



NO Is Not the Same as GSNO in the Regulation of Fe Deficiency Responses by Dicot Plants

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Abstract: Iron (Fe) is abundant in soils but with a poor availability for plants, especially in calcareous soils. To favor its acquisition, plants develop morphological and physiological responses, mainly in their roots, known as Fe deficiency responses. In dicot plants, the regulation of these responses is not totally known, but some hormones and signaling molecules, such as auxin, ethylene, glutathione (GSH), nitric oxide (NO) and S-nitrosoglutathione (GSNO), have been involved in their activation. Most of these substances, including auxin, ethylene, GSH and NO, increase their production in Fe-deficient roots while GSNO, derived from GSH and NO, decreases its content. This paradoxical result could be explained with the increased expression and activity in Fe-deficient roots of the GSNO reductase (GSNOR) enzyme, which decomposes GSNO to oxidized glutathione (GSSG) and NH₃. The fact that NO content increases while GSNO decreases in Fe-deficient roots suggests that NO and GSNO do not play the same role in the regulation of Fe deficiency responses. This review is an update of the results supporting a role for NO, GSNO and GSNOR in the regulation of Fe deficiency responses. The possible roles of NO and GSNO are discussed by taking into account their mode of action through post-translational modifications, such as S-nitrosylation, and through their interactions with the hormones auxin and ethylene, directly related to the activation of morphological and physiological responses to Fe deficiency in dicot plants.

Keywords: dicotyledonous; ethylene; glutathione; GSNO reductase; iron; nitric oxide; *S*-nitrosoglutathione; Fe deficiency responses

1. Introduction

Iron (Fe) is very abundant in most soils, mainly as Fe^{3+} , although its availability to plants is low, especially in calcareous soils [1,2]. This low availability is mainly related to the low solubility of Fe oxides and hydroxides at a high pH [2]. Dicot (Strategy I) plants, such as Arabidopsis and the tomato, need to reduce Fe³⁺, abundant in most soils, to Fe²⁺, by means of a ferric reductase (encoded by *FRO2* in Arabidopsis) at the root surface, prior to its subsequent uptake through an Fe²⁺ transporter (encoded by *IRT1* in Arabidopsis; Refs. [3,4]). When grown under an Fe deficiency, dicot plants develop several physiological and morphological responses, mainly in roots, known as Fe deficiency responses and aimed at facilitating Fe mobilization and uptake (see Section 4; Refs. [3,5]). Once Fe has been acquired in enough quantity, Fe deficiency responses need to be switched off, to save energy and to avoid toxicity. It should be noted that the responses spend a lot of energy and resources for being activated and that Fe in excess can be very toxic. Among other effects, Fe can cause the formation of extremely reactive hydroxyl radicals through the Fenton reaction [4,6]. To solve both problems, a low availability of Fe in soils and toxicity when Fe is acquired in excess, plants have evolved sophisticated mechanisms to



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Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). tightly control Fe acquisition and homeostasis [4]. In dicot plants, several hormones and signaling molecules, including ethylene, auxin, nitric oxide (NO) and glutathione (GSH), have been implicated in the activation of most physiological and morphological responses to Fe deficiency [3,5,7–13]. All the above cited substances enhance their production in Fe-deficient roots and are closely inter-related in a complex manner since some of them can affect the production and/or distribution of the other ones (see Section 6; Refs. [8,9,14]). Paradoxically, *S*-nitrosoglutathione (GSNO), which is formed from GSH and NO, decreases its production in Fe-deficient roots, where it has also been involved in the regulation of Fe deficiency responses [11,15,16]. These results suggest that GSNO, which is considered a relatively stable store for NO and a vehicle for its long-distance transport [17], does not play exactly the same roles that NO does in the regulation of Fe-deficient responses.

2. NO and GSNO in Plants

NO is a simple gaseous molecule (NO) which, due to its free radical nature, can react with cellular targets to form reactive nitrogen species, such as *S*-nitrosothiols, including *S*-nitrosoglutathione (GSNO; see below; Ref. [18]). NO can also bind to transition metal ions, such as Fe or Cu, to form metal–nitrosyl complexes, and to fatty acids to form nitro-fatty acids, which play an important role in the adaptation of plants to abiotic stresses [19,20]. NO is lipophilic and can easily diffuse across membranes [21]. In the 1980s, NO was recognized as a signaling molecule in mammals and later on, around the 1990s, also in plants [19,21]. NO has been involved in a myriad of developmental and physiological processes of plants, including seed germination, stomatal closure, flower development, root branching and senescence [20,22–25]. In addition, NO has been implicated in the responses of plants to both biotic and abiotic stresses, including pathogen infection, salinity, drought stress, nutrient deficiencies, an excess of heavy metals and others (see Section 3; Refs. [20,22,23,26–32]).

