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Modulation of nitric oxide bioactivity by plant haemoglobins

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Abstract

Nitric oxide (NO) is a highly reactive signalling molecule that has numerous targets in plants. Both enzymatic and non-enzymatic synthesis of NO has been detected in several plant species, and NO functions have been characterized during diverse physiological processes such as plant growth, development, and resistance to biotic and abiotic stresses. This wide variety of effects reflects the basic signalling mechanisms that are utilized by virtually all mammalian and plant cells and suggests the necessity of detoxification mechanisms to control the level and functions of NO. During the last two years an increasing number of reports have implicated non-symbiotic haemoglobins as the key enzymatic system for NO scavenging in plants, indicating that the primordial function of haemoglobins may well be to protect against nitrosative stress and to modulate NO signalling functions. The biological relevance of plant haemoglobins during specific conditions of plant growth and stress, and the existence of further enzymatic and non-enzymatic NO scavenging systems, suggest the existence of precise NO modulation mechanisms in plants, as observed for different NO sources.

Key words: Nitric oxide, non-symbiotic haemoglobin, plant haemoglobin.

Introduction

NO is a small reactive molecule that rapidly diffuses and permeates cell membranes. Its broad chemistry involves an

array of interrelated redox forms with different reactivities (Delledonne, 2005). Because of its unique chemistry, which permits its stability and reactivity, NO and its redox-activated forms are intra- and intercellular signalling molecules (Durner *et al.*, 1998).

In plants, NO has a role in several physiological processes including disease resistance and abiotic stress responses as well as growth and development (Neill *et al.*, 2003; Romero-Puertas *et al.*, 2004). The complexity of NO signalling involves various messenger molecules such as cGMP, cADP ribose, and Ca²⁺ (Durner *et al.*, 1998; Wendehenne *et al.*, 2001; Lamotte *et al.*, 2004; Romero-Puertas *et al.*, 2004), which both directly and indirectly modulate several physiological functions and alter the expression of specific genes (Polverari *et al.*, 2003; Parani *et al.*, 2004). Furthermore, the NO signalling pathways involve post-translational modification of target proteins such as NO-dependent tyrosine nitration and reversible cysteine S-nitrosylation, which can modulate the activity and function of different proteins (Sokolovski and Blatt, 2004; Feechan *et al.*, 2005; Lindermayr *et al.*, 2005). Although the existence of multiple mechanisms for NO action renders the dissection of specific pathways difficult, it may explain the incomplete inhibition observed when individual steps in specific NO-mediated pathways are blocked (Clarke *et al.*, 2000).

Both cytotoxic and cyto-protecting/stimulating properties of NO have been described in plants (Beligni and Lamattina, 1999). Therefore, the wide variety of sources of NO and its effects suggests the necessity of detoxification mechanisms to control its level, reactivity, and signalling functions. In this review, recent publications that have provided new insights into NO regulation are presented that

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Abbreviations: cADPR, cyclic ADP ribose; cGMP, cyclic GMP; flavoHbs, flavohaemoglobins; GSNO, S-nitroso-L-glutathione; GSNOR, GSNO reductase; H₂O₂, hydrogen peroxide; Hb, haemoglobin; HR, hypersensitive response; NO, nitric oxide; NO₂, nitrogen dioxide; NO₃⁻, nitrate; NOS, nitric oxide synthase; NR, nitrate reductase; nsHb, non-symbiotic haemoglobin; O₂, oxygen; O₂⁻, superoxide anion; OH[·], hydroxyl radical; ONOO⁻, peroxynitrite; ROS, reactive oxygen species; SA, salicylic acid; SAR, systemic acquired resistance; SOD, superoxide dismutase; SNO, S-S-nitroso thiol.

aid in the elucidation of the specific role of haemoglobin (Hb)-based control of NO under different conditions in plants.

