Nitric oxide molecular targets: reprogramming plant development upon stress

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Abstract

Plants are sessile organisms that need to complete their life cycle by the integration of different abiotic and biotic environmental signals, tailoring developmental cues and defense concomitantly. Commonly, stress responses are detrimental to plant growth and, despite the fact that intensive efforts have been made to understand both plant development and defense separately, most of the molecular basis of this trade-off remains elusive. To cope with such a diverse range of processes, plants have developed several strategies including the precise balance of key plant growth and stress regulators [i.e. phytohormones, reactive nitrogen species (RNS), and reactive oxygen species (ROS)]. Among RNS, nitric oxide (NO) is a ubiquitous gasotransmitter involved in redox homeostasis that regulates specific checkpoints to control the switch between development and stress, mainly by post-translational protein modifications comprising S-nitrosation of cysteine residues and metals, and nitration of tyrosine residues. In this review, we have sought to compile those known NO molecular targets able to balance the crossroads between plant development and stress, with special emphasis on the metabolism, perception, and signaling of the phytohormones abscisic acid and salicylic acid during abiotic and biotic stress responses.

Keywords: Abiotic, biotic, developmental cues, nitration, nitric oxide, post-translational modifications, reactive nitrogen species, S-nitrosation.

Introduction

Nitric oxide (NO) is a simple molecule whose production is regulated by complex mechanisms, given the large number of synthesis and scavenging pathways that influence NO homeostasis. Apart from being the most abundant reactive nitrogen species (RNS) in plants, NO is considered a gasotransmitter with a pivotal role in a plethora of physiological processes throughout the plant life cycle, from the regulation of growth and development to biotic and abiotic stress tolerance.

The distribution, concentration, and regulation of NO levels at the specific sites of action are important to exert different physiological functions. These features make NO a versatile and broad-spectrum signaling molecule, able to regulate numerous processes in a very precise way (Sanz et al., 2015). Considering the impact of NO levels in plants, either deficiency or overaccumulation greatly impair growth and development. Thus, reported mutants with altered NO levels show stunted growth immediately after germination which become visible in adult plants (Fig. 1), although the pleiotropic defects in these mutants may have wider impacts than just NO generation.
The mode of action of NO as a signaling effector includes the modification of molecules of biological relevance (e.g. proteins, fatty acids, cGMP, DNA, and RNA). Essentially, RNS derived from NO interact with biomolecules to modify both their structure and function. With special emphasis on protein structure, these modifications lead to conformational changes whose result may be an increased or decreased stability, activation or inhibition of activity, disruption of the interactome, translocation, and, in the case of transcription factors, an influence on DNA binding to alter gene expression. To perform these effects in such a diverse range of processes, NO modifies certain proteins through two post-translational mechanisms, the nitration of Tyr residues and the \(S\)-nitrosation of Cys residues and metals.

**NO post-translational modifications of key regulators by Tyr nitration**

The nitration of Tyr residues is carried out mainly by peroxynitrite (ONOO\(^-\)) and by the nitrogen dioxide radical (\(^{\cdot}\)NO\(_2\)). ONOO\(^-\) results from the reaction of NO with the superoxide radical (O\(_2^\cdot\)), which modifies position 3 of the phenolic ring, adding a nitro group (\(-NO_2\)). \(^{\cdot}\)NO\(_2\) comes from the reactions of NO in the presence of oxidants, such as H\(_2\)O\(_2\) and O\(_2\)\(^{-}\), and transition metals (Radi et al., 2004). Within a protein, not all Tyr residues are susceptible to nitration and depend on the conformational state in order to be more exposed to the redox environment (Abello et al., 2009; Corpas et al., 2013a) and the properties of surrounding amino acids (Souza et al., 1999; Ischiropoulos, 2003; Chaki et al., 2009; Lozano-Juste et al., 2011).

Similar to other RNS, ONOO\(^-\) has been considered one of the most potent molecules to produce oxidative damage to nucleic acids and lipid peroxidation. However, emerging evidence also highlights the great relevance of this molecule for signaling (Arasimowicz-Jelonek and Floryszak-Wieczorek, 2011; Vandelle and Delledonne, 2011). Considering global protein regulation, nitration is an important point of interaction with other signals, since Tyr residues are also susceptible to phosphorylation (Galetskiy et al., 2011). Likewise, NO is able to regulate the amount of ONOO\(^-\) through the inhibition of PrxIIE by \(S\)-nitrosation, which detoxifies this compound, promoting its accumulation (Romero-Puertas et al., 2007).

Numerous nitrated proteins, the so-called nitroproteome, have been identified under both normal growth (Lozano-Juste et al., 2011; Chaki et al., 2009, 2012; Begara-Morales et al., 2013) and stress conditions (Ceconi et al., 2009; Begara-Morales et al., 2013). Some studies have focused on the analysis of the effect of ONOO\(^-\) on specific proteins, with a predominantly inhibitory action (Table 1). Although nitration was classified initially as an irreversible protein modification, the existence of enzymes with denitrase activity in animals has been reported (Irie et al., 2003; Smallwood et al., 2007; Deeb et al., 2013).

**\(S\)-Nitrosation of Cys and metals in key molecular players**

Protein \(S\)-nitrosation is a post-translational modification that consists of the covalent attachment of an NO molecule to a thiol group of a Cys, forming an \(S\)-nitrosothiol (SN0). This modification appears to be the main mechanism by which NO, in its protonated form (NO\(^+\)) or in a greater state of oxidation (N\(_2\)O\(_3\)) (Hill et al., 2010), exerts its effect. \(S\)-Nitrosation is highly specific, since it depends not only on the proximity between NO and the target protein, but also on the conformation and amino acid sequence (Lindermayr and Durner,
Table 1. Targets and effects of protein nitration described in plants

| Protein                                                                 | Process                                                                 | Reference               |
|------------------------------------------------------------------------|------------------------------------------------------------------------|-------------------------|
| Catalase                                                               | Inhibition of activity against pathogens                                | Clark et al. (2000)     |
| S-Adenosyl homocysteine hydrolase (SAHH)                                | Inhibition of activity                                                  | Chaki et al. (2009)     |
| Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)                       | Inhibition of activity                                                  | Lozano-Juste et al. (2011) |
| Complexes of PSI and PSII                                               | Inactivation and disassembly of complexes dependent on light conditions | Galetskiy et al. (2011) |
| Ferredoxin-NADP oxidoreductase                                          | Inhibition of activity, causing changes in photosynthetic activity      | Chaki et al. (2011)     |
| O-Acetylserine (thiol) lyase 1                                          | Inhibition of activity under stress conditions to regulate cysteine and glutathione metabolism | Alvarez et al. (2011)   |
| Glutamine synthetase (GS1a)                                             | Inhibition of activity to regulate N metabolism in nodules              | Melo et al. (2011)      |
| NADP-isocitrate dehydrogenase (ICDH)                                   | Inhibition of activity for the reprogramming of metabolism and redox homeostasis during senescence | Begara-Morales et al. (2013) |
| NADH-hydroxyypyruvate reductase (HPR1)                                  | Inhibition of activity, changes in peroxisomal metabolism               | Corpas et al. (2013b)   |
| Ascorbate peroxidase (APX)                                              | Inhibition of activity                                                  | Clark et al. (2000); Begara-Morales et al. (2014) |
| Monodehydro-ascorbate reductase                                         | Inhibition of activity                                                  | Begara-Morales et al. (2015) |
| Superoxide dismutases (MSD1, FSD3, CSD3)                               | Inhibition of activity                                                  | Holzmeister et al. (2015) |
| Pyrabactin resistance1/ PYR1-like/regulatory component of ABA receptor (PYR/PYL/ RCAR) | Inhibition of activity                                                  | Castillo et al. (2015)  |
| Leghemoglobin (Lb)                                                     | Putative protective role, scavenging ONOO⁻                              | Sainz et al. (2015)     |

2009; Lamotte et al., 2014). It remains elusive to what extent this modification is mediated by non-enzymatic mechanisms (through the action of free NO/N₂O₃), or by transfer reactions (through the interaction between two components) known as transnitrosation [i.e. from S-nitrosogluthatine (GSNO) to other molecules], since mutants that accumulate either NO (cue1/nox1) or GSNO (gsnor1) do not behave in a similar way (Fig. 1) (Kneeshaw et al., 2014). A landmark in NO biology is the ability to maintain an optimal concentration at the specific site of action. Thus, the control of nitrosated proteins represents an important point of regulation. Reports on certain enzyme systems able to denitrosate proteins comprise the glutathione/GSNO reductase (GR/GSNOR) and thioredoxin/thioredoxin reductase (Trx/TrxR) systems (Tada et al., 2008; Malik et al., 2011; Paris et al., 2013). Remarkably, NPR1 denitrosation has been described by the system composed of thioredoxin TRXH5 and thioredoxin reductase NTRA (Kneeshaw et al., 2014). Given the high specificity shown by S-nitrosation, the regulation of denitrosation may also display such a specific pattern, as described for glyceraldehyde phosphate dehydrogenase (GAPDH; Zaffagnini et al., 2013). Non-enzymatic mechanisms able to eliminate the SNO moiety have also been reported, including exposure to reducing agents, nucleophilic compounds, or transition metals, together with heat or light (Kovacs and Lindermayr, 2013). Extensive literature refers to the multitude of processes in which this modification is involved (Mengel et al., 2013; Paris et al., 2013; Romero-Puertas et al., 2013) and to the numerous proteins susceptible to S-nitrosation described so far (Lindermayr et al., 2005) by using the biotin switch technique (Jaffrey and Snyder, 2001) (Table 2).

The third and less known NO-driven post-translational modification is the nitrosation of transition metals present in metalloproteins (namely iron, zinc, and copper) causing conformational changes that affect protein activity (Astier and Lindermayr, 2012) (Table 3). A clear example is the binding to the heme group of phytohoglobins, affecting the transport/scavenging of NO (Gupta et al., 2011). Interestingly, a self-nitrosation mechanism has been described in animals by intramolecular transfer from the heme group to a Cys in the globin domain (Jia et al., 1996; Gow and Stamler, 1998).

Having outlined the NO-dependent post-translational modifications for NO action and provided a compilation of those NO protein targets described so far, here we emphasized the balanced role of NO in different developmental cues through its interaction with phytohormones during abiotic and biotic stresses.

NO impact on plant development and abiotic stress trade-off

Changing environmental conditions compromise successful plant growth, thus being a critical step that reflects the need for a development and stress trade-off for plant establishment. In this context, abiotic stresses such as drought, hypoxia, salinity, or extreme temperatures are detrimental for plant survival. The phytohormone abscisic acid (ABA) plays a major role in abiotic stress responses such as stomatal closure (Desikan et al., 2002; García-Mata and Lamattina, 2002; Neill et al., 2002; Eisenach et al., 2017), water deficit (Christmann et al., 2007), or high light conditions (Galvez-Valdivieso et al., 2009), but also controlling pathogen responses (Adie et al., 2007). From a developmental point of view, ABA is involved in dormancy maintenance, biosynthesis of embry storage compounds, seed size and seed germination inhibition (Lopez-Molina et al., 2002; Kanno et al., 2010; Cheng et al., 2014; Albertos et al., 2015), and sophisticated regulation of root development (Dietrich et al., 2017; Belda-Palazon et al., 2018), among others.
The crosstalk between ABA and NO governs the main molecular mechanisms able to integrate external signals to program internal networks leading to plant adaptation (reviewed in Arc et al., 2013; León et al., 2014; Albertos et al., 2015; Wang et al., 2015a, b; Lombardo and Lamattina, 2018). NO is able to interact with a wide range of ABA metabolism, perception, and signaling targets, modulating protein function and impacting gene expression.

**NO effect on ABA synthesis and catabolism**

ABA levels are determined by the ratio between synthesis and catabolism. Key steps during ABA synthesis are controlled by zeaxanthin epoxidase (ZEP), 9-cis-epoxycarotenoid dioxygenase (NCED), short-chain alcohol dehydrogenase (ABA2), and a final step catalyzed by an abscisic aldehyde oxidase (AOO3) which is activated by the molybdenum cofactor (MoCo) sulfurase ABA3 (reviewed in Nambara and Marion-Poll, 2005; Finkelstein, 2013). ABA catabolism takes place mainly through the ABA 8′-hydroxylase pathway catalyzed by the cytochrome P450 enzyme ABA 8′-hydroxylase. In Arabidopsis, these enzymes are encoded by the CYP707A family. Among them, CYP707A1 and CYP707A3 are the most important enzymes required in mid-seed development, and CYP707A2 during the end of seed development and germination (Kushiro et al., 2006). A decrease in ABA is mandatory for seed dormancy breakdown and germination in Arabidopsis. An NO-induced ABA sensitivity reduction correlates with the transcription induction of CYP707A2 and protein accumulation (Liu et al., 2009) (Fig. 2). This NO effect was also evidenced by using genetic approaches with NO-deficient mutants, nia1nia2 and

| Protein | Process | Reference |
|---------|---------|-----------|
| Phytoglobin1 (Phytogb1) | Modulation of NO/O2 levels | Perazzolli et al. (2004) |
| Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) | Inhibition of activity | Lindemayr et al. (2005); Zaffagnini et al. (2013); Zhang et al. (2017) |
| Methionine adenosyltransferase (MAT1) | Inhibition of activity | | |
| Peroxiredoxin II E (PrxIIIE) | Inhibition of activity resulting in an increase of ONOO\textsuperscript{−}, which triggers Tyr residues nitration | Romero-Puertas et al. (2007) |
| Metacaspase M9C (unprocessed form) | Inhibition of autoprocessing and proteolytic activity | Belenghi et al. (2007) |
| MYB domain protein (MYB2) | Inhibition of DNA binding | Serpa et al. (2007) |
| Nonexpresser of PR genes 1 (NPR1) | Conformational changes (oligomerization) in cytoplasm | Tada et al. (2008) |
| Salicylic acid-binding protein 3 (SABP3) | Prevents salicylic acid (SA) binding and inhibits the activity | Wang et al. (2009) |
| Glycine decarboxylase complex (GDC) | Inhibition of activity | Palmieri et al. (2010) |
| TGACG sequence-specific binding protein 1 (TGA1) | Promotes DNA binding in the presence of NPR1 | Lindemayr et al. (2010) |
| Aldolase | Conformational change resulting in the inhibition of activity | van der Linde et al. (2011) |
| NADPH oxidase (RBOHD) | Inhibition of activity, minimizing the synthesis of ROIs (ROS intermediaries) | Yun et al. (2011) |
| Transport inhibitor response 1 (TIR1) | Facilitates interaction with Aux/IAA, promoting its degradation and triggering auxin response | Terrile et al. (2012) |
| Cell division cycle 48 (CDC48) | Inhibition of ATPase activity | Astier et al. (2012) |
| Histidine phosphotransfer protein 1 (AHP1) | Inhibition of phosphorylase activity, negatively regulating the cytokinin (CK) signaling pathway | Feng et al. (2013) |
| Ascorbate peroxidase (APX) | Promotes the activity | Begara-Morales et al. (2014); Yang et al. (2015) |
| GSNO reductase (GSNOR) | Inhibition of activity | Frungillo et al. (2014) |
| MYB domain protein (MYB30) | Inhibition of DNA binding | Tavares et al. (2014) |
| Open stomata 1/Sucrose nonfermenting 1-related protein kinase 2.6 (OST1/SnRK2.6) | Inhibition of activity, negative regulation of ABA responses | Wang et al. (2015) |
| ABA Insensitive 5 (ABI5) | Protein destabilization, promoting proteasome degradation | Albertos et al. (2015) |
| Peroxiredoxin II F (PrxIIIF) | Inhibition of peroxidase activity and acquisition of transnitrosylase activity, preventing the aggregation of citrate synthase | Camejo et al. (2015) |
| Other glycolysis enzymes [fructose 1,6-biphosphate aldolase, triosephosphate isomerase, 2-phosphoglycerate hydrase (enolase) and phosphoglycerate kinase] | Inhibition of activity | Zhang et al. (2017) |
| ATP synthase CF1 α-chain and β-chain | Inhibition of activity | Zhang et al. (2017) |
| Vascular-Related NAC-Domain7 (VND7) | Inhibition of transactivation activity | Kawabe et al. (2018) |
Table 3. Targets and effects of metal nitrosation described in plants