NO synthesis has been reported in different plant organs, including roots, stems, leaves and flowers, and, at the subcellular level, both in the apoplast and in the symplast, and in different organelles, such as mitochondria, chloroplasts and peroxisomes [20,33]. NO can be synthesized by both enzymatic and non-enzymatic pathways [19,20,22,24,33]. In mammals, NO synthases (NOS) catalyze the conversion of L-arginine to NO and citrulline. However, although there is some evidence of NOS-like activity in plants, until now, no functional NOS protein has been isolated and characterized in higher plants [20,22]. It seems that, in plants, nitrate reductase (NR) plays the main role in the enzymatic NO production [19,20]. There are mutants impaired in NO production, including the Arabidopsis *nia1nia2* mutants, altered in the *NIA1* and *NIA2* genes, encoding NRs [19,34], and mutants that overproduce NO, such as the Arabidopsis *cue/nox1* mutants [19,35,36]. NO is usually detected and determined by using the permeable NO-sensitive fluorophore 4-amino-5-methylamino-2',7'-difluoro-fluorescein diacetate (DAF-FM DA) [13,34].

NO is considered a phytohormone for some authors [37] while other ones do not consider it as such since no specific receptors for NO have been identified [21]. The action of NO is mainly mediated with its roles through post-translational modifications, including tyrosine nitration, metal nitrosylation and *S*-nitrosylation [19,25]. Tyrosine nitration is mediated with the peroxynitrite anion (OONO⁻), formed from NO and a superoxide radical, while metal nitrosylation is due to the interaction of NO with metalloproteins [19,25]. *S*-nitrosylation is a redox-based covalent addition of NO to the sulfhydryl group of a cysteine on a target protein and is the most prominent of the post-translational modifications caused with NO [19,25]. It can affect protein activity (activation or inhibition), translocation and protein function [38]. *S*-nitrosylation. The nitrosylation is considered a non-enzymatic process mediated directly with NO, or indirectly with *S*-nitrosothiols (e.g., GSNO) or other NO-derived compounds [19,25]. The specificity of the protein *S*-nitrosylation is mainly determined with the structure of the target protein and the local NO concentration in its vicinity [19]. Denitrosylation is mediated by the thioredoxin system and the

transnitrosylation, the transfer of a NO group from one protein to another, is mediated by transnitrosylases, not yet found in plants [19,25].

As previously stated, S-nitrosothiols are NO-derived compounds. Among them, GSNO is the most abundant low-molecular one and is formed non-enzymatically from glutathione (GSH) and NO under aerobic conditions (Figure 1; Refs. [17,18,32,39]. GSH and NO are inter-related since NO can influence GSH synthesis in roots [40]. Since the NO lifetime is relatively short (less than 10 s), GSNO is considered a relatively stable store for NO, being its main reservoir and a vehicle for its long-distance transport [17,18,39,41]. The levels of GSNO can be determined with several methods, including LC-ES/MS, chemiluminescencebased methods and a diamino-rhodamine fluorimetric-based method [15,42]. GSNO is tightly controlled with the GSNO reductase (GSNOR) enzyme, which decomposes it to oxidized glutathione (GSSG) and NH₃ (Figure 1; Refs. [41,43,44]). GSNOR is a class III Alcohol Dehydrogenase, which was originally identified as a GSH-dependent Formaldehyde Dehydrogenase [18,43,45–48]. GSNOR is expressed in both roots and shoots [49]. In Arabidopsis, GSNOR1 is the only gene encoding this enzyme [50]. There are Arabidopsis mutants that present a loss of AtGSNOR1 function, such as the gsnor1-3 mutant, which has higher GSNO contents, and Arabidopsis mutants that overexpress *AtGSNOR1*, such as the gsnor1-1 mutant, which has lower GSNO contents [19,36,50]. Besides mutants, there are also transgenic lines that overexpress GSNOR, and transgenic lines where GSNOR is blocked by RNAi [51–53]. In addition to its decomposition with GSNOR, GSNO can be non-enzymatically decomposed to generate NO and GSSG in the presence of reductants (including GSH and ascorbate) and Cu (Figure 1; Refs. [17,18,32]).