NO functions in plants

NO is a widespread signalling molecule that plays a crucial role in the modulation of several physiological processes during the entire life of the plant (Crawford and Guo, 2005) from germination (Bethke *et al.*, 2004b; Simontacchi *et al.*, 2004; Zhang *et al.*, 2005) to fruit maturation and senescence (Leshem *et al.*, 1998; Beligni and Lamattina, 2001). In roots, NO operates in the auxin signalling pathway that leads to root organogenesis (Pagnussat *et al.*, 2003; Correa-Aragunde *et al.*, 2004) and it also plays an important role in modulation of the gravitropic response (Hu *et al.*, 2005). In leaves, NO mediates abscisic acid-induced stomatal closure (Desikan *et al.*, 2002, 2004; Garcia-Mata and Lamattina, 2002), modulates the rate of leaf expansion (Leshem and Haramaty, 1996), and may affect metabolic processes such as photosynthesis (Hill and Bennett, 1970) and respiration (Zottini *et al.*, 2002). Furthermore, NO also seems to be involved in programmed cell death during xylem differentiation (Gabaldon *et al.*, 2005) and is a key signal for the control of flowering timing (He *et al.*, 2004) and for the orientation of pollen tube growth (Prado *et al.*, 2004).

NO is also involved as a control signal during several abiotic stress responses, including salinity and osmotic stress, temperature, UV light stress, and anoxia (Rockel *et al.*, 2002; An *et al.*, 2005; Shimoda *et al.*, 2005). In particular, NO increases resistance to different abiotic stress such as drought, salt, and oxidative stress (Zhao *et al.*, 2004; Shi *et al.*, 2005).

NO is produced during biotic stress in both pathological and non-pathological plant–microbe interactions (Romero-Puertas *et al.*, 2004; Wendehenne *et al.*, 2004; Zeidler *et al.*, 2004). Its accumulation under conditions that are concomitant with the avirulent gene-dependent oxidative burst has been linked to the induction of the hypersensitive cell death (Delledonne *et al.*, 1998; de Pinto *et al.*, 2002) and to cell-to-cell spread of apoptotic signals (Zhang *et al.*, 2003; Tada *et al.*, 2004). The NO produced during biotic stress is also involved in the activation of systemic acquired resistance (Durner *et al.*, 1998) through the up-regulation of defence genes (Polverari *et al.*, 2003). Furthermore, NO production was recently observed during the response to necrotrophic pathogens and insect herbivores (Jih *et al.*, 2003; Huang *et al.*, 2004; Van Baarlen *et al.*, 2004) in addition to a beneficial plant–microbe interaction, as demonstrated in *Lotus japonicus* with the symbiotic rhizobium *Mesorhizobium loti* (Shimoda *et al.*, 2005).

The above observations indicate that NO plays a key role in plant metabolism, signalling, defence, and development, suggesting that control of the level of NO in plants is

required in order to activate proper signalling functions. As for animal systems, where different nitric oxide synthases (NOS) have been identified (Stuehr *et al.*, 2004), different NO sources in plants also seem to be involved in NO production during specific processes (Neill *et al.*, 2003; Romero-Puertas *et al.*, 2004). Recently, the presence of a plant NOS gene has been shown in *Arabidopsis* (*AtNOS1*; Guo *et al.*, 2003). *AtNOS1* plays an important role in plant growth, fertility, and hormone signalling (Guo *et al.*, 2003; He *et al.*, 2004) and it is also involved in the plant–pathogen response (Zeidler *et al.*, 2004).

Another enzymatic source of NO is nitrate reductase (NR), an enzyme with a fundamental role in nitrogen assimilation, which can produce NO from nitrite when photosynthetic activity is inhibited or when its substrate nitrite accumulates (Yamasaki and Sakihama, 2000; Rockel *et al.*, 2002; Lamattina *et al.*, 2003). NR is an important source of abscisic acid-induced NO synthesis in stomata guard cells (Desikan *et al.*, 2002; Garcia-Mata and Lamattina, 2003), although no significant effects of NR have been observed with regard to NO accumulation during pathogenic infection (Zhang *et al.*, 2003) or during wounding stress (Garces *et al.*, 2001).