| Protein                     | Process                                                                 | Reference                  |
|-----------------------------|-------------------------------------------------------------------------|----------------------------|
| Lipoygenase-1               | Redox regulation                                                        | Nelson (1987)              |
| Catalase                    | Inhibition of activity to modulate pathogen response                    | Clark et al. (2000)        |
| Ascorbate peroxidase        | Inhibition of activity to modulate pathogen response                    | Clark et al. (2000)        |
| Nitric oxide-dependent      | GTP hydrolysis, NO-dependent generation of cGMP                        | Mulauzdi et al. (2011)     |
| guanylate cyclase (NOGC1)   |                                                                         |                             |
| Phytoglobin1                | Modulation of NO/O2 levels                                              | Perazzolli et al. (2004)   |
| Phytoglobin1 (Phytogb1)     |                                                                         |                             |
| Aconitase                   | Inhibition of activity for metabolism                                   | Gupta et al. (2012)        |

nia1nia2noa1-2, which show increased dormancy and ABA-mediated germination inhibition (Lozano-Juste and León, 2010), and by using NO donors (Bethke et al., 2004, 2006, 2007; Sarath et al., 2007). Additionally, the MoCo sulfurase ABA3 has been identified as a target of protein nitration (Lozano-Juste et al., 2011), which could alter its activity (Fig. 2).

NO alterations of ABA perception and signaling

ABA perception and signal transduction depend on the core PYRABACTIN RESISTANCE (PYR)/PYR1-LIKE (PYL)/REGULATORY COMPONENT OF ABA RECEPTOR (RCAR) (Ma et al., 2009; Park et al., 2009), PROTEIN PHOSPHATASE 2C (PP2C) (Umezawa et al., 2009; Vlad et al., 2009), and SNF1-RELATED PROTEIN KINASE2 (SnRK2) kinases (Mustilli et al., 2002; Yoshida et al., 2006; Nakashima et al., 2009; Umezawa et al., 2009). In the presence of ABA, the formation of PYR/PYL/RCAR–PP2C complexes inhibits the activity of the PP2Cs, thereby activating SnRK2s, which in turn controls AREB/ABF-type basic/region leucine zipper (bZIP) transcription factors (Fujii et al., 2009). These bZIP transcription factors bind to cis-regulatory elements known as ABA-responsive elements (ABREs) and regulate downstream gene expression (Choi et al., 2000; Uno et al., 2000; Kang et al., 2002; Finkelstein et al., 2005; Reeves et al., 2011; Gao et al., 2016; reviewed in Banerjee and Roychoudhury, 2017).

The control by NO of ABA perception and signaling pathways occurs at different levels (Fig. 2). First, PYR/PYL/RCAR receptors are inhibited by Tyr nitration (Castillo et al., 2015), enabling activation of PP2C which in turn inactivates SnRKs. An additional control point falls in the inhibition of the activity of SnRKs 2.2, 2.3, and 2.6 by S-nitrosation and SnRK2.6 down-regulation by NO treatment impairing seed germination and stomatal closure (Wang et al., 2015a, b; Zhao et al., 2016). Interestingly, the nia1nia2 NO-deficient mutant is affected in genes involved in the ABA perception core, where RCAR1, RCAR11, RCAR12, and RCAR14 are up-regulated, and also presents a higher PP2C activity (Zhao et al., 2016), in accordance with up-regulation of PP2C transcription by exogenous NO treatment (Castillo et al., 2018). Finally, NO regulates the ABI5 bZIP transcription factor through S-nitrosation of Cys153. This modification targets ABI5 to the proteasome by promoting the interaction with CULLIN4-based and KEEP ON GOING E3 ligases (Albertos et al., 2015). In addition, ABI5 is sumoylated by the SUMO E3 ligase SIZ1 (Miura et al., 2009), which is considered to be a Tyr nitration target (Lozano-Juste et al., 2011).

ABI5 is a key player in ABA-triggered processes (Finkelstein and Lynch, 2000; Lopez-Molina et al., 2001) and also emerges as a molecular hub in the NO-mediated balance between early development and stress (Albertos et al., 2015). ABI5 expression and protein levels increase during the last steps of seed maturation (Brocard et al., 2002; Bensmihen et al., 2005) and overexpression of ABI5 confers hypersensitivity to ABA, which promotes its transcription and stabilization (Brocard et al., 2002). ABI5 functions in the ABA signaling pathway by blocking seed germination (Lopez-Molina et al., 2001; Albertos et al., 2015; reviewed in Skubacz et al., 2016) and seedling establishment upon exposure to stress conditions such as drought or salinity (Lopez-Molina et al., 2001; Tezuka et al., 2013). ABI5 also promotes CATALASE1 transcription during seed germination (Bi et al., 2017), whose protein activity is inhibited by Tyr nitration and metal nitrosation in tobacco (Clark et al., 2000).

Similarly to ABI5, other group A bZIP transcription factors are involved in different developmental cues, including embryo development and seed maturation (Jakoby et al., 2002), and stress responses. Thus, bZIP67 regulates fatty acid composition (Mendes et al., 2013), bZIP14 is necessary for flowering and meristem identity (Gorham et al., 2018), bZIP12/EEL counteracts ABI5’s action on the transcription of Late Embryogenesis Abundant (LEA) genes (Finkelstein and Lynch, 2000; Lopez-Molina et al., 2002; Bensmihen et al., 2002), and the subfamily of ABFs (ABRE-binding factors) constitute key signaling transcription factors mediating ABA responses during seed germination, drought, and osmotic stresses (Choi et al., 2000; Finkelstein et al., 2005; Fujita et al., 2005; Yoshida et al., 2010, 2015; Fernando et al., 2018). Since ABI5 is an NO target, other members from group A of bZIPs are found to be susceptible to modification by S-nitrosation when analyzed using GPS-SNO software (Fig. 3).

The ABA signaling pathway is linked to chromatin remodeling (Saez et al., 2008; Han et al., 2012, 2015), histone deacetylation (Luo et al., 2012; Ryu et al., 2014), and histone demethylation (Zhao et al., 2015), and epigenetic changes appear as mechanisms involved in the response to stress conditions (reviewed in Nonogaki, 2014). In this context, accumulation of histone acetylation marks in Arabidopsis is promoted by the NO donor GSNO while it is decreased by the NO scavenger 2-(4-carboxyphenyl)-4,4,5,5-tetramethylimidazoline-1-oxyl-3-oxide (cPTIO). This fact correlates with inhibition of the activity of histone deacetylases (HDACs) (Mengel et al., 2017) probably associated with S-nitrosation, as previously described in mammals for HDAC2 and HDAC6 (Nott et al., 2008; Okuda et al., 2015). This post-translational modification
linked to the chromatin state can also be responsible of the reprogramming of expression triggered by NO (Huang et al., 2002; Polverari et al., 2003; Palmieri et al., 2008; Hussain et al., 2016; Imran et al., 2018). SWI/SNF chromatin-remodeling ATPase BRAHMA (BRM), whose switch activity is modulated by phosphorylation/dephosphorylation mediated by
SnRK2/PP2CA (Peirats-Llobet et al., 2016), is also susceptible to S-nitrosation, as revealed by GPS-SNO analysis. In addition, BRAHMA represses ABI5 transcription in the absence of ABA (Han et al., 2012).

Hormonal networks regulate developmental and stress processes in response to internal and external cues. Thus, ABA and gibberellins (GAs) play antagonistic roles in many physiological events (reviewed in Liu and Hou, 2018) where NO represents a key modulator between both pathways. The NO donor sodium nitroprusside (SNP) promotes DELLA protein accumulation by repressing E3 ubiquitin ligase SLEEPY1 (SLY1), inhibiting GA signaling (Lozano-Juste and León, 2011). This result was also demonstrated by genetic evidence using nia1,2noa1-2 NO-deficient mutant seedlings (Lozano-Juste and León, 2011). In addition, GA20ox3, involved in GA biosynthesis, is up-regulated in nia1,2noa1-2 and down-regulated upon NO treatment (Lozano-Juste and León, 2011). Nevertheless, NO plays a synergistic role with GAs during seed dormancy break (Bethke et al., 2007), in accordance with the NO burst detected during early seed germination (Simontacchi et al., 2004, Albertos et al., 2015). In wheat roots, an increase in GA content after the addition of SNP under aluminum stress has also been described (He et al., 2012). In this framework, NO controls the specific hormonal balance, leading to a continuous reprogramming of the signaling pathways that govern stress and developmental networks.
NO and ABA network during drought, salinity, and extreme temperatures

ABA acts to save water and energy during stress conditions. This phytohormone prevents turgor loss under low water availability mainly through stomatal closure (Eisenach et al., 2017) and contribution to the synthesis of osmoprotectants (Verslues and Bray, 2006), thus improving plant cell adaptation to drought. NO is also a key player inside the network required for stomatal closure since nitrate reductase (NR) and NOS-like activities linked to NO production are mandatory for the ABA signal transduction cascade in guard cells (García-Mata and Lamattina, 2001, 2002; Desikan et al., 2002; Neill et al., 2002). In Arabidopsis guard cells, ABA correlates with H$_2$O$_2$ and NO in the regulation of stomatal closure. ABA increases the generation of endogenous H$_2$O$_2$, which promotes NO production in order to regulate stomatal movement (Bright et al., 2006). In addition, pea and Arabidopsis guard cells are able to generate NO in response to ABA, while removal of NO with scavengers inhibits ABA-induced stomatal closure (García-Mata and Lamattina, 2002). However, genetic evidence showed that stomata from the nia1nia2noa1-2 NO-deficient mutant were hypersensitive to ABA during stomatal closure (Lozano-Juste and León, 2010). The involvement of NO in ABA perception and signaling has been described above. Specifically, SnRK2.6, which is preferentially expressed in guard cells, is inhibited through S-nitrosation (Fujii and Zhu, 2009; Wang et al., 2015b). SnRK2.6 phosphorylates the slow (S-type) anion channel associated1 (SLAC1) and inward potassium channel in Arabidopsis thaliana 1 (KAT1) promoting stomatal closure (Vahisalu et al., 2008; Geiger et al., 2009; Sato et al., 2009). Nevertheless, pharmacological assays showed that NO application triggered stomatal closure, whereas this was inhibited by the NO scavenger cPTIO (Neill et al., 2002), suggesting a positive role for NO in stomatal closure. Other studies reported that NO may affect KAT1 (García-Mata et al., 2003; Sokolovski and Blatt, 2004), SLAC1 (Vahisalu et al., 2008), and nitrated cGMP generation (Joudoi et al., 2013). Consequently, NO-dependent modulation of ion channels at the plasma membrane of guard cells facilitates osmotic solute loss, reducing guard cell turgor and promoting stomatal closure. Fu et al. (2016) showed promotion of stomatal development by NO up-regulation of the basic helix–loop–helix (bHLH) genes SPEECHLESS (SPCH), MUTE, and SCRIM2, and down-regulation of MITOGEN-ACTIVATED PROTEIN KINASE 6 (MPK6) expression. Further research will be necessary to decipher these NO dual effects, where the level of channel modulation promotes stomatal development and stomatal closure while SnRK2.6 S-nitrosation inhibits this closure.

Soil salinity becomes one of the main threats for crop production. A reduction in the protein S-nitrosation pattern under salt treatment was previously reported (Camejo et al., 2013). NO promotes salt tolerance by different mechanisms, including the increase in transcription of H$^+$/ATPase and the Na$^+$/H$^+$ antiporter in Avicennia marina in order to maintain ion homeostasis (Chen et al., 2010), synthesis of protective metabolites, and induction of the oxidative defense system (Fan and Du, 2012; Manai et al., 2014; Ahmad et al., 2016). Additionally, NO ameliorates salinity stress through stomatal closure by reducing water loss as mentioned above. Oxidative stress constitutes a common effect linked to drought, salinity, or osmotic stress. In rice, exogenous treatment with the NO donor SNP increases enzyme activity related to redox control, such as guaiacol peroxidase (POX), superoxide dismutase (SOD), and ascorbate peroxidase (APX) (Uchida et al., 2002). APX is modulated by NO at the post-translational level by S-nitrosation of Cys residues, which in turn promotes its activity (Begara-Morales et al., 2014), and by metal nitrosation and Tyr nitrination, which both inhibit its activity (Clark et al., 2000; Begara-Morales et al., 2014). Furthermore, other NO targets are SOD, since Tyr nitrination decreases its activity (Holzmeister et al., 2015), and pea Prx III, where S-nitrosation inhibits its activity (Camejo et al., 2013). Phosphoenolpyruvate carboxylyase-kinase (PEPCK) regulates photosynthetic C$_4$ phosphoenolpyruvate carboxylase in sorghum, is enhanced by salinity, and presents a high activity under short NO treatments (Monreal et al., 2013), highlighting a novel role for NO in linking carbon fixation with salt stress mitigation. ABA exogenous application, drought, and salt stress induce ABI5 at early post-germinative stages (Lopez-Molina et al., 2001). ABI5 together with ABI3 modulate the expression of Em1 and Em6 (class I LEA proteins) genes which are involved in desiccation tolerance (Lopez-Molina et al., 2002; Carles et al., 2002). The ABI5 mutant allele abi5-9 shows ABA and salinity insensitivity (Tezuka et al., 2013), highlighting another point of ABA–NO crosstalk during abiotic stresses. Other ABFs are involved in salt, osmotic, and drought stresses. ABI3 transcription is up-regulated during salt treatment while ABAF1 and ABAF4 are repressed (Fujita et al., 2005; Fernando et al., 2018). In addition, ABI3 and ABAF4 display putative Cys residues susceptible to be modulated by NO through S-nitrosation (Fig. 3). All together, these findings demonstrate a key role for NO during salinity stress alleviation.