Figure 1. Inter-relationship between ethylene, auxin, GSH, NO and GSNO in Fe-deficient roots of dicot plants. Fe deficiency causes an increased production of ethylene (ET), auxin, glutathione (GSH) and nitric oxide (NO) in dicot roots, as well as an increased GSNOR expression and activity, which diminishes *S*-nitrosoglutathione (GSNO) content. GSNO can be enzymatically decomposed (1) to oxidized glutathione (GSSG) and NH₃ by GSNOR or non-enzymatically (2) to generate GSSG and NO. NO (also the one originated from GSNO) and/or GSNO can influence ethylene synthesis by positively affecting the transcription of the *MTK*, *SAMS*, *ACS* and *ACO* genes; by positively affecting ACO activity with *S*-nitrosylation; or by negatively affecting SAMS activity with *S*-nitrosylation. GSH itself can also affect ethylene synthesis by affecting the transcription of *ACS* genes and NO synthesis. NO can affect GSH synthesis, and both NO and ethylene can affect auxin accumulation, distribution and signaling. Based on [8,9,11,13–16,35,38,40,53–57]. Nsy: Nitrosylation (^ or \rightarrow : promotion; -||: inhibition). Green arrows and words indicate steps and compounds implicated in ethylene synthesis.

Similarly to NO, GSNO and, consequently, GSNOR have also been involved in the responses of plants to different biotic and abiotic stresses [27,39,43–45,48,50,52]. GSNOR activity generally increases under stress conditions [45,48]. Recently, Rudolf et al. [23] proposed that GSNO promotes the methylation of the repressive chromatin mark H3K9, which would impair the expression of stress-responsive genes. According to this proposal, GSNOR, by degrading GSNO, would positively affect the expression of stress-responsive genes [23].

3. Role of NO and GSNO in the Responses of Plants to Mineral Stresses

A mineral stress is related to the sub-optimal availability of essential elements or toxicity of essential and non-essential elements, including Al, Na, Cl and others [58]. As previously stated, both NO and GSNO/GSNOR participate in the responses of plants to many abiotic stresses, including mineral stresses, salinity, drought and others (see Section 2; Refs. [26,46,48]). In relation to mineral stresses, NO and/or GSNO have been implicated in several of them, including responses to heavy metals (e.g., Cu, Fe, Cd or Al; Refs. [27,32,59–61]), to metalloids [62], to salinity [37,63,64] or to nutrient deficiencies (see below). In general, NO production increases in roots under several mineral stresses. In addition, and similarly to what occurs with Fe deficiency (see Section 5), this increased MO production can be accompanied by an increased GSNOR activity and a decreased GSNO content. For example, Leterrier et al. [65] found increased NO and GSNOR activity in arsenic-treated *Arabidopsis* plants while GSNO decreased.

NO and GSNO/GSNOR have been found to play key roles in the regulation of Fe deficiency responses by dicot (Strategy I) plants (see Section 5) but also in responses and adaptations to other nutrient deficiencies [56,66–70]. NO has been involved in the regulation of responses to P deficiency, including the development of cluster roots and root hairs, and the upregulation of phosphate transporters [66,69]. In relation to S deficiency, NO improves the adaption of plants to the oxidative stress caused by this deficiency, probably by maintaining the redox state through the ascorbate-GSH cycle [70]. Under a Mg deficiency, as occurs with Fe and P deficiency, NO has been implicated in the development of subapical root hairs [56,67]. In the studies about the role of NO in the regulation of P, S or Mg deficiency responses, exogenous GSNO has been used as a NO donor but what rarely has been studied is the role of endogenous GSNO and GSNOR in the regulation of these responses [71]. Nonetheless, *GSNOR1* expression also increases in P- and S-deficient roots, as occurring under an Fe deficiency (see Section 5; Ref. [15]).

4. Fe Deficiency Responses in Dicot Plants

When grown under an Fe deficiency, dicot (Strategy I) plants develop several physiological and morphological responses, mainly in roots, known as Fe deficiency responses and aimed at facilitating Fe mobilization and uptake [3–5,72]. Among the physiological responses are an enhanced ferric reductase activity (due to a higher expression of the FRO gene); an enhanced Fe^{2+} uptake capacity (due to a higher expression of the *IRT1* gene); the acidification of the rhizosphere (due to a higher expression of HA (H⁺-ATPase) genes); and an increase in the synthesis and release of organic acids (e.g., citrate and malate), phenols (e.g., coumarins) and flavins to the medium [2–5,72–74]. The acidification facilitates the solubilization of Fe hydroxides and the functioning of the ferric reductase, which has an optimum pH around 5.0 [73]. Organic acids, phenols and flavins can act as chelating and/or reducing agents for Fe in the soil or inside the plant [2,3,74]. Among the morphological responses are the development of subapical root hairs, of cluster roots and of transfer cells, all of them aimed at increasing the surface of contact with the soil [3,9]. Both physiological and morphological responses are located in the subapical regions of the roots [3]. The activation of the Fe deficiency responses is not fully understood, but in recent years, several transcription factors (TFs) that participate in the upregulation of most of their associated genes have been found [3-6,72]. In Arabidopsis, the master regulator of most of these genes is FIT (bHLH29), a homolog of the tomato FER gene (Figure 2; Refs. [3,6]). The FIT regulatory network comprises other bHLH TFs of the Ib subgroup, including bHLH38, bHLH39, bHLH100 and bHLH101 (Figure 2). All of them have redundant functions and can interact with FIT to form heterodimers that activate the expression of the Fe acquisition genes *FRO2* and *IRT1* [4,5,72]. *FIT* is exclusively induced in roots in response to Fe deficiency while the other *Ib* bHLH genes cited above are induced in both roots and leaves in response to Fe deficiency [5].