Recent studies have shown other nitrite-mediated NO sources in plants, including the enzymatic production of NO in mitochondria under anoxia (Planchet *et al.*, 2005) and the membrane associated nitrite-NO oxidoreductase in roots (Stöhr *et al.*, 2001). Other potential enzymatic NO sources such as xanthine oxidoreductase, horseradish peroxidase, or cytochrome P450 should be also considered (Corpas and del Rio, 2004), as well as non-enzymatic mechanisms, including the spontaneous liberation of NO from nitrite in the presence of acid pH and reducing agents (Yamasaki and Sakihama, 2000; Bethke *et al.*, 2004a) and the carotenoid-mediated NO production in the presence of nitrite and light (Cooney *et al.*, 1994).

Therefore, different NO sources are most likely required to control the production of NO during specific processes, although the physiological significance of NO production in different instances and identification of the precise source of NO depending on the physiological process and its regulation or interrelation with other possible sources requires further investigation.

NO reactions

NO and its exchangeable redox-activated forms are well known as intra- and intercellular signalling molecules, since NO can rapidly diffuse across biological membranes and contribute to transient cell-to-cell signalling for brief periods of time (Beligni and Lamattina, 2001). As free NO is highly reactive, several reactions that are controlled by both the concentration and redox state of NO and the availability and reactivity of target groups can occur without enzyme

catalysis (Crawford and Guo, 2005). These reactions regulate the signalling and toxicity of NO and may also modulate its levels. The free radical NO has a half-life of just a few seconds and rapidly reacts with O₂ to form nitrogen dioxide (NO₂), which degrades to nitrite and nitrate in aqueous solutions (Neill *et al.*, 2003). NO can also react with the free radical superoxide (O₂⁻) to form the reactive molecule peroxyxynitrite (ONOO⁻), which can lead to the formation of NO₂ and the potent oxidant hydroxyl radical (OH[•]). OH[•] is a very strong oxidizing specie that can rapidly attack biological membranes and all types of biomolecules such as DNA and proteins leading to irreparable damage, metabolic dysfunction, and cell death (del Rio *et al.*, 2003). By itself, ONOO⁻ is responsible for tyrosine nitration and oxidation of thiol residues to sulphenic and sulphonic acids (Lamattina *et al.*, 2003) and it is considered the major toxic reactive nitrogen species in animal cells (Stamler *et al.*, 1992), but not for plant cells (Delledonne *et al.*, 2001).

As a consequence, the effect of NO on animal cells depends on many complex conditions, such as the rate of production and diffusion, the concentration of reactive oxygen species (ROS), and the level of enzymes involved in ROS scavenging, such as superoxide dismutase and catalase (Tamir *et al.*, 1993). In plants, the accumulation of NO and H₂O₂ during the hypersensitive disease resistance response (HR) is responsible for the execution of the cell death program (Delledonne *et al.*, 1998; Clarke *et al.*, 2000; de Pinto *et al.*, 2002). Since the independent increase of only one component of this binary system has little effect on the induction of cell death (Delledonne *et al.*, 2001), the relative rates of production of NO and O₂⁻ are critical in modulating the effects of NO. This can paradoxically offer protection against oxidative damage by intercepting reactive species and converting them to less damaging and/or more easily detoxified products. Thus, whereas H₂O₂ is the noxious partner of NO to induce cell death, O₂⁻ may be considered as a chemical NO scavenger that controls the level of NO in plant cells through the formation of ONOO⁻ (Delledonne *et al.*, 2001).