Low and high temperatures promote changes in the S-nitrosoproteome and nitrination level as described in Brassica juncea and pea plants (Corpas et al., 2008; Abat and Deswal, 2009), showing that NO is involved in plant tolerance to chilling and freezing (reviewed in Puyaubert and Baudouin, 2014). Recently, NO has been proposed to scavenge ROS and regulate the levels of polyamines, osmoprotective metabolites, and hormonal balance, since NO-deficient mutants are more tolerant to cold stress (Zhao et al., 2009; Fan et al., 2015; Costa-Broseta et al., 2018). Other NO mechanisms involve the negative regulation of the synthesis of phosphorylated sphingolipids during cold transduction (Cantrel et al., 2011). GSNOR controls the S-nitrosothiol concentration, which is modulated by cold conditions at the level of gene expression and activity but, depending on the species analyzed, can be promoted or repressed (Ziqgas et al., 2013; Kubienová et al., 2014; Lv et al., 2017). NO is also involved in heat responses since previous exogenous treatment led to a better thermotolerance acquisition while this effect is blocked by the NO scavenger cPTIO (Song et al., 2013). This molecule is able to modulate heat stress alleviation at different levels, including the induction of genes belonging to subunits of the PSII core reaction center (Psb) complex (psbA, psbB, and psbC) (Chen et al., 2013), the
increase in DNA binding of heat shock transcription factors, and heat shock protein18.2 (HSP18.2) accumulation through calmodulin 3 (CaM3) (Xuan et al., 2010) and the promotion of HSP26 transcription (Uchida et al., 2002).

**NO and hypoxic stress crosstalk**

As aerobic organisms, plants have evolved to maintain specific requirements for oxygen (O$_2$) that lead to a correct respiratory energy supply. A close relationship between both O$_2$ and NO sensing is mediated by the N-degron pathway, which operates through N-terminal recognition that targets proteins for degradation, and by phytoglobins, which are able to modulate the level of diatomic gases such as carbon monoxide, NO, and O$_2$. Hypoxic conditions lead to an increase in NO levels, suggesting a key role for the NO/O$_2$ balance during this stress (Dordas et al., 2003; Borisjuk et al., 2011, controlling its transport, scavenging, and detoxification (Arredondo-Peter et al., 1998). There are three types of phytoglobins, symbiotic (SymPhytogb), non-symbiotic (Phytogb1 and 2), and truncated (Phytogb3). Phytogb1 and 2 have a significant function in regulating NO and O$_2$ levels mainly during cellular hypoxic conditions (Dordas et al., 2003, 2004). Phytogb1 overexpression regulates NO levels and improves growth and development under hypoxic stress (Hunt et al., 2002; Perazzolli et al., 2004; Thiel et al., 2011). A complex self-regulatory mechanisms closes this cycle since Phytogb1 is S-nitrosated both in the Cys and in the metal (Perazzolli et al., 2004), and leghemoglobin is modulated by Tyr nitration (Sainz et al., 2015), leading to a specific and fine-controlled NO/O$_2$ balance, closely related to inhibition or promotion of plant development.

The N-degron pathway is involved not only in hypoxic stress (Gibbs et al., 2011; Licausi et al., 2011) but also in seed storage mobilization (Zhang et al., 2018a, b), germination (Holman et al., 2009; Gibbs et al., 2014), photomorphogenesis (Abbas et al., 2015), shoot and leaf development (Graciet et al., 2009), stomatal closure (Gibbs et al., 2014), flowering (Vicente et al., 2017), vernalization (Gibbs et al., 2018), leaf senescence (Yoshida et al., 2002), and pathogen attack (de Marchi et al., 2016; Vicente et al., 2019). This pathway senses O$_2$ and NO through the regulation of ethylene response factor (ERF) Group VII transcription factors, which are degraded via PROTEOLYSIS6 (PRT6) in the presence of both gases due to a characteristic conserved motif at the N–terminus initiating with Met–Cys. In Arabidopsis and rice, ERFVIIIs are associated with hypoxia responses, and their protein stabilization improves growth under this abiotic stress (Gibbs et al., 2011; Licausi et al., 2011). ABA also participates in the response to hypoxic conditions, such as root flooding (Hsu et al., 2011) or seed environment before germination (Benech-Arnold et al., 2006), and its exogenous application promotes hypoxia tolerance in roots (Ellis et al., 1999). In fact, ABA perception and signaling constitute a key hormonal network affected by the N-degron pathway (Holman et al., 2009; Vicente et al., 2017). Gibbs et al. (2014) identified a mechanism for NO/O$_2$ sensing during ABA signaling through degradation of ERFVIIIs, which are ABI5 transcriptional activators. ERFVIIIs are degraded in the presence of both NO and O$_2$, affecting seed germination, although NO-mediated ABI5 degradation is independent of this pathway (Albertos et al., 2015). In addition, the ABI5 transcriptional repressor BRAHMA could be modulated by ERFVII (Vicente et al., 2017). This mechanism integrates NR-dependent NO production with the regulation of the chromatin-remodeling ATPase BRAHMA mediated by ERFVII, ending in a genetic reprogramming that controls development and stress responses to enhance plant survival. A deregulation in PYL2 ABA receptor transcription in the pty6 knockout mutant is dependent on ERFVII, RAP2.12, RAP2.2, and RAP2.3 (Zhang et al., 2018b). Additionally, the interaction between RAP2.3 and DELLA contributes to regulate hormonal networks able to control the balance between growth and stress responses (Marín-de la Rosa et al., 2014). Recently, the NO modulation by S-nitrosation of GSNOR has been described, which promotes a conformational change that drives its autophagy–dependent degradation, linking hypoxia and NO to selective autophagy (Zhan et al., 2018). At the physiological level, GSNOR degradation regulates NO cellular homeostasis, which is involved in low-O$_2$ tolerance and promotion of seed germination by modulating ABI5 expression. These results confirm the key function of the N-degron pathway in the regulation of genetic and molecular networks through NO/O$_2$ balance sensing.

**NO signaling at the crossovers between plant development and biotic stress**

Upon pathogen attack, the plant must resume growth. In this context, whether the plant uses the same arsenal of molecules for both development and defense, or if a genetic reprogramming occurs between these two key processes, constitutes a major question concerning the complex cellular environment. Pieterse et al. (2009) asserted that the contribution of plant growth regulators (i.e., hormone signaling pathways) to plant immunity is indicative of an extensive crosstalk between development and defense. Consequently, it is hypothesized that both are regulated by a network of interconnecting signaling pathways in a cost-efficient manner. Several phytohormones have been related to plant defense, among them salicylic acid (SA), jasmonate (JA), ethylene (ET), and ABA within the context of disease suppression. Of particular importance is the NO–SA interaction during biotic stress responses, based on the well-known molecular effectors and the extensive literature that places NO at the center of both SA synthesis and signaling pathways.

*Interconnections between NO and SA during plant immunity and developmental cues*

SA has been linked to plant response to abiotic stresses such as drought (Munné-Bosch and Peñuelas, 2003; Chini et al., 2004; Horváth et al., 2007), chilling (Janda et al., 1999; Ding et al., 2008), heavy metal tolerance (Pál, 2002; Metwally et al., 2013).
2003), heat (Dat et al., 1998; Shi et al., 2006), and osmotic stress (Borsani et al., 2001). Furthermore, SA participates in plant growth and developmental processes such as seed germination, vegetative growth, flower formation, respiration, photosynthesis, stomatal closure, and gene expression associated with senescence, among others (reviewed in Rivás-San Vicente et al., 2011). Nevertheless, the most prominent SA function falls into the local and systemic response against microbial pathogens (Durner and Klessig, 1995; Innes, 2018).

In plant immunity, NO was first described as a molecule with a role in plant disease resistance, being a signal that is activated upon pathogen attack (Delledonne et al., 1998; Durner et al., 1998; Bellin et al., 2013). Knowledge of the involvement of NO in plants has increased greatly and it has been shown to be involved in many cellular processes, not only immune response related, but also growth and development associated (reviewed in Sanz et al., 2015). In this framework, it is difficult to separate NO, and other RNS, from ROS molecules, as both are considered as signaling effectors undergoing reciprocal regulation, which is pivotal in early stages of biotic interactions (Scheler et al., 2013; Del Río, 2015). Nowadays some controversy still surrounds the NO homeostasis in plant immunity, at the level of both production and turnover (reviewed in Vandelle et al., 2016).

Accordingly, GSNO, which is not only a bioactive NO species but also a stable NO reservoir and NO transport form (Kovacs et al., 2015), is becoming increasingly relevant (Feechan et al., 2005; Frungillo et al., 2014). In turn, GSNO is irreversibly degraded by GSNOR (Liu et al., 2001). GSNOR is present in almost all plant tissues and participates in numerous plant processes throughout the plant life cycle. The Arabidopsis GSNOR null mutant gsno1-3, also known as SENSITIVE TO HOT TEMPERATURE5 (HOT5) from a thermotolerance genetic screening (Lee et al., 2008), presents enhanced levels of SNO and proteome-wide increased S-nitrosation (Hu et al., 2015). This translates into pleiotropic deficiencies in multiple plant growth and development pathways and physiological processes (Kwon et al., 2012), and altered responses to biotic and abiotic stresses (Feechan et al., 2005; Lee et al., 2008; Chen et al., 2009; Kwon et al., 2012). It is noteworthy that gsno mutants have altered chlorophyll content and photosynthetic properties (Hu et al., 2015) and, additionally, they show early flowering, a loss of apical dominance due to a higher number of axillary shoots, reduced hypocotyl elongation and primary root growth, impaired germination, and decreased seed production, among other aspects.

It should be noted that the crosstalk between NO and targets of SA synthesis and signaling affects phenylalanine ammonia lyase expression in the former (Klessig et al., 2000), and the expression of pathogenesis-related genes in particular or the systemic acquired response in general in the latter (Song and Goodman, 2001; Rustérucci et al., 2007; Espanyu et al., 2012; Mur et al., 2013). Another example is the participation of both molecules, SA and NO, in mitigating the toxicity caused by heavy metals and, thus, enhancing plant development (Zhou et al., 2009; Singh et al., 2009, 2017). It has been described that GSNO influences the function of proteins related to plant defensive responses but, interestingly, these proteins also affect developmental processes (Table 2). S-Nitrosation of SA-binding protein 3 (SABP3) is prompted by bacterial infection and inhibits SA binding capacity and carbonic anhydrase (CA) activity. Since CA activity is required for the establishment of plant disease resistance, this post-translational modification could participate in a negative feedback loop in the modulation of the SA-dependent plant defense mechanism (Slaymaker et al., 2002; Wang et al., 2009). Loss or overexpression of CA activity causes defective tapetal cell differentiation in early anther development (Huang et al., 2017). Similarly, S-nitrosation of the NADPH oxidase AtRBOHD abolishes its ability to synthesize ROS, giving a role to NO in limiting the hypersensitive response (Torres and Dangl, 2005; Yun et al., 2011). Once more, this enzyme, together with AtRBOHF, negatively regulates lateral root development by changing the accumulation of superoxide in Arabidopsis roots (Li et al., 2015). Interestingly, there is a reduced NADPH oxidase activity in gsno mutants, probably because of inhibition of AtRBOHD by S-nitrosation (Karapetyan and Dong, 2018).

NO also targets several ROS-detoxifying enzymes by nitration or S-nitrosation (Tables 1, 2), including APX, monodehydroascorbate reductase, CAT, SODs, PrxIIE, and PrxIII, all of which are related to H2O2 detoxification (Romero-Puertas et al., 2007; Lin et al., 2012; Ortega-Galisteo et al., 2012; de Pinto et al., 2013; Begara-Morales et al., 2013, 2016; Holzmeister et al., 2015; Yang et al., 2015). Recently, the contribution of many of these enzymes to plant tolerance to chilling temperatures, having an effect in vegetative tissues, has been described in a priming process providing plant memory formation (Baier et al., 2019).

Regulation of the nonexpressor of pathogenesis-related genes (NPR) family mediated by NO

The Arabidopsis genome contains six members of the nonexpressor of pathogenesis-related genes (NPR) family including NPR1-4, NPR5/BLADE-ON-PETIOLE2 (BOP2), and NPR6/BLADE-ON-PETIOLE1 (BOP1) (Fig. 4). The corresponding proteins have in common two BTB/POZ, (Broad-Complex, Transtrack, and Bric-a-brac/Pox virus and Zinc finger) domains for protein–protein interaction, involved in degradation by the ubiquitin–proteasome system, and a series of four ankyrin repeats, which allow the interaction with the TGA (TGACG motif-binding protein) family of transcription factors (Aravind and Koonin, 1999, Sedgwick and Smerdon, 1999).

NPR1 is a transcription cofactor (reviewed in Withers and Dong, 2016) key in SA perception and signaling since the npr1 mutant is SA insensitive (Cao et al., 1997; Canet et al., 2010a, b). However, not all the genes induced by SA depend on NPR1 (Blanco et al., 2009), mostly due to the function of other family members such as NPR3 and NPR4 (Canet et al., 2010a, b). NPR1 is also involved in the induced systemic resistance (ISR) (Pieterse et al., 1998) and in the crosstalk between SA and JA (Spoel et al., 2003). NPR1 function is regulated at the post-translational level by a monomerization/oligomerization mechanism dependent on the cellular redox state and determines protein subcellular localization (Fig. 5). During pathogen
attack, SA concentration increases, promoting the partial reduction of the oligomer NPR1 (formed by disulfide bridges in the cytoplasm) to a monomer in the nucleus, then targeted by a C-terminal nuclear localization sequence (Mou et al., 2003; Spoel et al., 2009). In addition to other post-translational modifications that regulate NPR1, such as phosphorylation (reviewed in Withers and Dong, 2016), it was later discovered that S-nitrosation of Cys156 facilitates protein oligomerization in vivo, providing a negative regulation of defense-related gene expression by NO. Upon pathogen infection or SA accumulation, changes in cellular redox potential lead to the reduction of Cys through the activity of thioredoxins (mainly TRX-h5), and NPR1 monomers are released to the nucleus (Tada et al., 2008; Kneeshaw et al., 2014). In the cell nucleus, the mechanism proposed to modulate NPR1 gene expression is through its interaction with the TGA family of bZIP transcription factors, which bind specifically to SA response elements. However, it has also been observed that NPR1 can be present in the nucleus when SA levels are low (Després et al., 2000). Rivas-San Vicente et al. (2011) suggested an additional function of NPR1 in regulating genes related to germination, plant growth, and development; in fact, NPR1 has been related to the promotion of cell division and/or suppression of endoreduplication during leaf development (Vanacker et al., 2001). Moreover, redox changes related to the circadian clock motivated by SA upon pathogen infection act via NPR1 to trigger a transcriptional reprogramming, thus minimizing fitness costs on plant growth (Zhou et al., 2015). For this reason, NPR1 could be suggested to be a key molecular player in the balance between defense and growth.