Figure 2. Working model proposed to explain the role of ethylene, NO and GSNO in the regulation of Fe acquisition genes by Arabidopsis. Fe deficiency causes an increased production of ethylene (ET), glutathione (GSH) and nitric oxide (NO), and a decreased GSNO content (see Figure 1). Ethylene activates the transcription of the Fe acquisition genes FRO2 and IRT1 by affecting FIT transcription and activity through the EIN3/EIL1 TFs, which interact with the MEDIATOR TFs MED16 and MED25. FIT transcription could also be affected by GSNO through the GRF11 TF, and FIT stability with GSNO, perhaps through S-nitrosylation. NO/GSNO could also activate the transcription of the Ib bHLH genes, by affecting the S-nitrosylation of the SKB1 protein. When denitrosylated, SKB1 is an epigenetic negative modulator that controls the expression of the *lb bHLH* genes. GSNO could also affect the activity of the Ib bHLH TFs with their direct S-nitrosylation. FIT, along with Ib bHLH TFs, would activate FRO2 and IRT1 expression. ERF72, implicated in the inhibition of the expression of Fe acquisition genes, could be degraded by the N-degron (previously, N-end rule) pathway with the participation of NO. On the other hand, ERF72 can inhibit NO production. Based on [3,7,12,13,15,16,34,75-81]. (^ or \rightarrow : promotion; -: inhibition). Red lines indicate the processes probably affected by NO and blue lines indicate the ones probably affected by GSNO. NO (NblueOblue) indicates NO originated from GSNO while NO' (NredOblue) indicates NO originated from either NO or GSNO. Green lines and words indicate steps and components implicated in ethylene signaling.

The expression of *FIT* and *Ib bHLHs* is induced with homo- and hetero-dimers formed with IVc-subgroup bHLH TFs: bHLH34, bHLH104, bHLH105 (ILR3) and bHLH115 [4,72]. Upstream of the IVc subgroup, there are other bHLH TFs, such as bHLH121 (URI), and the BRUTUS (BTS) and BTS-LIKE (BTSL) proteins [4,72]. BTS and BTSL proteins are E3 ligases, which act as potential Fe sensors that interact with IVc bHLH TFs and FIT, targeting them for proteasomal degradation. Since FIT and the IVc bHLH TFs act as positive regulators

of Fe deficiency responses, BTS and BTSL proteins act as negative regulators [4,72,82–84]. In recent years, it has been found that some peptides or small proteins, called IMAs (Iron Man/Fe-Uptake-Inducing Peptide: IMA/FEP), play a key role in the activation of Fe deficiency responses [83–87]. IMAs could impair the interaction of BTS and BTSL proteins with FIT and IVc bHLH TFs, thus diminishing their proteasomal degradation and, consequently, favoring the activation of Fe deficiency responses in Arabidopsis roots [83,84].

5. Role of NO and GSNO in the Regulation of Fe Deficiency Responses by Dicot Plants

The influence of hormones and signaling molecules in the regulation of morphological and physiological responses to Fe deficiency by dicot plants has been studied since the beginning of the 1980s, with the pioneering works of Landsberg, Römheld and Marschner suggesting a role for auxin in such a process (reviewed in Romera et al. [9]). After that, Romera and Alcántara [88], based on the use of ethylene inhibitors and precursors, proposed a similar role for the plant hormone ethylene, another simple gaseous molecule (C_2H_4), in such a regulation. The ethylene hypothesis has been further confirmed with different experimental results, including the higher ethylene production of Fe-deficient roots; the higher expression of both ethylene synthesis and signaling genes in Fe-deficient roots; the role of ethylene in the expression of many key Fe-related genes, including *FIT(FER)*, *FRO* and *IRT1*; and the alteration of Fe deficiency responses in ethylene defective mutants (see Section 6; Refs. [3,7,9,89–91]). Ethylene has also been implicated in the regulation of the responses to other nutrient deficiencies [92–95].