NO can also react rapidly with thiol- and transition metal-containing proteins, including a wide functional spectrum of proteins such as receptors, transcription factors and cellular messengers (Stamler *et al.*, 2001). For example, the NO-dependent activation of guanylate cyclase by binding to the haem iron established a function for NO in signal transduction (Murad, 1986). NO can react with glutathione to form *S*-nitrosoglutathione (GSNO), which can function as a mobile reservoir of NO bioactivity (Feechan *et al.*, 2005) or a *S*-nitrosylating agent. *S*-nitrosylation is represented by binding of a NO group to the thiol side chain of a cysteine residue. In animals, this modification is involved in a large part of the almost ubiquitous influence of NO on cellular signal transduction (Hess *et al.*, 2005), and during the last few years over 100 proteins have been identified

as targets of *S*-nitrosylation (Stamler *et al.*, 2001). Temporal and spatial regulation of *S*-nitrosylation allows post-translational modification to function as a mechanism that conveys redox-based signalling (Hess *et al.*, 2005). Very little is known about *S*-nitrosylation in plants, although numerous proteins have been obtained from the deduced *Arabidopsis* proteome that have a degenerate *S*-nitrosylation motif (Huber and Hardin, 2004). Recently, a proteomic approach using the biotin switch method (Jaffrey *et al.*, 2001) identified 63 proteins from *Arabidopsis* cell culture extracts treated with GSNO and 52 proteins from NO-treated *Arabidopsis* leaves as putative targets for *S*-nitrosylation in plants (Lindermayr *et al.*, 2005). The characterization of mechanisms regulating *S*-nitrosylation/de-nitrosylation will undoubtedly aid in an improved understanding of the functional consequences and relevance of *S*-nitrosylation in plants, and might identify possible mechanisms to control the levels of NO and NO-related species.

Haemoglobins detoxify NO

The wide variety of NO sources and biological effects suggests the requirement of detoxification mechanisms in plants to control the levels of NO as well as its reactivity and signalling functions. Haemoglobins (Hbs) are most commonly recognized for their ability to act either as O₂ carriers or stores to facilitate O₂ delivery, even though they are also well known regulators of NO homeostasis. In humans, Hbs regulate the activity of NO through either detoxification (Joshi *et al.*, 2002) or delivery through *S*-nitrosylation reactions (Gow *et al.*, 1999). Bacterial flavohaemoglobins (flavoHbs) consume NO enzymatically through a NO reductase/denitrosylase activity (Gardner *et al.*, 1998; Hausladen *et al.*, 1998) to protect bacterial cells from NO, as also observed for truncated Hbs (Quellet *et al.*, 2002). *Ascaris* Hb has a NO consumption activity that involves the intermediacy of *S*-nitrosylated Hb (Minning *et al.*, 1999). Thus, the primordial function of Hbs, present not only in erythrocytes but also in microorganisms, invertebrates, and plants may well be to protect against nitrosative stress and modulate the signalling functions of NO.

In plants, there are at least three distinct types of Hbs that have been classified as symbiotic, non-symbiotic Hbs (nsHb), and truncated Hbs. The latter are the most recently discovered plant Hbs; they are characterized by a three-dimensional structure with a 2-on-2 arrangement of α -helices (Watts *et al.*, 2001) and appear to be ubiquitous in the plant kingdom (Vieweg *et al.*, 2005). Symbiotic Hbs are found specifically in symbiotic legume root nodules where they scavenge and transport O₂ to protect *Rhizobium* nitrogenase from inactivation (Appleby, 1984). The nsHbs appear to be ubiquitous in the plant kingdom and are organized in two classes. Class-1 Hbs have an extremely

high affinity for O_2 and are induced in plants during hypoxic stress, whereas class-2 nsHbs have lower affinity for O_2 , are induced by low temperature, and are expressed during plant development (Trevaskis *et al.*, 1997; Hunt *et al.*, 2001).