Except for a minor role in SA perception (Canet et al., 2010b), the functions of NPR2, the NPR1 paralog with greater homology in the primary sequence, are unknown. Interestingly, NPR3 and NPR4 have been characterized as SA receptors, able to bind the hormone with different affinities and regulate the degradation of NPR1 via the ubiquitin–proteasome by a mechanism dependent on SA concentration (Fu et al., 2012). A role for NPR3 in root growth and storage compound accumulation in seeds has also been proposed, as a result of repression of the basal pathogen immune system (Shi et al., 2013). In

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**Fig. 4.** S-Nitrosation analysis in group D of bZIP transcription factor and NONEXPRESSOR OF PATHOGENESIS-RELATED GENES (NPR) families. (A) Dendrograms of TGA members of the group D bZIP transcription factor family and NPR-like proteins. The branch length is proportional to the number of substitutions per site (http://phylogeny.lirmm.fr/). (B) *In silico* prediction of S-nitrosation Cys (C) targets by using the GPS-SNO 1.0 software (Xue et al., 2010). The analysis shows target Cys in red, orange, and yellow depending on the S-nitrosation score (high, medium, and low, respectively). The Cys residues highlighted in blue correspond to *in vivo* and/or *in vitro* S-nitrosation.
addition, BOP1 and BOP2 are the most divergent proteins of the NPR family, both lacking a recognizable nuclear localization sequence. Although a role for these proteins as mediators of the methyl jasmonate-induced resistance in plant immunity has been described (Canet et al., 2012), the most studied function is as regulators of development; especially in the establishment of axes of asymmetry in the organogenesis of leaf and flower (Hepworth et al., 2005).

**Group D of bZIP transcription factors are NO targets**

Group D of bZIP transcription factors comprises the so-called TGA factors, according to their conserved TGACG DNA-binding motif. All of them are characterized by a short zipper domain consisting of three repeats, two conserved Q-rich domains in the C-terminus, and a more variable N-terminal part (Dröge-Laser et al., 2018). In the Arabidopsis genome, 10 members of the TGA family are present, falling into five clades (Jakoby et al., 2002) (Fig. 4). Clade I comprises TGA1 and TGA4, and Clade II consists of three closely interconnected factors TGA2, TGA5, and TGA6, which contain a shorter N-terminus than the other TGA proteins. TGA3 and TGA7 constitute clade III. PERIANTHIA or TGA8 comprise clade IV, and TGA9 and TGA10 form clade V.

The presence of TGACG motifs in the promoters of different plant glutathione S-transferase genes (Ellis et al., 1993; van der Zaal et al., 1996) opened up the hypothesis that TGA proteins trigger plant stress responses. In the case of TGA1 and TGA4, both are related to control of basal resistance against pathogens (reviewed in Gatz, 2013). These proteins present a regulation through Cys residues sensitive to the cellular redox state. Thus, in the absence of SA, Cys260 and Cys266 of these proteins form an intramolecular disulfide bond that prevents interaction with NPR1; this link is reduced after the accumulation of SA, allowing this interaction and improving their binding to defense-related gene promoter regions (Després et al., 2003). The Cys residues 260 and 266 of TGA1 are regulated by both S-nitrosation and S-glutathionylation, affecting protein conformation and preventing formation of disulfide bonds (Lindermayr et al., 2010). At the same time, NPR1 ameliorates not only the DNA binding activity of the reduced TGA1 (Després et al., 2003), but also the DNA binding activity of TGA1-SNO. Although TGA1 and TGA4 regulate target genes involved in systemic acquired resistance (SAR, Sun et al., 2018), they also modulate nitrate responses in Arabidopsis roots (Alvarez et al., 2014).

TGA2, TGA5, and TGA6 play key roles in pathways linked to SA (Zhang et al., 2003; Kesarwani et al., 2007), JA/ET (Zander et al., 2010, 2012, 2014), xenobiotics, and reactive oxylipin signaling (Fode et al., 2008; Mueller et al., 2008; Findling et al., 2018). Interestingly, tga2tga5tga6 triple mutant roots are considerably shorter than those of the wild type in control medium (Stotz et al., 2013). The interaction between NPR1 and TGA2 protein to stimulate the DNA binding activity to the SA-responsive element in the PR-1 gene promoter has also been reported (Wu et al., 2012).

The TGA3 transcription factor mediates NPR1 SA-dependent gene expression in planta (Sarkar et al., 2018) and its role in the hormonal crosstalk between SA and cytokinin has also been reported (Choi et al., 2010). Apart from that, TGA3 is also related to metal detoxification (Fang et al., 2017). TGA9 and TGA10 play essential roles in anther development.

**Fig. 5.** Crosstalk of NO during developmental cues and biotic stress responses. Upon pathogen attack, a redox change in the cellular context promotes NONEXPRESSOR OF PATHOGENESIS-RELATED GENES1 (NPR1) monomerization and interaction with different TGAs in the nucleus to activate the expression of stress-related genes. Similarly, a hypothetical model shows the interaction of other NPR-like proteins with TGA members to activate developmental gene expression. BLADE-ON-PETIOLE1/2 (BOP1/2) proteins interact with PERIANTHIA (PAN) in the nucleus where PAN binds DNA under reducing conditions. The putative role of Cys S-nitrosation (SNO) is included. Arrows indicate positive effects and dotted arrows putative regulations.
by the action of two CC-type floral glutaredoxins, ROXY1 and ROXY2 (Murmu et al., 2010), again exemplifying a redox-regulated TGA factor function in plants.

PERIANTHIA (PAN)/TGA8, which is part of an independent clade of the TGA family, has important functions in plant development, as a negative regulator of floral organ initiation and the number of petals and sepals (Running and Meyerowitz, 1996; Chuang et al., 1999). PAN functions in floral development are mediated by the positive regulation of the AGAMOUS (AG) gene, which antagonizes the meristematic activity by repression of WUSCHEL (WUS) (Das et al., 2009). pan mutants have flowers with five petals, similar to those of the AGAMOUS/WUSCHEL (WUS) double mutant, and pan1 is co-expressed with BOP1/2 during floral development. Hepworth et al. (2005) demonstrated by yeast two-hybrid assays that, similarly to NPR1, BOP1 and BOP2 interact with transcription factors of the TGA family but with different specificities, showing preference for PAN. This fact was corroborated by a bimolecular fluorescence complementation (BiFC) assay in Arabidopsis mesophyll protoplasts which verified their location in the cell nucleus (Xu et al., 2010). Indeed, BOP1/2–PAN interaction was described in the binding to regulatory sequences of the APII promoter, as a mechanism to promote the identity of the floral meristem. Although initially PAN was described as a regulator of the development of aerial parts of the plant, PAN also has a fundamental role in the stem cell niche of the root apical meristem (de Luis Balaguer et al., 2017).

At the biochemical level, PAN ability to bind DNA (and, specifically, AG-regulating elements) is altered according to the cell redox conditions. PAN contains an N-terminal end with five Cys residues able to form intramolecular disulfide bridges, which is in agreement to the regulatory mechanism of other TGAs (Gutsche and Zachgo, 2016). In addition, a sixth Cys residue at the C-terminal end, Cys340, is essential for PAN function because it undergoes S-glutathionylation in a specific manner (Li et al., 2009; Gutsche and Zachgo, 2016). Remarkably, the ROXY1 CC-type glutaredoxin negatively regulates PAN protein (Li et al., 2009).

In summary, NPR-like proteins interact with TGA factors, which in turn are regulated by glutaredoxins. A clear parallelism seems to have evolved between the mechanism regulating the defense responses and that regulating floral development (Gatz, 2013) (Fig. 5).

Concluding remarks

Our understanding of the molecular basis for plant development and stress trade-off is still very limited, although the balanced function of plant growth and stress regulators is known to contribute to plant survival and fitness. The severe growth and developmental defects of NO-deficient and NO-oversaturator mutants (even though they have complex pleiotropic phenotypes), together with impaired responses to biotic and abiotic stresses, may be indicative of a prominent role for this gasotransmitter in these trade-offs.

Thus, to gain full appreciation of how NO post-translational protein modification controls transcriptional reprogramming of plant development upon stress, the future challenge is to uncover the reversible post-translational regulation and those molecular targets across different interconnected signaling pathways.

As we move away from Arabidopsis to other model species (i.e. the low redundancy species Marchantia polymorpha) and crops, it is important to have a clear vision not only of NO function and target specificity, but also of gene abundance and the evolutionary signaling pathways for translational biology.

Future research should reveal if precise amino acid substitutions in key targets will lead to the design of more accurate molecular tools for biotic and abiotic stress tolerance and improvement in growth and development in crops.

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References

Abat JK, Deswal R. 2009. Differential modulation of S-nitrosoproteome of Brassica juncea by low temperature: change in S-nitrosylation of Rubisco is responsible for the inactivation of its carboxylase activity. Proteomics 9, 4368–4380.

Abbas M, Berckhan S, Rooney DJ, et al. 2015. Oxygen sensing coordinates photomorphogenesis to facilitate seedling survival. Current Biology 25, 1483–1488.

Abello N, Kerstiens HA, Postma DS, Bischoff R. 2009. Protein tyrosine nitration: selectivity, physicochemical and biological consequences, denitration, and proteomics methods for the identification of tyrosine-nitrated proteins. Journal of Proteome Research 8, 3222–3238.

Adie BA, Pérez-Pérez J, Pérez-Pérez MM, Godoy M, Sánchez-Serrano JJ, Schmelz EA, Solano R. 2007. ABA is an essential signal for plant resistance to pathogens affecting JA biosynthesis and the activation of defenses in Arabidopsis. The Plant Cell 19, 1665–1681.

Ahmad P, Abdel-Latef AA, Hashem A, Abdel-Allah EF, Guçel S, Tran LS. 2016. Nitric oxide mitigates salt stress by regulating levels of osmolytes and antioxidant enzymes in chickpea. Frontiers in Plant Science 7, 367.

Albertos P, Romero-Puertas MC, Tatematsu K, Mateos I, Sánchez-Vicente I, Nambara E, Lorenzo O. 2015. S-Nitrosylation triggers ABI5 denitration, and proteomics methods for the identification of tyrosine-nitrated proteins. Journal of Biological Chemistry 286, 578–586.

Alvarez JM, Riveras E, Vidal EA, et al. 2014. Systems approach identifies TGA1 and TGA4 transcription factors as important regulatory components of the nitrate response of Arabidopsis thaliana roots. The Plant Journal 80, 1–13.

Arawind L, Koonin EV. 1999. Fold prediction and evolutionary analysis of the POZ domain: structural and evolutionary relationship with the potassium channel tetramerization domain. Journal of Molecular Biology 285, 1353–1361.

Arasimowicz-Jelonek M, Floryszak-Wieczorek J. 2011. Understanding the fate of peroxynitrite in plant cells—from physiology to pathophysiology. Phytochemistry 72, 681–688.

Arc E, Sechet J, Corbineau F, Rajjou L, Marion-Poll A. 2013. ABA crosstalk with ethylene and nitric oxide in seed dormancy and germination. Frontiers in Plant Science 4, 63.
Arredondo-Peeter R, Hargrove MS, Moran JF, Sarath G, Klucos RV. 1998. Plant hemoglobins. Plant Physiology 118, 1121–1125.

Astier J, Besson-Bard A, Lamotte O, Bertoldo J, Bourque S, Terenzi H, Wendehenne D. 2012. Nitric oxide inhibits the AtPase activity of the chaperone-like AAA+-AtPase CDC48, a target for S-nitrosylation in cryptogean signalling in tobacco cells. The Biochemical Journal 447, 249–260.

Astier J, Lindermay C. 2012. Nitric oxide-dependent posttranslational modification in plants: an update. International Journal of Molecular Sciences 13, 15193–15208.

Baier M, Bittner A, Prescher A, van Buer J. 2019. Preparing plants for improved cold tolerance by priming. Plant, Cell & Environment 42, 782–800.

Banerjee A, Roychoudhury A. 2017. Abscisic-acid-dependent basic leucine zipper (bZIP) transcription factors in plant abiotic stress. Protoplasma 254, 3–16.

Begara-Morales JC, Chaki M, Sánchez-Calvo B, Mata-Pérez C, Leterrier M, Palma JM, Barroso JB, Corpsas FJ. 2013. Protein tyrosine nitration in pea roots during development and senescence. Journal of Experimental Botany 64, 1121–1134.

Begara-Morales JC, Sánchez-Calvo B, Chaki M, Mata-Pérez C, Valderrama R, Padilla MN, López-Jaramillo J, Luque F, Corpsas FJ, Barroso JB. 2015. Differential molecular response of monodehydroascorbate reductase and glutathione reductase by nitration and S-nitrosylation. Journal of Experimental Botany 66, 5983–5996.

Begara-Morales JC, Sánchez-Calvo B, Chaki M, Valderrama R, Mata-Pérez C, López-Jaramillo J, Padilla MN, Carreras A, Corpsas FJ, Barroso JB. 2014. Dual regulation of cytosolic ascorbate peroxidase (APX) by tyrosine nitration and S-nitrosylation. Journal of Experimental Botany 65, 527–538.

Begara-Morales JC, Sánchez-Calvo B, Chaki M, Valderrama R, Mata-Pérez C, Padilla MN, Carreras A, Corpsas FJ, Barroso JB. 2016. Antioxidant systems are regulated by nitric oxide-mediated post-translational modifications (NO-PTMs). Frontiers in Plant Science, 152.

Bellin D, Asai S, Delledonne M, Brackenier A, Inzé D, Delledonne M, Van Breusegem F. 2007. Metacaspase activity of Arabidopsis thaliana is regulated by S-nitrosylation of a critical cysteine residue. Journal of Biological Chemistry 282, 1532–1538.