Several years after the implication of ethylene in the regulation of Fe deficiency responses, it was found that NO played a similar role in such a regulation (see Section 6; Ref. [34]). These authors showed that NO production was enhanced in Fe-deficient tomato roots; that the NO-scavenger 2-(4-carboxyphenyl)-4,4,5,5-tetramethylimidazoline-1-oxyl-3oxide (cPTIO) blocked the enhanced ferric reductase activity and the expression of several key Fe acquisition genes, including FER, FRO1 and IRT1, in Fe-deficient tomato roots; that the NO donor GSNO induced the development of subapical root hairs and the expression of several Fe acquisition genes in roots of tomato plants grown under low Fe conditions; and that NO-deficient mutants, such as the NR-deficient tomato *nia* mutants, were impaired in the activation of Fe deficiency responses [34]. After that, similar results have been found by other authors in different dicot plant species by determining NO in roots; by using NO scavengers (e.g., cPTIO), NR inhibitors (e.g., tungstate) or NOS inhibitors (e.g., L-NAME); by using NO donors (e.g., sodium nitroprusside, diethylamine-NONOate or GSNO); and by using NO-defective mutants [7,10,11,13,15,16,20,24,66,71,76,96–102]. It should be noted that sodium nitroprusside is not an adequate NO donor for Fe studies since it contains an Fe atom [20].

Besides the above results, it has also been found that NO participates in other processes related to Fe deficiency responses and/or to Fe acquisition. In relation to Fe deficiency responses, NO has also been implicated in the stabilization of the FIT protein, probably because, in its presence, FIT protein is less likely to be a target of proteasomal degradation [76]. Additionally, it has been found that the 14-3-3 protein GRF11 acts downstream of NO to upregulate *FIT* expression, which can activate the expression of Fe acquisition, NO has been implicated in Fe immobilization in the root apoplast by decreasing the pectin methylation of the cell wall [104,105].

In addition to NO, GSNO has also been involved in the regulation of Fe deficiency responses similarly to what occurs with GSH [10–13,15,16]. Some authors have proposed that GSNO specifically mediates the Fe deficiency signal through FIT (see Section 7; Ref. [16]). Very recently, Shee et al. [12] found that FIT and some Ib bHLH TFs, including bHLH38 and bHLH101, can be *S*-nitrosylated, probably by GSNO, which would improve their stability (Figure 2). The expression of the *Ib bHLH* genes can be negatively affected by the Shk1 binding protein 1 (SKB1/PRMT5), because of its positive effect on the chromatin package [3,106]. Since SKB1 can be nitrosylated [107], it is possible that NO/GSNO, through the *S*-nitrosylation of SKB1, could activate the expression of *Ib bHLH* genes (Figure 2; Refs. [3,106]). In supporting this view, several *Ib bHLH* genes, including *bHLH38*, *bHLH39* and *bHLH100*, are upregulated in leaves of the Arabidopsis *gsnor1-3* mutant, which has a higher GSNO content [44].

Both NO and GSH production, in the same way that ethylene does, increase in Fedeficient roots (Table 1; Refs. [9,11,15,34,66,101,108]). However, GSNO content, in contrast to its precursors GSH and NO, decreases in Fe-deficient Arabidopsis WT roots (Table 1; Refs. [11,15,16]). Moreover, GSNO levels in Fe-sufficient Arabidopsis *opt3-2* mutant roots and pea *dgl* mutant roots, which present the constitutive activation of Fe deficiency responses, are also lower than those in their respective Fe-sufficient WT roots [15]. So, it seems that increased NO but decreased GSNO is a prerequisite for the induction of Fe deficiency responses. These paradoxical results could be explained with the increased GSNOR activity in Fe-deficient roots of dicot plant species, such as Arabidopsis and the tomato [15,53], since GSNOR decomposes GSNO (see above). In accordance with these results, Fe-sufficient Arabidopsis *opt3-2* mutant roots (see above) present higher *GSNOR1* expression and activity than the Fe-sufficient WT ones [15]. In agreement with all these results, Wen et al. [53] found that *GSNOR* overexpression in tomato plants causes an enhancement of the ferric reductase activity and the upregulation of the Fe acquisition genes *FRO1* and *IRT1*.

Table 1. Effects of Fe deficiency and Fe excess in the production of ethylene (ET), glutathione (GSH), nitric oxide (NO) and *S*-nitrosoglutatione (GSNO) by roots of different dicot plant species.

	Fe Sufficiency	Fe Deficiency	Fe Excess	Plant Species	References
ET	+	+ + + +	+ + + +	Pea Cucumber Squash Arabidopsis (*)	[9,89,108–110]
GSH	+	+ + + +	+ + + +	Sugar beet Arabidopsis Rice (**)	[11,15,111]
NO	+	++++	+ + + +	Lupinus Tomato Arabidopsis Peanut	[15,66,101,104, 112]
GSNO	+ + + +	+ +	n.d.	Arabidopsis Pea	[11,15,16]

(*) Ramírez et al. [113] did not find increased GSH in Fe-deficient Arabidopsis roots; (**) rice presents characteristics of Strategy I (dicot) and Strategy II (graminaceous) plants [114]; n.d.: not determined. +: an arbitrary quantity; + +: Increase in quantity; + + + +: a significative higher quantity.