Although the presence of stress-induced nsHbs is widespread in the plant kingdom, their function has only been recently elucidated and their cellular localization is not clearly understood. In particular, alfalfa class-1 nsHb has been shown to localize in both the nucleus and cytosol (Seregélyes *et al.*, 2000), although the main nsHbs activity involved in NO degradation was found to be localized in the soluble cytosolic fraction (Igamberdiev *et al.*, 2004) in agreement with the previous protein sequence analysis of rice and *Arabidopsis* class-1 nsHb (Arredondo-Peter *et al.*, 1997; Trevaskis *et al.*, 1997). In contrast to symbiotic Hb, the nsHbs exhibit an iron hexacoordination in which the ligand binding site on the haem prosthetic group is occupied by a His residue similar to many Hbs (Kundu *et al.*, 2003). For example, the human neuroglobins show a hexacoordinated structure, are up-regulated during hypoxia, and their expression is directly associated with protection against hypoxic challenge (Sun *et al.*, 2001, 2003). Similarly, class-1 nsHbs are strongly expressed during hypoxia or similar stresses, and are required for survival of plants after a severe hypoxic challenge (Hunt *et al.*, 2002; Dordas *et al.*, 2003b). However, these nsHbs possess a high affinity for O_2 and slow O_2 dissociation rate constants and are, therefore, unlikely to function as O_2 transporters (Kundu *et al.*, 2003). On the other hand, hypoxia is a stress condition that generates copious amounts of NO (Dordas *et al.*, 2003b) suggesting other possible Hb-based cell-protection mechanisms.

Class-1 nsHbs from *Arabidopsis* (Perazzolli *et al.*, 2004), barley (Igamberdiev *et al.*, 2004), and alfalfa (Seregélyes *et al.*, 2004) are now known to detoxify NO to nitrate in an NAD(P)H-dependent manner. Biochemical evidence indicates that rapid nitrate accumulation is accompanied by NO-dependent oxidation of oxygenated to oxidized nsHb (Dordas *et al.*, 2004; Perazzolli *et al.*, 2004). Furthermore, this Fe(III) intermediate of haem can be directly reduced by NADPH, as for nsHb from *Arabidopsis*, which catalyses an enzymatic cycle for NO metabolism with continuous nitrate accumulation in the presence of excess NO and NADPH (Fig. 1A; Perazzolli *et al.*, 2004). Otherwise, oxidized nsHb might be reduced by a mixture of NADH and FAD, as for alfalfa nsHb (Seregélyes *et al.*, 2004), or by a methaemoglobin reductase, as for barley nsHb (Igamberdiev *et al.*, 2004).

The demonstration that class-1 nsHb from *Arabidopsis* can also metabolize GSNO through production of *S*-nitrosohaemoglobin (Fig. 1B; Perazzolli *et al.*, 2004) suggests a conserved role of haemoglobin *S*-nitrosothiols in processing NO and *S*-nitroso compounds across humans, nematodes, and plants. Hexacoordinate plant Hbs appear to