Bellin D, Asai S, Delledonne M, Yoshioka H. 2013. Nitric oxide as a mediator for defense responses. Molecular Plant-Microbe Interactions 26, 271–277.

Benczúr Arnold RL, Gualano N, Leymarie J, Côme D, Corbineau F. 2006. Hypoxia interacts with ABA metabolism and increases ABA sensitivity in embryos of dormant barley grains. Journal of Experimental Botany 57, 1423–1430.

Bensmihen S, Giraudat J, Parcy F. 2005. Characterization of three homologous basic leucine zipper transcription factors (bZIP) of the ABI5 family during Arabidopsis thaliana embryo maturation. Journal of Experimental Botany 56, 597–603.

Bensmihen S, Rippa S, Lambert G, Jublot D, Pautot V, Granier F, Giraudat J, Parcy F. 2002. The homologous ABI5 and EEL transcription factors function antagonistically to fine-tune gene expression during late embryogenesis. The Plant Cell 14, 1391–1403.

Bethke PC, Gubler F, Jacobsen JV, Jones RL. 2004. Dormancy of Arabidopsis seeds and barley grains can be broken by nitric oxide. Planta 219, 847–855.

Bethke PC, Libourel IG, Aoyama N, Chung YY, Still DW, Jones RL. 2007. The Arabidopsis aleurone layer responds to nitric oxide, gibberellin, and abscisic acid and is sufficient and necessary for seed dormancy. Plant Physiology 143, 1173–1188.

Bethke PC, Libourel IG, Jones RL. 2006. Nitric oxide reduces seed dormancy in Arabidopsis. Journal of Experimental Botany 57, 517–526.

Bi C, Ma Y, Wu Z, Yu YT, Liang S, Lu K, Wang XF. 2017. Arabidopsis ABI5 plays a role in regulating ROS homeostasis by activating CATALASE 1 transcription in seed germination. Plant Molecular Biology 94, 197–213.

Blanco F, Salinas P, Cecchini NM, Jordana X, Van Hummelen P, Alvarez ME, Holuaigue L. 2009. Early genomic responses to salicylic acid in Arabidopsis. Plant Molecular Biology 70, 79–102.

Boríjsk J, Machereel D, Bensmihen S, Wobus U, Rolletschek H. 2007. Low oxygen sensing and balancing in plant seeds: a role for nitric oxide. New Phytologist 176, 813–823.

Borsani O, Valpuesta V, Botella MA. 2001. Evidence for a role of salicylic acid in the oxidative damage generated by NaCl and osmotic stress in Arabidopsis seedlings. Plant Physiology 126, 1024–1030.

Brilli J, Desikan R, Hancock JT, Weis IS, Neill SJ. 2006. ABA-induced NO generation and stomatal closure in Arabidopsis are dependent on H2O2 synthesis. The Plant Journal 45, 113–122.

Brocard IM, Lynch TJ, Finkelstein RR. 2002. Regulation and role of the Arabidopsis abscisic acid-insensitive 5 gene in abscisic acid, sugar, and stress response. Plant Physiology 129, 1533–1543.

Camejo D, Ortiz-Espin A, Lázaro JJ, Romero-Puertas MC, Lázaro-Payo A, Sevila F, Jiménez A. 2015. Functional and structural changes in plant mitochondrial Pxxl F caused by NO. Journal of Proteomics 119, 122–125.

Camejo D, Romero-Puertas Mdl C, Rodríguez-Serrano M, Sandalio LM, Lázaro JJ, Jiménez A, Sevila F. 2013. Salinity-induced changes in S-nitrosylation of pea mitochondrial proteins. Journal of Proteomics 79, 87–99.

Canet JV, Dobón A, Fajmonová J, Tornero P. 2012. The BLADE-ON-PETIOLE genes of Arabidopsis are essential for resistance induced by methyl jasmonate. BMC Plant Biology 12, 199.

Canet JV, Dobón A, Ibáñez F, Perales L, Tornero P. 2010a. Resistance and biomass in Arabidopsis: a new model for salicylic acid perception. Plant Biotechnology Journal 8, 126–141.

Canet JV, Dobón A, Roig A, Tornero P. 2010b. Structure–function analysis of npr1 alleles in Arabidopsis reveals a role for its paralogs in the perception of salicylic acid. Plant, Cell & Environment 33, 1911–1922.

Cantrel T, Vazquez T, Puyaubert J, Rezé N, Lesch M, Kaiser WM.

Dutilleul C, Guillás I, Zachowski A, Baudouin E. 2011. Nitric oxide participates in cold-responsive phospholipid formation and gene expression in Arabidopsis thaliana. New Phytologist 189, 415–427.

Cao H, Glazebrook J, Clarke JD, Volko S, Dong X. 1997. The Arabidopsis NPR1 gene that controls systemic acquired resistance encodes a novel protein containing ankyrin repeats. Cell 88, 57–63.

Carles C, Bies-ETHene N, Aspat L, Léon-Kloosterziel KM, Koomnreef M, Echeverria M, Delseny M. 2002. Regulation of Arabidopsis thaliana Enr genes: role of ABI5. The Plant Journal 30, 373–383.

Castillo MC, Coego A, Costa-Broseta Á, Léon J. 2018. Nitric oxide responses in Arabidopsis hypocotyls are mediated by diverse phytohormone pathways. Journal of Experimental Botany 69, 5265–5279.

Castillo MC, Lozano-Juste J, González-Guzmán M, Rodriguez L, Rodríguez PL, León J. 2015. Inactivation of PVR-PYL/RCAR ABA receptors by tyrosine nitration may enable rapid inhibition of ABA signaling by nitric oxide. Science Signaling 8, ra99.

Cecconi D, Orzetti S, Vandelie E, Rinalducci S, Zolla L, Delledonne M. 2009. Protein nitration during defense response in Arabidopsis thaliana. Electrophoresis 30, 2460–2468.

Chaki M, Valderrama R, Fernández-Ocaña AM, et al. 2009. Protein targets of tyrosine nitration in sunflower (Helianthus annuus L.) hypocotyls. Journal of Experimental Botany 60, 4221–4234.

Chaki M, Valderrama R, Fernández-Ocaña AM, et al. 2011. High temperature triggers the metabolism of S-nitrosothiols in sunflower mediating a process of nitrosative stress which provokes the inhibition of ferredoxin-NADP reductase by tyrosine nitration. Plant, Cell & Environment 34, 1803–1818.

Chaki M, Valderrama R, Fernández-Ocaña AM, et al. 2012. Protein targets of tyrosine nitration in sunflower (Helianthus annuus L.) hypocotyls (correction). Journal of Experimental Botany 63, 5377.

Chen J, Xiao Q, Wu F, Dong X, He J, Pei Z, Zheng H. 2010. Nitric oxide enhances salt secretion and Na+ sequestration in a mangrove plant, Avicennia marina, through increasing the expression of H+-ATPase and Na+/H+ antiporter under high salinity. Tree Physiology 30, 1570–1585.

Chen K, Chen L, Fan J, Fu J. 2013. Allelopathy of heat damage to photosystem II by nitric oxide in tall fescue. Photosynthesis Research 116, 21–31.
Chen R, Sun S, Wang C, et al. 2009. The Arabidopsis PARAOQUAT RESISTANT2 gene encodes an S-nitrosothiol reductase that is a key regulator of cell death. Cell Research 18, 1377–1397.

Cheng RJ, Zhang XY, Shao XX, Wang F, Zhang Z, Liu YG, Zhang Y, Zhang XS. 2014. Abscisic acid regulates early seed development in Arabidopsis by ABA5-mediated transcription of SHORT HYPOCYTOL UNDER BLUE1. The Plant Cell 26, 1053–1068.

Chini A, Grant JJ, Seki M, Shinozaki K, Loake GJ. 2004. Drought tolerance establishment by enhanced expression of the CC-NBS-LRR gene, ADR1, requires salicylic acid, EDS1 and ABI1. The Plant Journal 38, 810–822.

Choi H, Hong J, Ha J, Kang J, Kim SY. 2000. ABFs, a family of ABA-responsive element binding factors. Journal of Biological Chemistry 275, 1723–1730.

Choi J, Huh SU, Kojima M, Sakakibara H, Paek KH, Hwang I. 2010. The cytokinin-activated transcription factor ARR2 promotes plant immunity via TGA3/4/NIM1-dependent salicylic acid signaling in Arabidopsis. Developmental Cell 19, 234–245.

Christmann A, Weiler EW, Steudle E, Grill E. 2007. A hydraulic signal in root-to-shoot signalling of water shortage. The Plant Journal 49, 167–174.

Chuang CF, Running MP, Williams RW, Meyerowitz EM. 1999. The PERIANTHIA gene encodes a bZIP protein involved in the determination of floral organ number in Arabidopsis thaliana. Genes & Development 13, 334–344.

Clark D, Durner J, Navarre DA, Klessig DF. 2000. Nitric oxide inhibition of tobacco catalase and ascorbate peroxidase. Molecular Plant-Microbe Interactions 13, 1380–1384.

Corpas FJ, Dordas C, Hasinoff BB, et al. 2016. The N-end rule pathway controls redox homeostasis via the degradation of ascorbate peroxidase. Structure 24, 1383–1394.

Desikan R, Griffiths R, Hancock J, Neill S. 2002. A new role for an old enzyme: nitrate reductase-mediated nitric oxide generation is required for abscisic acid-induced stomatal closure in Arabidopsis thaliana. Proceedings of the National Academy of Sciences, USA 99, 16314–16318.

Després C, Chubak C, Rochon A, Clark R, Bethune T, Desveaux D, Fobert PR. 2003. The Arabidopsis NPR1 disease resistance protein is a novel modulator of the pathogen response that confers redox regulation of DNA binding activity to the basic domain/leucine zipper transcription factor TGA1. The Plant Cell 15, 2181–2191.

Després C, DeLong C, Glaze S, Liu E, Fobert PR. 2000. The Arabidopsis NPR1/NIM1 protein enhances the DNA binding activity of a subgroup of the TGA family of bZIP transcription factors. The Plant Cell 12, 279–290.

Dietrich D, Pang L, Kobayashi A, et al. 2017. Root hydrotopism is controlled via a cortex-specific growth mechanism. Nature Plants 3, 17057.

Ding X, Cao Y, Huang L, Zhao J, Xu C, Li X, Wang S. 2008. Activation of the indole-3-acetic acid-amido synthetase GH3-8 suppresses expansin expression and promotes salt-tolerance- and jasmonate-independent basal immunity in rice. The Plant Cell 20, 228–240.

Dordas C, Hasinoff BB, Igamberdiev AU, Matanich N, Rivoal J, Hill RD. 2003. Expression of a stress-induced hemoglobin affects NO levels produced by alfalfa root cultures under hypoxic stress. The Plant Journal 35, 763–770.

Dordas C, Hasinoff BB, Rivoal J, Hill RD. 2004. Class-1 hemoglobins, nitrate and NO levels in anoxic maize cell-suspension cultures. Planta 219, 66–72.

Dröge-Laser W, Snoek BL, Snel B, Weiste C. 2018. The Arabidopsis bZIP transcription factor family—an update. Current Opinion in Plant Biology 45, 36–49.

Durner J, Klissig DF. 1995. Inhibition of ascorbate peroxidase by salicylic acid and 2,6-dichloroisonicotinic acid, two inducers of plant defense responses. Proceedings of the National Academy of Sciences, USA 92, 11312–11316.

Durner J, Wendehenne D, Klessig DF. 1998. Defense gene induction in tobacco by nitric oxide, cyclic GMP, and cyclic ADP-ribose. Proceedings of the National Academy of Sciences, USA 95, 10328–10333.

Eisenach C, Baetz U, Huck NV, Zhang J, De Angeli A, Beckers GJM, Martinova E. 2017. ABA-induced stomatal closure involves ALMT4, a phosphorylation-dependent vacuolar anion channel of Arabidopsis. The Plant Cell 29, 2552–2569.

Ellis JG, Tokuhisa JG, Llewellyn DJ, Bouchez D, Singh K, Dennis ES, Peacock WJ. 1993. Does the ecs-element occur as a functional component of the promoters of plant genes? The Plant Journal 4, 433–443.

Ellis MH, Dennis ES, Peacock WJ. 1999. Arabidopsis roots and shoots have different mechanisms for hypoxic stress tolerance. Plant Physiology 119, 57–64.

Espunya MC, De Michele R, Gómez-Cadenas A, Martínez MC. 2012. S-Nitrosoglutathione is a component of wound- and salicylic acid-induced systemic resistance in Arabidopsis thaliana. Journal of Experimental Botany 63, 3219–3227.

Fan HF, Du CX. 2012. Effect of nitric oxide on proline metabolism in cucumber seedlings under salinity stress. Journal of the American Society for Horticultural Science 137, 127–133.

Fan J, Chen K, Amombo E, Hu Z, Chen L, Fu J. 2015. Physiological and molecular mechanism of nitric oxide (NO) induced in Bermudagrass response to cold stress. PLoS One 10, e0132991.

Fang H, Liu Z, Long Y, Liang Y, Jin Z, Zhang L, Liu D, Li H, Zhai J, Pei Y. 2017. The Ca2+ /calmodulin2-binding transcription factor TGA3 ele-
corporates redox homeostasis, enhances ABA-regulated expression and promotes salicylate- and jasmonate-independent basal immunity in rice. The Plant Journal 810–822.

Fang H, Liu Z, Long Y, Liang Y, Jin Z, Zhang L, Liu D, Li H, Zhai J, Pei Y. 2017. The Ca2+ /calmodulin2-binding transcription factor TGA3 ele-
corporates redox homeostasis, enhances ABA-regulated expression and promotes salicylate- and jasmonate-independent basal immunity in rice. The Plant Journal 810–822.

Feng J, Wang C, Chen Q, Chen H, Ren B, Li X, Zuo J. 2013. S-Nitrosylation of phosphotransfer proteins represses cytokinin signaling. Nature Communications 4, 1529.

Fernando VCD, Al Kateeb W, Belmonte MF, Schroeder DF. 2018. Role of Arabidopsis ABF1/3 during det1 germination in salt and osmotic stress conditions. Plant Molecular Biology 97, 149–163.

Findling S, Stotz HU, Zoller M, Krischke M, Zander M, Gatz C, Berger S, Mueller MJ. 2018. TGA2 signaling in response to reactive electrophile species is not dependent on cysteine modification of TGA2. PLoS One 13, e0195398.