The role of NO in the regulation of Fe deficiency responses by dicot plants is also supported with other experimental results, besides the ones previously described. It has been found that beneficial rhizosphere microorganisms eliciting induced systemic resistance (ISR) can also induce Fe deficiency responses. The root-specific MYB72 TF, involved in both processes (ISR and Fe deficiency responses), and NO are required for the activation of both kinds of responses [115–118].

In addition to their role under Fe-deficient conditions, GSH and NO, similarly to ethylene, also play a role in the responses of plants to Fe excess. All these substances, ethylene, GSH and NO, increase their production upon Fe excess too (Table 1; Refs. [109–112]). In the case of GSNO, although it has not been determined under Fe excess conditions, it is known that GSNOR is required for root tolerance to Fe toxicity, probably by preventing cell death via inhibiting Fe-dependent nitrosative and oxidative cytotoxicity [60].

6. Interactions of NO and GSNO with Ethylene and Auxin in the Regulation of Fe Deficiency Responses by Dicot Plants

NO can interact with many hormones, such as strigolactones, salicylic acid, abscisic acid, auxin and ethylene, and signaling molecules, such as polyamines, reactive oxygen species and hydrogen sulfide, to exert its functions in the regulation of responses to biotic and abiotic stresses [18,29,33,55,71,119–124]. In the regulation of Fe deficiency responses by dicot plants, some of these interactions have already been described [8,9,24,71,105]. Nonetheless, to simplify the description of all the possible interactions, in this review, we will only describe the interactions of NO with ethylene and auxin. NO, ethylene and auxin have all been implicated in the activation of both morphological and physiological responses to Fe deficiency in dicot plants, and all of them activate the expression of similar key Fe acquisition genes [3,7–9,13,15,71,93,96,125]. In the case of NO and ethylene, all the Fe-related genes upregulated by NO in Fe-deficient roots of Arabidopsis and cucumber plants are similarly upregulated by ethylene [7,13]. Moreover, auxin, ethylene and NO have been described as the downstream signals more closely related to the direct activation of the morphological and physiological responses. As examples, the EIN3/EIL1 TFs, related to ethylene, directly interact with the master regulator FIT; the GRF11 protein, regulated with NO, affects *FIT* transcription; and auxin acts downstream of ethylene and NO in the development of subapical root hairs (Figure 2; Refs. [67,75,77,126]). Since hormones and signaling molecules are inter-related between them, it is possible that some other ones involved in the regulation of Fe deficiency responses could finally act through ethylene, auxin or NO [9,93,105].

As previously stated, ethylene participates in the activation of Fe deficiency responses by dicot plants (see Section 5). Ethylene is synthetized from the methionine amino acid, through a pathway including SAMS (SAM Synthetase), ACS (ACC Synthase) and ACO (ACC Oxidase) (Figure 1; Ref. [127]):

SAMS ACS ACO

Methionine \rightarrow SAM \rightarrow ACC \rightarrow Ethylene (ET)

Its proposed mode of action (Figure 2; Refs. [80,128]) is

ET-ET receptors \rightarrow CTR1-EIN2 \rightarrow EIN3/EILs \rightarrow ERFs \rightarrow ET responses

In this pathway, CTR1 is a kinase, EIN2 is a protein located in the endoplasmic reticulum membrane and EIN3, EILs and ERFs are TFs [80,128]. Mutants in the CTR1 protein present constitutive responses to ethylene while those mutated in EIN2 or EIN3 are insensitive to ethylene [80,128]. Very recently, our group [91] found that Arabidopsis *ein2* mutants are impaired in the upregulation of the Fe acquisition genes *FRO2* and *IRT1*. This clearly suggests that EIN2, and consequently ethylene, is implicated in the activation of Fe acquisition genes. Furthermore, it has been shown that EIN3 and EIL1, two TFs in the ethylene signaling pathway (see above), are implicated in the transcription and activity of the master regulator FIT (Figure 2; Refs. [75,126].