Finkelstein R. 2013. Abscisic acid synthesis and response. The Arabidopsis Book 11, e0166.
Finkelstein R, Gampala SS, Lynch TJ, Thomas TL, Rock CD. 2005. Redundant and distinct functions of the ABA response loci ABI-SENSITIVE(ABI)5 and ABI-BINDING FACTOR (ABF)3. Plant Molecular Biology 59, 253–267.

Finkelstein RR, Lynch TJ. 2000. The Arabidopsis abscisic acid response gene ABI5 encodes a basic leucine zipper transcription factor. The Plant Cell 12, 599–609.

Fode B, Siemens T, Thurow C, Weigel R, Gatz C. 2008. The Arabidopsis GRAS protein SCL14 interacts with class II TGA transcription factors and is essential for the activation of stress-inducible promoters. The Plant Cell 20, 3122–3135.

Frungillo L, Skelly MJ, Loake GJ, Spool SH, Salgado I. 2014. S-Nitrosothiols regulate nitric oxide production and storage in plants through the nitrogen assimilation pathway. Nature Communications 5, 5401.

Fu ZQ, Yan S, Saleh A, et al. 2012. NPR3 and NPR4 are receptors for the immune signal salicylic acid in plants. Nature 486, 228–232.

Fu ZW, Wang YL, Lu YT, Yuan TT. 2016. Nitric oxide is involved in stomatal development by modulating the expression of stomatal regulator genes in Arabidopsis. Plant Science 252, 282–289.

Fujii H, Chinnusamy V, Rodrigues A, Rubio S, Antoni R, Park SY, Cutler SR, Sheen J, Rodriguez PL, Zhu JK. 2009. In vitro reconstitution of an abscisic acid signaling pathway. Nature 462, 660–664.

Fujii H, Zhu JK. 2009. Arabidopsis mutant deficient in 3 abscisic acid-activated protein kinases reveals critical roles in growth, reproduction, and stress. Proceedings of the National Academy of Sciences, USA 106, 8380–8385.

Fujita Y, Fujita M, Satoh R, Maruyama K, Parvez MM, Seki M, Hiratsu K, Ôhme-Takagi M, Shinozaki K, Yamaguchi-Shinozaki K. 2005. AREB1 is a transcription activator of novel ABRE-dependent ABA signaling that enhances drought stress tolerance in Arabidopsis. The Plant Cell 17, 3470–3488.

Galetskiy D, Lohscheider JN, Kononikhin AS, Popov IA, Nikolaev EN, Adamska I. 2011. Phosphorylation and nitration levels of photosynthetic activated protein kinases reveals critical roles in growth, reproduction, and stress downstream of the receptor-like kinase EMS1. The Plant Cell 24, 4892–4906.

Han SK, Sang Y, Rodrigues A, Wu MF, Rodriguez PL, Wagner D; BIO425 F2010. Wu MF, Rodriguez PL, Wagner D. 2012. The SWI/SNF2 chromatin remodeling ATPase BRAHMA represses abscisic acid responses in the absence of the stress stimulus in Arabidopsis. The Plant Cell 24, 4902–4906.

He HY, He LF, Gu MH, Li XF. 2012. Nitric oxide improves aluminum tolerance by regulating hormonal equilibrium in the root apices of rye and wheat. Plant Science 183, 123–130.

Hepworth SR, Zhang Y, McKim S, Li X, Haughn GW. 2005. BLADE-ON-PETIOLE-dependent signaling controls leaf and floral patterning in Arabidopsis. The Plant Cell 17, 1434–1448.

Hill BG, Dranka BP, Bailey SM, Lancaster JR Jr, Darley-Usmar VM. 2010. What part of NO don’t you understand? Some answers to the cardinal questions in nitric oxide biology. Journal of Biological Chemistry 285, 19699–19704.

Holman TJ, Jones PD, Russell L, et al. 2009. The N-end rule pathway promotes seed germination and establishment through removal of ABA sensitivity in Arabidopsis. Proceedings of the National Academy of Sciences, USA 106, 4549–4554.

Holzmeister C, Gaupe S, Scherzer O, Root L, Sussmann R, Durner J. 2015. Differential inhibition of Arabidopsis superoxide dismutases by peroxynitrite-mediated tyrosine nitration. Journal of Experimental Botany 66, 989–999.

Horváth E, Pál M, Szalai G, Pádli E, Janda T. 2007. Exogenous 4-hydroxybenzoic acid and salicylic acid modulate the effect of short-term drought and freezing stress on wheat plants. Biologia Plantarum 51, 480–487.

Hoy JA, Hagrove MS. 2008. The structure and function of plant hemoglobins. Plant Physiology and Biochemistry 46, 371–379.

Hsu FC, Chou MY, Peng HP, Chou SJ, Shih MC. 2011. Insights into hypoxic systemic responses based on analyses of transcriptional regulation in Arabidopsis. PLoS One 6, e28888.

Hu J, Huang X, Chen L, Sun X, Lu C, Zhang L, Wang Y, Zuo J. 2015. Site-specific nitrosoproteomic identification of endogenous S-nitrosylated proteins in Arabidopsis. Plant Physiology 167, 1731–1746.

Huang J, Li Z, Biener G, Xiong E, Malik S, Eaton N, Zhao C, Raicu V, Kong H, Zhao D. 2017. Carbonic anhydrases function in anther cell differentiation downstream of the receptor-like kinase EMS1. The Plant Cell 29, 1335–1356.

Huang X, von Rad U, Durner J. 2002. Increased level of hemoglobin 1 enhances survival of hypoxic systemic responses based on analyses of transcriptional regulation in Arabidopsis. PLoS One 6, e0153810.

Hu J, Huang X, Chen L, Sun X, Lu C, Zhang L, Wang Y, Zuo J. 2015. Site-specific nitrosoproteomic identification of endogenously S-nitrosylated proteins in Arabidopsis. Plant Physiology 167, 1731–1746.

Huang J, Li Z, Biener G, Xiong E, Malik S, Eaton N, Zhao C, Raicu V, Kong H, Zhao D. 2017. Carbonic anhydrases function in anther cell differentiation downstream of the receptor-like kinase EMS1. The Plant Cell 29, 1335–1356.

Huang X, von Rad U, Durner J. 2002. Increased level of hemoglobin 1 enhances survival of hypoxic systemic responses based on analyses of transcriptional regulation in Arabidopsis. PLoS One 6, e28888.

Hup W, Klok EJ, Trevaskis B, Watts RA, Ellis MH, Peacock WJ, Dennis ES. 2002. Increased level of hemoglobin 1 enhances survival of hypoxic stress and promotes early growth in Arabidopsis thaliana. Proceedings of the National Academy of Sciences, USA 99, 17197–17202.

Hussain A, Mun BG, Imran QM, Lee SU, Adamu TA, Shahid M, Kim KM, Yun BW. 2016. Nitric oxide mediated transcription profiling of peroxynitrite-dependent signaling kinases reveals critical roles in growth, reproduction, and stress downstream of the receptor-like kinase EMS1. The Plant Cell 29, 1335–1356.
reveals activation of multiple regulatory pathways in Arabidopsis thaliana. Frontiers in Plant Science 7, 975.

Imran QM, Hussain A, Lee SU, Mun BG, Falak N, Loake GJ, Yun BW. 2018. Transcriptome profile of NO-induced Arabidopsis transcription factor genes suggests a putative regulatory role in multiple biological processes. Scientific Reports 8, 7711.

Innes R. 2018. The positives and negatives of NPR: a unifying model for salicylic acid signaling in plants. Cell 173, 1314–1315.

Irie Y, Saeki M, Kamisaki Y, Martin E, Murad F. 2003. Histone H1.2 is a substrate for denitrosylation, as an activity that reduces nitrosylation in mammalian proteins. In Proceedings of the National Academy of Sciences, USA 100, 5634–5639.

Ischiropoulos H. 2003. Biological selectivity and functional aspects of protein tyrosine nitration. Biochemical and Biophysical Research Communications 305, 776–783.

Jaffrey SR, Snyder SH. 2001. The biotin switch method for the detection of S-nitrosoylated proteins. Science’s STKE 2001, p1.

Jakoby B, Weisshaar B, Dröge-Laser W, Vicente-Carbajosa J, Tiedemann J, Kroe T, Parfy C. bZIP Research Group. 2002. bZIP transcription factors in Arabidopsis. Trends in Plant Science 7, 106–111.

Janda T, Szalai G, Tari I, Paldi E. 1999. Hydroporionic treatment with salicylic acid decreases the expression of chilling injury in maize (Zea mays L.) plants. Planta 208, 175–180.

Jia L, Bonaventura C, Bonaventura J, Stamler JS. 1996. S-Nitrosotriamethinolobin: a dynamic activity of blood involved in vascular control. Nature 380, 221–226.

Joudoi T, Shichiri Y, Kamizono N, Akaile T, Sawa T, Yoshitake J, Yamada N, Iwai S. 2013. Nitrated cyclic GMP modulates guard cell signaling in Arabidopsis. The Plant cell 25, 558–571.

Kang JY, Choi HI, Im MY, Kim SY. 2002. Arabidopsis basic leucine zipper proteins that mediate stress-responsive abscisic acid signaling. The Plant Cell 14, 343–357.

Kanno Y, Jikumaru Y, Hanada A, Nambara E, Abrams SR, Kamiya Y, Nambara E, Abrams SR. 2002. Arabidopsis N终止 R1-dependent defense signaling in Arabidopsis thaliana. New Phytologist 156, 317–328.

Karapetyan S, Dong X. 2018. Redox and the circadian clock in plant immunity: a balancing act. Free Radical Biology & Medicine 119, 56–61.

Kawabe H, Ohtani M, Kurata T, Sakamoto T, Demura T. 2009. Regulators of PP2C phosphatase activity function as abscisic acid and GA receptors in Arabidopsis. The Plant Cell 21, 429–441.

Kawabe H, Ohtani M, Kurata T, Sakamoto T, Demura T. 2009. Regulators of PP2C phosphatase activity function as abscisic acid receptors in Arabidopsis. The Plant Cell 21, 429–441.

Kubienová L, Tichá T, Jahnová J, Luhová L, Mieslerová B, Perata P, van Dongen JT. 2011. Oxygen sensing in plants is mediated by an N- and rule pathway for protein destabilization. Nature 479, 419–422.

Liu A, Wang Y, Tang J, Xue P, Li C, Liu H, Bu Y, Yang F, Loake GJ, Chu C. 2012. Nitric oxide and protein S-nitrosylation are integral to hydrogen peroxide-induced leaf cell death in rice. Plant Physiology 158, 451–464.

Lindermayr C, Durner J. 2009. S-Nitrosylation in plants: pattern and function. Journal of Proteomics 73, 1–9.

Lindermayr C, Saalbach G, Bahnweg G, Durner J. 2006. Differential inhibition of Arabidopsis methionine aconitases transfers by protein S-nitrosylation. Journal of Biological Chemistry 281, 4285–4291.

Lindermayr C, Saalbach G, Durner J. 2005. Proteomic identification of S-nitrosylated proteins in Arabidopsis. Plant Physiology 137, 921–930.

Lindermayr C, Sell S, Müller B, Leister D, Durner J. 2010. Redox regulation of the NPR1–TGA1 system of Arabidopsis thaliana by nitric oxide. The Plant Cell 22, 2894–2907.

Liu L, Hausladen A, Zeng M, Que L, Heitman J, Stamler JS. 2001. A metabolite enzyme for S-nitrosothiol conserved from bacteria to humans. Nature 410, 490–494.

Liu X, Hou X. 2018. Antagonistic regulation of ABA and GA in metabolism and signaling pathways. Frontiers in Plant Science 9, 251.

Liu Y, Shi L, Ye N, Liu R, Jia W, Zhang J. 2009. Nitric oxide-induced rapid decrease of abscisic acid concentration is required in breaking seed dormancy in Arabidopsis. New Phytopathologist 183, 1030–1042.

Lombardo MC, Lamattina L. 2018. Abscisic acid and nitric oxide modulate cytoskeleton organization, root hair growth and ectopic hair formation in Arabidopsis. Nitric Oxide: Biology and Chemistry 80, 89–97.

Lopez-Molina L, Mongrand S, Chua NH. 2001. A postgermination developmental arrest checkpoint is mediated by abscisic acid and requires the ABI5 transcription factor in Arabidopsis. Proceedings of the National Academy of Sciences, USA 98, 4782–4787.

Lopez-Molina L, Mongrand S, McLachlin DT, Chalt BT, Chua NH. 2002. ABI5 acts downstream of ABI3 to execute an ABA-dependent growth arrest during germination. The Plant Journal 32, 317–328.

Lozano-Juste J, Colom-Moreno R, León J. 2011. In vivo protein tyrosine nitration in Arabidopsis thaliana. Journal of Experimental Botany 62, 3501–3517.

Lozano-Juste J, León J. 2010. Enhanced abscisic acid-mediated responses in nia1nia2nog1-2 triple mutant impaired in NIA/NR- and ANO1-dependent nitric oxide biosynthesis in Arabidopsis. Plant Physiology 152, 891–903.

Lozano-juste J, Leon J. 2011. Nitric oxide regulates DELLA content and PIF expression to promote photomorphogenesis in Arabidopsis. Plant Physiology 156, 1410–1423.

Luo M, Wang YY, Liu X, Yang S, Lu Q, Cui Y, Wu K. 2012. HD2C2 interacts with HD2A and is involved in ABA and salt stress response in Arabidopsis. Journal of Experimental Botany 63, 3237–3248.

Lv X, Ge S, Jalal Ahammed G, Xiang X, Guo Z, Yu J, Zhou Y. 2012. HD2C interacts with ROXY1, a glutaredoxin interacting with TGA factors, is required for flower development in Arabidopsis thaliana. The Plant Cell 24, 1397–1410.

Liu Y, Shi L, Ye N, Liu R, Jia W, Zhang J. 2009. Nitric oxide-induced rapid decrease of abscisic acid concentration is required in breaking seed dormancy in Arabidopsis. New Phytopathologist 183, 1030–1042.

Lombardo MC, Lamattina L. 2018. Abscisic acid and nitric oxide modulate cytoskeleton organization, root hair growth and ectopic hair formation in Arabidopsis. Nitric Oxide: Biology and Chemistry 80, 89–97.

Lopez-Molina L, Mongrand S, Chua NH. 2001. A postgermination developmental arrest checkpoint is mediated by abscisic acid and requires the ABI5 transcription factor in Arabidopsis. Proceedings of the National Academy of Sciences, USA 98, 4782–4787.

Lopez-Molina L, Mongrand S, McLachlin DT, Chalt BT, Chua NH. 2002. ABI5 acts downstream of ABI3 to execute an ABA-dependent growth arrest during germination. The Plant Journal 32, 317–328.

Lozano-Juste J, Colom-Moreno R, León J. 2011. In vivo protein tyrosine nitration in Arabidopsis thaliana. Journal of Experimental Botany 62, 3501–3517.

Lozano-Juste J, León J. 2010. Enhanced abscisic acid-mediated responses in nia1nia2nog1-2 triple mutant impaired in NIA/NR- and ANO1-dependent nitric oxide biosynthesis in Arabidopsis. Plant Physiology 152, 891–903.

Lozano-juste J, Leon J. 2011. Nitric oxide regulates DELLA content and PIF expression to promote photomorphogenesis in Arabidopsis. Plant Physiology 156, 1410–1423.

Luo M, Wang YY, Liu X, Yang S, Lu Q, Cui Y, Wu K. 2012. HD2C2 interacts with HD2A and is involved in ABA and salt stress response in Arabidopsis. Journal of Experimental Botany 63, 3237–3248.

Lv X, Ge S, Jalal Ahammed G, Xiang X, Guo Z, Yu J, Zhou Y. 2012. Crosstalk between nitric oxide and MPK1/2 mediates cold acclimation-induced chilling tolerance in tomato. Plant & Cell Physiology 53, 1963–1975.

Ma Y, Szostkiewicz I, Korte A, Moeis D, Yang Y, Christmann A, Grill E. 2009. Regulators of PPO2 phosphate activity function as abscisic acid sensors. Science 324, 1064–1068.

Ma Z, Marsolais F, Bykova NV, Igamberdiev AU. 2016. Nitric oxide and reactive oxygen species mediate metabolic changes in barley seed embryo during germination. Frontiers in Plant Science 7, 138.
Malik SI, Hussain A, Yun BW, Spoel SH, Loake GJ. 2011. GSNO-mediated de-nitrosylation in the plant defence response. Plant Science 181, 540–544.

Mamidi J, Kalai T, Goula H, Corsap FJ. 2014. Exogenous nitric oxide (NO) ameliorates salinity-induced oxidative stress in tomato (Solanum lycopersicum) plants. Journal of Soil Science and Plant Nutrition 14, 433–446.

Marín-de la Rosa N, Sotillo B, Miskolczi P, et al. 2014. Large-scale identification of gibberellin-related transcription factors defines group VII ETHYLENE RESPONSE FACTORS as functional DELLA partners. Plant Physiology 166, 1022–1032.

Melo PM, Silva LS, Ribeiro I, Seabra AR, Carvalho HG. 2011. Glutamine synthetase is a molecular target of nitric oxide in root nodules of Medicago truncatula and is regulated by tyrosine nitration. Plant Physiology 157, 1505–1517.

Mendes A, Kelly AA, van Erp H, Shaw E, Powers SJ, Kurup S, Eastmond PJ. 2013. bZIP57 regulates the omega-3 fatty acid content of Arabidopsis seed oil by activating fatty acid desaturase3. The Plant Cell 25, 3104–3116.

Mengel A, Ageeva A, Georgii E, Bernhardt J, Wu K, Durner J, Lindermayr C. 2017. Nitric oxide modulates histone acetylation at stress genes by inhibition of histone deacetylases. Plant Physiology 173, 1434–1452.

Mengel A, Chaki M, Shekarisefahlan A, Lindermayr C. 2013. Effect of nitric oxide on gene transcription—S-nitrosylation of nuclear proteins. Frontiers in Plant Science 4, 293.

Metwally A, Finkemeier I, Georgi M, Dietz KJ. 2003. Salicylic acid alleviates the cadmium toxicity in barley seedlings. Plant Physiology 132, 272–281.

Miura K, Lee J, Jin JB, Yoo CY, Miura T, Hasegawa PM. 2009. Sumoylation of ABI5 by the Arabidopsis SUMO E3 ligase SI2 negatively regulates abscisic acid signaling. Proceedings of the National Academy of Sciences, USA 106, 5418–5423.

Monreal JA, Arias-Baldrich C, Tossi V, Feria AB, Rubio-Casal A, Garcia-Mata C, Lamattina L, Garcia-Maurino S. 2013. Nitric oxide regulation of leaf phosphoenolpyruvate carboxylase-kinase activity: implication in sorghum responses to salinity. Plant Cell 23B, 859–869.

Mou Z, Fan W, Dong X. 2003. Inducers of plant systemic acquired resistance regulate NPR1 function through redox changes. Cell 113, 935–944.

Mueller S, Hilbert B, Dueckershoff K, Roitsch T, Krischke M, Mueller MJ, Berger S. 2008. General detoxification and stress responses are mediated by oxidized lipids through TGA transcription factors in Arabidopsis. The Plant Cell 20, 768–785.

Mulaudzi T, Ludidi N, Ruzvidzo O, Morse M, Hendricks N, Iwuoha E, Gehring C. 2011. Identification of a novel Arabidopsis thaliana nitric oxide-binding molecule with guanylate cyclase activity in vitro. FEBS Letters 585, 2693–2697.

Munné-Bosch S, Peñuelas J. 2003. Photo- and antioxidative protection by abscisic acid and acts upstream of reactive oxygen species production in sorghum responses to salinity. Planta 215, 2015–2023.

Nakamura K, Fujita Y, Kanamori N, et al. 2009. Three Arabidopsis SnRK2 protein kinases, SnRK2D/SnRK2.2, SnRK2E/SnRK2.6/OST1 and SnRK2P/SnRK2.3, involved in ABA signaling are essential for the control of seed development and dormancy. Plant & Cell Physiology 50, 1345–1363.

Nambara E, Marion-Poll A. 2002. Nitric oxide is a novel component of abscisic acid signaling in stomatal guard cells. Plant Physiology 128, 13–16.

Nelson MJ. 1987. The nitric oxide complex of ferrous soybean lipoygenase-1. Substrate, pH, and ethanol effects on the active-site iron. Journal of Biological Chemistry 262, 12137–12142.

Noguchi H. 2014. Seed dormancy and germination—emerging mechanisms and new hypotheses. Frontiers in Plant Science 5, 233.

Nott A, Watson PM, Robinson JD, Repoldi L, Riccio A. 2008. S-Nitrosylation of histone deacetylase 2 induces chromatin remodelling in neurons. Nature 455, 411–415.

Okamoto M, Kuwahara A, Seo M, Kusihito T, Asami T, Hirai N, Kamiya Y, Koshiba T, Nambara E. 2006. CYP707A1 and CYP707A2, which encode abscisic acid hydroxylases, are indispensable for proper control of seed dormancy and germination in Arabidopsis. Plant Physiology 141, 97–107.

Okuda K, Ito A, Uehara T. 2015. Regulation of histone deacetylation activity via S-nitrosylation. Biological & Pharmaceutical Bulletin 38, 1434–1437.

Ortega-Galisteo AP, Rodriguez-Serrano M, Pazmiño DM, Gupta DK, Sandalio LM, Romero-Puertas MC. 2012. S-Nitrosylated proteins in pea (Pisum sativum L.) leaf peroxisomes: changes under abiotic stress. Journal of Experimental Botany 63, 2089–2103.

Pál M. 2002. Effect of salicylic acid during heavy metal stress. Acta Biologica Szegediensis 46, 119–120.

Palmieri MC, Lindermayr C, Bauwe H, Steinhauser C, Durner J. 2010. Regulation of plant glycine decarboxylase by S-nitrosylation and glutathionylation. Plant Physiology 152, 1514–1528.

Palmieri MC, Sell S, Huang X, Scherf M, Werner T, Durner J, Lindermayr C. 2008. Nitric oxide-responsive genes and promoters in Arabidopsis thaliana: a bioinformatics approach. Journal of Experimental Botany 59, 177–186.

Park SY, Fung P, Nishimura et al. 2009. Abscisic acid inhibits type 2C protein phosphatases via the PYR/PYL family of START proteins. Science 324, 1068–1071.

Paris R, Iglesias MJ, Terrile MC, Casalongué CA. 2013. Functions of S-nitrosylation in plant hormone networks. Frontiers in Plant Science 4, 294.

Perazzoli M, Dominici P, Romero-Puertas MC, Zago E, Zeier J, Sonoda M, Lamb C, Delellonde M. 2004. Arabidopsis nonsymbiotic hemoglobin AB1 modulates nitric oxide bioactivity. The Plant Cell 16, 2785–2794.

Peirats-Llobet M, Han SK, Gonzalez-Guzman M, Jeong CW, Rodriguez L, Belda-Palazon B, Wagner D, Rodriguez PL. 2016. A direct link between abscisic acid signaling and the chloratin-remodeling ATPase BRAHMA via core ABA signaling pathway components. Molecular Plant 9, 136–147.

Pieterse CM, Leon-Reyes A, Van der Ent S, Van Wees SC. 2009. Networking by small-molecule hormones in plant immunity. Nature Chemical Biology 5, 308–316.

Pieterse CM, van Wees SC, van Pelt JA, Knoester M, Maan R, Gerrits H, Weisbeek PJ, van Loon LC. 1998. A novel signaling pathway controlling induced systemic resistance in Arabidopsis. The Plant Cell 10, 1517–1520.

Polverari A, Molesini B, Pezzotti M, Buonauro R, Marte D, Delledonne M. 2003. Nitric oxide-mediated transcriptional changes in Arabidopsis thaliana. Molecular Plant-Microbe Interactions 16, 1094–1105.

Puyaubert J, Baudouin E. 2014. New clues for a cold case: nitric oxide response to low temperature. Plant, Cell & Environment 37, 2623–2630.

Radi R. 2004. Nitric oxide, oxidants, and protein tyrosine nitration. Proceedings of the National Academy of Sciences, USA 101, 4003–4008.

Reeves WM, Lynch TJ, Mobin R, Finkelstein RR. 2011. Direct targets of the transcription factors ABA-insensitive (ABI4) and ABI5 reveal synergistic action by ABI4 and several bZIP ABA response factors. Plant Molecular Biology 75, 347–363.

Rivas-San Vicente M, Plasencia J. 2011. Salicylic acid beyond defence: its role in plant growth and development. Journal of Experimental Botany 62, 3321–3338.

Romero-Puertas MC, Laxa M, Matté A, Zainotto F, Finkemeier I, Jones AM, Perazzoli M, Vavasseur A, Dietz KJ, Delellonde M. 2007. S-Nitrosylation of peroxiredoxin II E promotes peroxynitrite-mediated tyrosine nitration. The Plant Cell 19, 4120–4130.

Romero-Puertas MC, Rodriguez-Serrano M, Sandalio LM. 2013. Protein S-nitrosylation in plants under abiotic stress: an overview. Frontiers in Plant Science 4, 373.
Running MP, Meyerowitz EM. 1996. Mutations in the PERIANTHIA gene of Arabidopsis specifically alter floral organ number and initiation pattern. Development 122, 1261–1269.

Rustén-C, Eguren MC, Díaz M, Chabannes M, Martínez MC. 2007. S-Nitrosothiol reductase affords protection against pathogens in Arabidopsis, both locally and systemically. Plant Physiology 143, 1282–1292.

Ryu H, Cho H, Bae W, Hwang I. 2014. Control of early seedling development by BES1/TPL/HDA19-mediated epigenetic regulation of ABI3. Nature Communications 5, 4138.

Saez A, Rodrigues A, Santiago J, Rubio S, Rodríguez PL. 2008. HAB1–SWI38 interaction reveals a link between ascorbic acid signaling and putative SWI/SNF chromatin-remodeling complexes in Arabidopsis. The Plant Cell 20, 2972–2988.

Sainz M, Calvo-Beguerra L, Pérez-Rontomé C, Wienkoop S, Abián J, Staudinger C, Bartesaghi S, Radi R, Becana M. 2015. Lighthemoglobin is nitrated in functional legume nodules in a tyrosine residue within the heme cavity by a nitrite/peroxide-dependent mechanism. The Plant Journal 81, 723–735.

Sanz L, Albertos P, Mateos I, Sánchez-Vicente I, Lechón T, Fernández-Marcos M, Lorenzo O. 2015. Nitric oxide (NO) and phytohormones cross-talk during early plant development. Journal of Experimental Botany 66, 2857–2868.

Sarah G, Hou G, Baird LM, Mitchell RB. 2007. Reactive oxygen species, ABA and nitric oxide interactions on the germination of warm-season C4-grasses. Planta 226, 697–708.

Sarkar S, Das A, Khandagale P, Maiti IB, Chattopadhyay S, Dey N. 2018. Interaction of Arabidopsis TGA3 and WRKY63 transcription factors on Cestrum yellow leaf curling virus (CmYLCV) promoter mediates salicylic acid-dependent gene expression in plants. Planta 247, 181–199.

Sato A, Sato Y, Fukao Y, et al. 2009. Threonine at position 306 of the KAT1 potassium channel is essential for channel activity and is a target site for ABA-activated SnRK2/OST1/SnRK2;6 protein kinase. The Biochemical Journal 424, 439–448.

Scheler C, Durner J, Astier J. 2013. Nitric oxide and reactive oxygen species in plant biotic interactions. Current Opinion in Plant Biology 16, 534–539.

Sedgwick SG, Smerdon SJ. 1999. The ankyrin repeat: a diversity of interactions on a common structural framework. Trends in Biochemical Sciences 24, 311–316.

Serpa V, Vernal J, Lamattina L, Grotewold E, Lamattina L, Cassia R, Terenzi H. 2007. Inhibition of AtMYB23 DNA-binding by nitric oxide involves coxyline S-nitrosylation. Biochemical and Biophysical Research Communications 361, 1048–1053.

Shi Q, Bao Z, Zhu Z, Ying Q, Qian Q. 2013. The salicylic acid receptor NPR3 is a negative regulator of the transcriptional defense response during early flower development in Arabidopsis. Molecular Plant 6, 802–816.

Simontacchi M, Jasid S, Puntarulo S. 2004. Nitric oxide generation during early germination of sorghum seeds. Plant Science 167, 839–847.

Singh HP, Kaur S, Batish DR, Sharma VP, Sharma N, Kohli RK. 2009. Nitric oxide alleviates arsenic toxicity by reducing oxidative damage in the roots of Oryza sativa (rice). Nitric Oxide: Biology and Chemistry 20, 289–297.

Singh S, Tripathi DK, Singh S, Sharma S, Dubey NK, Chauhan DK, Vaculik M. 2017. Toxicity of aluminum on various levels of plant cells and organisms. A review: Environmental and Experimental Botany 137, 177–193.

Skubacz A, Daszkowska-Golec A, Szarejko I. 2016. The role and regulation of ABIs (ABA-Insensitive S) in plant development, abiotic stress responses and phytohormone crosstalk. Frontiers in Plant Science 7, 1884.