Since NO plays a similar role to ethylene in the regulation of Fe deficiency responses (see Section 5; Ref. [34]), the question arose as to whether NO acts downstream of ethylene, or ethylene acts downstream of NO, or if both act in conjunction. Results from our group and others have shown that ethylene, NO, GSH and GSNO are inter-related since each can influence the production of the others [7,8,13,14,56]. NO, GSNO or GSH applied to Fe-sufficient Arabidopsis plants greatly induced the expression in roots of many genes involved in ethylene synthesis, including *SAMS*, *ACS*, *ACO* and 5-methilthioribose kinase (*MTK*) (see Figure 1; Refs. [13,14]). The ethylene synthesis genes induced with NO are also induced under an Fe deficiency, which suggests that this deficiency probably upregulates them through NO. NO/GSNO could also affect ethylene synthesis with the *S*-nitrosylation of ethylene synthesis enzymes (Figure 1). The Arabidopsis *SAMS* isoform, *SAMS1*, but not *SAMS2* and *SAMS3*, can be reversibly inhibited with *S*-nitrosylation, which would impair

ethylene synthesis [15,38,55]. In contrast, the S-nitrosylation of an ACO enzyme in a tomato improves ethylene synthesis [57]. In the opposite direction, ACC (an ethylene precursor) applied to Fe-sufficient Arabidopsis and cucumber plants caused NO accumulation in the subapical region of their roots (Figure 1; Refs. [13,43]). Moreover, the application of ACC to the Arabidopsis ethylene-insensitive mutant ein2-5 did not cause this NO accumulation [91]. Similarly, NO accumulation in Mg-deficient roots is impaired in this ein2-5 mutant [56]. Ethylene probably increases NO content by activating enzymes involved in its synthesis, such as NR and NOS [56]. All these results suggest that ethylene influences NO accumulation and vice versa and agree with other nutrient-related root processes showing a mutual and generally synergistic effect between NO and ethylene [21,129]. This mutual influence could probably lead to the amplification of activating signals involved in the upregulation of Fe- and other nutrient-related genes. There are also some processes, including fruit ripening, de-etiolation and lateral root formation, that are regulated with NO/ethylene antagonism [21,64,130]. In the same way, ethylene can also negatively affect NO by increasing the NO scavenger Phytoglobin1 under hypoxia [131]. Besides ethylene synthesis, NO can also affect ethylene signaling. The ethylene response factor ERF72 (also named RAP2.3), which negatively regulates Fe deficiency responses in Arabidopsis [79], belongs to the group VII ERFs, which are sensors of NO and can be targeted for proteolysis degradation by the N-degron (previously named the N-end rule) pathway in the presence of NO [78]. Reciprocally, RAP2.3 can negatively control NO homeostasis and signaling (Figure 2; Ref. [81]).

In relation to GSNO, its interaction with ethylene is also feasible. As described above, the SAM Synthetase SAMS1, involved in ethylene synthesis, can be inhibited with S-nitrosylation [15,38,55]. In this way, higher GSNO levels (such as those found in Fe-sufficient roots) could contribute to the S-nitrosylation of the SAMS1 enzyme, and, consequently, to the inhibition of ethylene synthesis. In contrast, lower GSNO levels (such as those found in Fe-deficient WT roots and in Fe-sufficient *opt3-2* and *dgl* roots) could contribute to the denitrosylation of the SAMS1 enzyme and, consequently, to an increase in ethylene synthesis [15]. In supporting this view, silencing GSNOR in *Nicotiana attenuate*, which leads to a higher GSNO content, decreased the herbivore-induced accumulation of ethylene [132]. In the opposite direction, ethylene could decrease GSNO content since it has been shown that ACC (ethylene precursor) can induce GSNOR1 expression [15]. The possible relationship between GSNO/GSNOR and ethylene is also feasible because both GSNOR [133] and several ethylene synthesis enzymes, such as MTK (Figure 1), induced in Fe-deficient roots [7,9] are located in the phloem [134]. In fact, GSNO is presumably phloem-mobile [39]. All the above results would imply that ethylene could simultaneously increase NO accumulation while decreasing GSNO content [15].

Similar to ethylene, auxin is also inter-related with NO. Several works have found that auxin can induce some Fe deficiency responses in plants by acting through NO [8,96,97,103, 135,136]. In contrast, it has been shown that NO can affect auxin transport, accumulation and signaling [8,54,67,137]. Auxin can also interact with ethylene, since auxin can enhance ethylene synthesis by affecting ACS enzymes, while ethylene can affect auxin accumulation and distribution [8,67].

In conclusion, ethylene, auxin and NO/GSNO are closely inter-related in the regulation of Fe deficiency responses. In some cases, it seems that auxin acts upstream of NO/GSNO and ethylene, such as in the regulation of Fe acquisition genes (Figure 2), but in other ones, auxin probably acts downstream of NO/GSNO and ethylene, such as in the development of root hairs.