Slaymaker DH, Navarre DA, Clark D, del Pozo O, Martin GB, Klessig DF. 2002. The tobacco salicylic acid-binding protein 3 (SABP3) is the chloroplast carbonic anhydrase, which exhibits antioxidant activity and plays a role in the hypersensitive defense response. Proceedings of the National Academy of Sciences, USA 99, 11640–11645.

Smallwood HS, Louttre NM, Boscheck CB, Bigelow DJ, Smith RD, Pasa-Tolic L, Squier TC. 2007. Identification of a denitrase activity against calmodulin in activated macrophages using high-field liquid chromatography–FTICR mass spectrometry. Biochemistry 46, 10498–10505.

Sokolovski S, Blatt MR. 2004. Nitric oxide block of outward-rectifying K+ channels indicates direct control by protein nitrosylation in guard cells. Plant Physiology 136, 4275–4294.

Song F, Goodman RM. 2001. Activity of nitric oxide is dependent on, but is partially required for function of, salicylic acid in the signaling pathway in tobacco systemic acquired resistance. Molecular Plant-Microbe Interactions 14, 1458–1462.

Song L, Zhao H, Hou M. 2013. Involvement of nitric oxide in acquired thermotolerance of rice seedlings. Russian Journal of Plant Physiology 60, 785–790.

Souza JM, Daikhin E, Yudkoff M, Raman CS, Ischiropoulos H. 1999. Factors determining the selectivity of protein tyrosine nitration. Archives of Biochemistry and Biophysics 371, 169–178.

Spoel SH, Koornneef A, Claessens SM, et al. 2003. NPR1 modulates cross-talk between salicylate- and jasmonate-dependent defense pathways through a novel function in the cytosol. The Plant Cell 15, 760–770.

Spoel SH, Mou Z, Tada Y, Spivey NW, Genschik P, Dong X. 2009. Proteasome-mediated turnover of the transcription coactivator NPR1 plays dual roles in regulating plant immunity. Cell 137, 860–872.

Stotz HU, Müller S, Zoeller M, Mueller MJ, Berger S. 2013. TGA transcription factors and jasmonate-independent COI1 signalling regulate specific plant responses to reactive oxygen species. Journal of Experimental Botany 64, 963–975.

Sun T, Gusta L, Zhang Q, Ding P, Jetter R, Zhang Y. 2018. TGACG-BINDING FACTOR 1 (TGA1) and TGA4 regulate salicylic acid and piperocic acid biosynthesis by modulating the expression of SYSTEMIC ACQUIRED RESISTANCE DEFICIENT 1 (SARD1) and CALMODULIN-BINDING PROTEIN 60g (CBP60g). New Phytologist 217, 344–354.

Tada Y, Spoel SH, Pajerowska-Mukhtar K, Mou Z, Song J, Wang C, Zou J, Dong X. 2008. Plant immunity requires conformational changes [corrected] of NPR1 via S-nitrosylation and thiooxidation. Science 321, 952–956.

Tavares CP, Vernal J, Delena RA, Lamattina L, Cassia R, Terenzi H. 2014. S-Nitrosylation influences the structure and DNA binding activity of AtMYB30 transcription factor from Arabidopsis thaliana. Biochimica et Biophysica Acta 1844, 810–817.

Terrile MC, Paris R, Calderón-Villalobos LI, Iglesias MJ, Lamattina L, Estelle M, Casalongué CA. 2012. Nitric oxide influences auxin signaling through S-nitrosylation of the Arabidopsis TRANSPORT INHIBITOR RESPONSE 1 auxin receptor. The Plant Journal 70, 492–500.

Tezuka K, Tajti T, Hayashi T, Sakata Y. 2013. A novel abii5 allele reveals the importance of the conserved Aai in the C3 domain for regulation of downstream genes and salt tolerance during germination in Arabidopsis. Plant Signaling & Behavior 8, e23455.

Thiel J, Rolletschek H, Friedel S, Lunn JE, Feyl R, Tsrichesch H, Müller M, Borisjuk L. 2011. Seed-specific elevation of non-symbiotic hemoglobin AtHb1: beneficial effects and underlying molecular networks in Arabidopsis thaliana. BMC Plant Biology 11, 48.

Torres MA, Dangl JL. 2005. Functions of the respiratory burst oxidase in biotic interactions, abiotic stress and development. Current Opinion in Plant Biology 8, 397–403.

Uchida A, Jagendorf AT, Hibino T, Takabe T, Takabe T. 2002. Effects of hydrogen peroxide and nitric oxide on both salt and heat stress tolerance in rice. Plant Science 163, 513–523.

Umezawa T, Sugiyama N, Mizoguchi M, Hayashi S, Myouga F, Yamaguchi-Shinozaki K, Ishihama Y, Hirayama T, Shinozaki K. 2009. Type 2C protein phosphatases directly regulate abscisic acid-activated protein kinases in Arabidopsis. Proceedings of the National Academy of Sciences, USA 106, 17588–17593.

Uno Y, Furihata T, Abe H, Yoshida R, Shinozaki K, Yamaguchi-Shinozaki K. 2000. Arabidopsis basic leucine zipper transcription factors involved in an abscisic acid-dependent signal transduction pathway under drought and high-salinity conditions. Proceedings of the National Academy of Sciences, USA 97, 11632–11637.

Vahisalu T, Kollist H, Wang YF, et al. 2008. SLAC1 is required for plant guard cell S-type anion channel function in stomatal signalling. Nature 452, 487–491.
Vanacker H, Lu H, Rate DN, Greenberg JT. 2001. A role for salicylic acid and NPR1 in regulating cell growth in Arabidopsis. The Plant Journal 28, 290–216.

Vandelle E, Delledonne M. 2011. Peroxynitrite formation and function in plants. Plant Science 181, 534–539.

Vandelle E, Ling T, Imanifard Z, Liu R, Delledonne M, Bellin D. 2016. Nitric oxide signaling during the hypersensitive disease resistance response. Advances in Botanical Research 77, 219–243.

dan van der Linde K, Gutsche N, Leffers HM, Lindermayr C, Müller B, Holtgrefe S, Scheibe R. 2011. Regulation of plant cytosolic aldolase functions by redox-modifications. Plant Physiology and Biochemistry 49, 946–957.

dan van der Zaal BJ, Droog FN, Pieterse FJ, Hooykaas PJ. 1996. Auxin-sensitive elements from promoters of tobacco GST genes and a consensus as-I-like element differ only in relative strength. Plant Physiology 110, 79–88.

Verslues PE, Bray EA. 2006. Role of abscisic acid (ABA) and Arabidopsis thaliana ABA-insensitive loci in low water potential-induced ABA and proline accumulation. Journal of Experimental Botany 57, 201–212.

Vicente J, Mendiondo GM, Movahedi M, et al. 2017. The Cys-Arg/N-end rule pathway is a general sensor of abiotic stress in flowering plants. Current Biology 27, 3183–3190.e4.

Vicente J, Mendiondo GM, Pauwels J, et al. 2019. Distinct branches of the N-end rule pathway modulate the plant immune response. New Phytologist 221, 988–1000.

Vlad F, Rubio S, Rodrigues A, Sirichandra C, Belin C, Robert N, Leung J, Rodriguez PL, Laurrière C, Merlot S. 2009. Protein phosphatases 2C regulate the activation of the Snf1-related kinase OST1 by abscisic acid in Arabidopsis. The Plant Cell 21, 3170–3184.

Wang P, Du Y, Hou YJ, Zhao Y, Hsu CC, Yuan F, Zhu X, Tao WA, Song CP, Zhu JK. 2015a. Nitric oxide negatively regulates abscisic acid signaling in guard cells by S-nitrosylation of OST1. Proceedings of the National Academy of Sciences, USA 112, 613–618.

Wang P, Zhu JK, Lang Z. 2015b. Nitric oxide suppresses the inhibitory effect of abscisic acid on seed germination by S-nitrosylation of SnRK2 proteins. Plant Signaling & Behavior 10, e1031939.

Wang YQ, Feechan A, Yun BW, et al. 2009. S-nitrosylation of AOSABP3 antagonizes the expression of plant immune. Journal of Biological Chemistry 284, 2131–2137.

Withers J, Dong X. 2016. Posttranslational modifications of NPR1: a single protein playing multiple roles in plant immunity and physiology. PLoS Pathogens 12, e1005707.

Wu Y, Zhang D, Chu JY, Boyle P, Wang Y, Brindle ID, De Luca V, Després C. 2012. The Arabidopsis NPR1 protein is a receptor for the plant defense hormone salicylic acid. Cell Reports 1, 659–677.

Xu M, Hu T, McKim SM, Murrell J, Haughn GW, Heworth SR. 2010. Arabidopsis BLADE-ON-PETIOLE1 and 2 promote floral meristem fate and determinacy in a previously undefined pathway targeting APETALA1 and AGAMOUS-LIKE24. The Plant Journal 63, 974–989.

Xuan Y, Zhou S, Wang L, Cheng Y, Zhao L. 2010. Nitric oxide functions as a signal and acts upstream of AtCaM3 in thermotolerance in Arabidopsis seedlings. Plant Physiology 153, 1895–1900.

Xue Y, Liu Z, Gao X, Jin C, Wen L, Yao X, Ren J. 2010. GPS-SNO: computational prediction of protein S-nitrosylation sites with a modified GPS algorithm. PLoS One 5, e11290.

Yang H, Mu J, Chen L, Feng J, Hu J, Li Z, Zhou JM, Zuo J. 2015. S-Nitrosylation positively regulates ascorbate peroxidase activity during plant stress responses. Plant Physiology 167, 1604–1615.

Yoshida R, Umezawa T, Mizoguchi T, Takahashi S, Takahashi F, Shinozaki K. 2006. The regulatory domain of SnRK2E/OST1/SnRK2.6 interacts with AB1 and integrates abscisic acid (ABA) and osmotic stress signals controlling stomatal closure in Arabidopsis. Journal of Biological Chemistry 281, 5310–5318.

Yoshida S, Ito M, Callis J, Nishida I, Watanabe A. 2002. A delayed leaf senescence mutant is defective in arginyl-tRNA:protein arginyltransferase, a component of the N-end rule pathway in Arabidopsis. The Plant Journal 32, 129–137.

Yoshida T, Fujita Y, Maruyama K, Mogami J, Todaka D, Shinozaki K, Yamaguchi-Shinozaki K. 2015. Four Arabidopsis ARET/ABF transcription factors function predominantly in gene expression downstream of SnRK2 kinases in abscisic acid signaling in response to osmotic stress. Plant, Cell & Environment 38, 35–49.

Yoshida T, Fujita Y, Sayama H, Kidokoro S, Maruyama K, Mizoi J, Shinozaki K, Yamaguchi-Shinozaki K. 2010. ARET1, ARET2, and ABF3 are master transcription factors that cooperatively regulate ABA-dependent ABA signaling involved in drought stress tolerance and require ABA for full activation. The Plant Journal 61, 672–685.

Yun BW, Feechan A, Yin M, et al. 2011. The Cys-Arg/N-end rule regulates cell death in plant immunity. Nature 478, 264–268.

Zaffagnini M, Morisse S, Bedhomme M, Marchand CH, Festa M, Rouhier N, Lemaire SD, Trost P. 2013. Mechanisms of nitrosylation and denitrosylation of cytoplasmic glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana. Journal of Biological Chemistry 288, 22777–22789.

Zander M, Chen S, Imkampe J, Thurow C, Gatz C. 2012. Repression of the Arabidopsis thaliana jasmonic acid/ethylene-induced defense pathway by TGA-interacting glutaredoxins depends on their C-terminal ALWL motif. Molecular Plant 5, 831–840.

Zander M, La Camera S, Lamotte O, Métraux JP, Gatz C. 2010. Arabidopsis thaliana class-II TGA transcription factors are essential activators of jasmonic acid/ethylene-induced defense responses. The Plant Journal 61, 200–210.

Zander M, Thurow C, Gatz C. 2014. TGA transcription factors activate the salicylic acid-suppressible branch of the ethylene-induced defense response by regulating ORA59 expression. Plant Physiology 165, 1671–1683.

Zhan N, Wang C, Chen L, et al. 2018. S-Nitrosylation targets GSNO reductase for selective autophagy during hypoxia responses in plants. Molecular Cell 71, 142–154.e6.

Zhang H, Gannon L, Hassall KL, Deery MJ, Gibbs DJ, Holdsworth MJ, van der Hoorn RAL, Lilley KS, Theodoulou FL. 2018a. N-terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway. New Phytologist 218, 1106–1126.

Zhang H, Gannon L, Jones PD, Rundle CA, Hassall KL, Gibbs DJ, Holdsworth MJ, Theodoulou FL. 2018b. Genetic interactions between ABA signaling and the Arg/N-end rule pathway during Arabidopsis seedling establishment. Scientific Reports 8, 15192.

Zhang Y, Tessaro MJ, Lassner M, Li X. 2003. Knockout analysis of Arabidopsis transcription factors TGA2, TGA6, and TGA6 reveals their redundant and essential roles in systemic acquired resistance. The Plant Cell 15, 2647–2653.

Zhang ZW, Luo S, Zhang GC, et al. 2017. Nitric oxide induces mono-saccharide accumulation through enzyme S-nitrosylation. Plant, Cell & Environment 40, 1834–1848.

Zhao C, Cai S, Wang Y, Chen ZH. 2016. Loss of nitrate reductases NIA1 and NIA2 impairs stomatal closure by altering genes of core ABA signaling components in Arabidopsis. Plant Signaling & Behavior 11, e1183088.

Zhao M, Yang S, Liu X, Wu K. 2015. Arabidopsis histone demethylases LDL1 and LDL2 control primary seed dormancy by regulating DELAY OF GERMINATION 1 and ABA signaling-related genes. Frontiers in Plant Science 6, 159.

Zhao MG, Chen L, Zhang LL, Zhang WH. 2009. Nitric reductase-dependent nitric oxide production is involved in cold acclimation and freezing tolerance in Arabidopsis. Plant Physiology 151, 755–767.

Zhou M, Wang W, Karapetyan S, Mwimba M, Marqués J, Buchler NE, Dong X. 2015. Redox rhythm reinforces the circadian clock to gate immune responses. Nature 523, 472–476.

Zhou ZS, Guo K, Elbaz AA, Yang ZM. 2000. Salicylic acid alleviates mercury toxicity by preventing oxidative stress in roots of Medicago sativa. Environmental and Experimental Botany 45, 27–34.

Zogas V, Tanou G, Filippou P, Diamantidis G, Vasilakakis M, Fotopoulos V, Molassiotis A. 2013. Nitrosative responses in citrus plants exposed to six abiotic stress conditions. Plant Physiology and Biochemistry 68, 115–126.