7. Why Is NO Not the Same as GSNO in the Regulation of Fe Deficiency Responses?

Since NO can react with GSH to generate GSNO, and GSNO can be decomposed to generate NO (Figure 1), it is difficult to assign a specific role to either NO or GSNO in the regulation of Fe deficiency responses, or in other processes. For example, upon the application of exogenous GSNO, we cannot know whether it will act by itself or by

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generating NO (Figure 1). Moreover, since GSH, NO and GSNO can stimulate ethylene synthesis (Figure 1), it is also difficult to know whether the final executor of their different effects on Fe deficiency responses is themselves or ethylene. A first attempt to decipher the different roles of NO and GSNO in the regulation of Fe deficiency responses by dicot plants is the one made by Dr. Yeh's group [16]. These authors, by using chemical screening, identified a small molecule, [3-amino-N-(3-methylphenyl)thieno [2,3-b]pyridine-2-carboxamide], named R7 ('R' denoting repressor) that downregulates *FIT* expression, and, consequently, *IRT1* and *FRO2* expression, but not the one of the *Ib* bHLH genes. R7 treatment did not affect cellular levels of NO or GSH but decreased the GSNO level in roots. Exogenously supplying GSNO, but not other NO donors, alleviated this inhibitory effect of R7 on *FIT* expression. After these results, the authors propose that GSNO specifically mediates the Fe deficiency signal to FIT while NO could mediate the signal to Ib bHLHs (Figure 2; Ref. [16]). Since *FIT* transcription can be activated by the GRF11 protein, which is upregulated with a GSNO treatment [77], it is possible that GSNO could mediate *FIT* transcription through the GRF11 protein while the one of *Ib* bHLH genes could be mediated with NO (Figure 2).

As stated above (see Section 5), it seems that increased NO but decreased GSNO in roots is a prerequisite for the induction of Fe deficiency responses. Nonetheless, it is also clear that GSNO content should not be too low, since R7, which inhibits GSNO accumulation, also blocks *FIT* transcription and the Fe deficiency responses depending on FIT [16]. In supporting this view, Guan et al. [51] found that *GSNOR* overexpression in Arabidopsis plants, which provokes a low GSNO content, causes a downregulation of the Fe acquisition gene *IRT1*. However, and as described in Section 5, Wen et al. [53] found that *GSNOR* overexpression in tomato plants causes an enhancement of the ferric reductase activity and the upregulation of the Fe acquisition genes *FRO1* and *IRT1*. So, in Arabidopsis, a lower GSNO content inhibits Fe deficiency responses while, in the tomato, it activates them. Perhaps, in Arabidopsis, *GSNOR* overexpression causes a too low GSNO content.

There are several possibilities to explain the differences between NO and GSNO. First, the NO lifetime is very short while GSNO is considered a relatively stable store for NO [17,18,39,41]. Second, the time course of NO and GSNO abundance after Fe starvation can be different: in fact, GSNOR is greatly upregulated in roots after very few hours of this deficiency [15]. Third, the NO and GSNO location can be different. Under an Fe deficiency, NO mainly accumulates in the subapical regions of the roots [13,118] while it is not yet known where the decrease in GSNO that occurs under this condition is located. At the cellular level, GSNOR is a nuclear and cytosolic enzyme while NO can also be synthesized in the apoplast or in organelles, such as chloroplasts [20,33,44,46,137]. Fourth, NO and GSNO do not always interact with the same protein thiols to cause *S*-nitrosylation [47,138]. Fifth, NO can also become covalently bound to transition metals (e.g., Fe), or to fatty acids (see Section 2; Refs. [19,20,36,39]). In fact, some authors consider that NO may have a wider range of biological activity relative to GSNO, and that both NO and GSNO can exhibit additive functions [36].

In the literature, there are results showing different effects of NO and GSNO on plant processes. As examples, NO causes salicylic acid accumulation while GSNO reduces its accumulation [39,52]; the phenotype of the Arabidopsis *gsnor1-3* mutant, which has higher GSNO contents, is different than the Arabidopsis *nox1* mutant, which overproduces NO [137].

8. Concluding Remarks and Future Perspectives

GSH, NO and GSNO have been involved in the activation of Fe deficiency responses by dicot plants. Both GSH and NO increase their production in Fe-deficient roots. However, GSNO, derived from GSH and NO, decreases its content in Fe-deficient roots. These paradoxical results could be explained with the increased expression and activity of the GSNOR enzyme, which decomposes GSNO, in Fe-deficient roots. The fact that NO content increases while GSNO decreases in Fe-deficient roots suggests that NO and GSNO do not play exactly the same role in the regulation of Fe deficiency responses. Since most of the effects of NO and GSNO in plant processes are related to post-translational modifications provoked with *S*-nitrosylation, it is tempting to speculate that perhaps both substances can modify different proteins. In this sense, some results, including those presented by Dr. Yeh's group, suggest that GSNO could act through the master regulator FIT while NO could act through other TFs, including the Ib bHLH TFs. Nonetheless, more research is needed to decipher the intriguing relationship between NO and GSNO, and between them and other signals implicated in the regulation of Fe deficiency responses, such as GSH, ethylene and auxin.

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