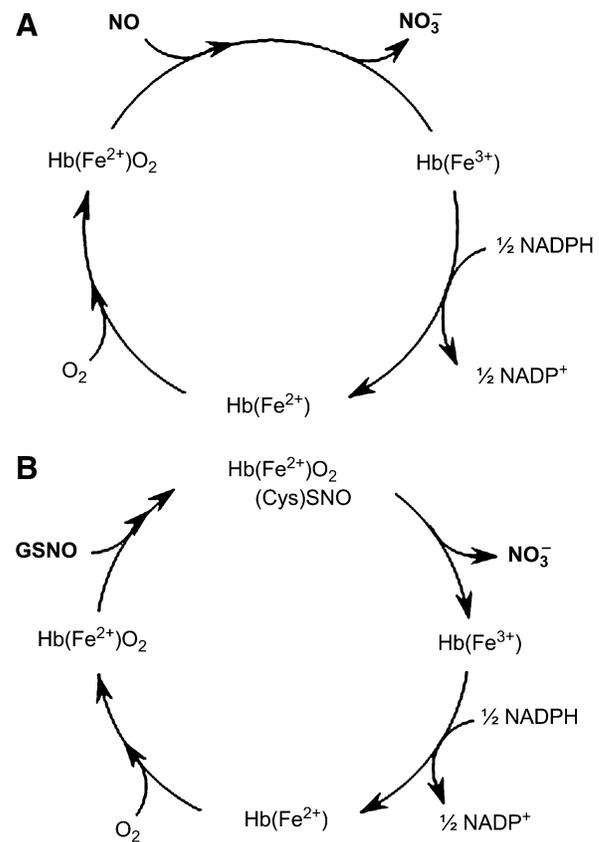


Fig. 1. Haemoglobin-based NO-detoxification reactions. (A) Reaction cycle for NO metabolism by *Arabidopsis* class-1 nsHb: oxygenated Hb is oxidized by NO with nitrate production. The recovery of oxygenated Hb for another NO degradation cycle is ensured by regeneration by NADPH and subsequent association with O_2 . This reduction of nsHb may be augmented *in vivo* by specific interaction with a methaemoglobin reductase system. (B). Reaction cycle for GSNO metabolism by *Arabidopsis* class-1 nsHb: oxygenated Hb is oxidized by GSNO with nitrate production through the formation of an *S*-nitrosoHb intermediate. The recovery of oxygenated Hb is ensured by regeneration by NADPH and subsequent association with O_2 . The reduction of nsHb may be augmented *in vivo* by specific interaction with a methaemoglobin reductase system as well.

operate as *Ascaris* Hb (Minning *et al.*, 1999), although they are structurally very different. Both *Arabidopsis* class-1 and *Ascaris* Hbs have evolved distal cysteine residues in the haem pocket, not present in human and bacterial Hbs, which are implicated in NO/SNO detoxification. *Arabidopsis* class-1 nsHb seem to retain the primitive function in NO/SNO detoxification by positioning cysteine residues in the distal haem pocket similar to *Ascaris* Hb, whereas NO delivery function in human haemoglobin is accomplished through the use of a proximal cysteine residue (Jia *et al.*, 1996).

A role of nsHbs in NO modulation has been largely demonstrated *in vitro* and *in vivo* only for the high O_2 affinity class-1. Conversely, the function of the strongly different class-2 nsHbs has not been investigated. Class-2 nsHbs seem to be exclusive to dicots (Hunt *et al.*, 2001), are induced by cold stress (Trevaskis *et al.*, 1997), and are

expressed in specific tissues of mature flowering plants (Hunt *et al.*, 2001). The *Arabidopsis* class-2 nsHb show lower O₂ affinity than class-1 nsHbs and might be involved in O₂ storage or transport (Trevaskis *et al.*, 1997). A possible interaction with NO, particularly in NO biosynthesis from nitrite at low O₂ levels, has recently been proposed (Crawford and Guo, 2005).

Haemoglobin-based NO modulation during hypoxic stress

The main physiological function for the NO scavenging activity of nsHb appears to be protection against nitrosative stress associated with hypoxia (Dordas *et al.*, 2003b, 2004; Perazzolli *et al.*, 2004). Overexpression of class-1 nsHb results in a greater cell viability and stronger plant growth under hypoxia in *Arabidopsis* (Hunt *et al.*, 2002; Perazzolli *et al.*, 2004) and in alfalfa cultures expressing the barley nsHb (Dordas *et al.*, 2003b), whereas the suppression of nsHb expression reduces organ growth under hypoxic stress (Dordas *et al.*, 2003b; Perazzolli *et al.*, 2004). This nsHb-mediated hypoxia tolerance depends on the high O₂ affinity of nsHbs and NO detoxification (Dordas *et al.*, 2003b; Perazzolli *et al.*, 2004), but it is not due to O₂ delivery (Hunt *et al.*, 2002).

Hypoxic stress activates NR leading to copious amounts of NO synthesis and elevated NO emission from plant tissues that are measurable by chemiluminescence (Rockel *et al.*, 2002; Perazzolli *et al.*, 2004) and electron paramagnetic resonance (Dordas *et al.*, 2003b, 2004). Hypoxia stimulated NO accumulation is dramatically suppressed in *Arabidopsis* plants expressing *Arabidopsis* class-1 nsHb (Fig. 2; Perazzolli *et al.*, 2004), in alfalfa root cultures overexpressing barley class-1 nsHb (Dordas *et al.*, 2003b) and in maize cell lines expressing the same barley nsHb (Dordas *et al.*, 2004); whereas the transgenic lines suppressed for nsHbs expression have enhanced levels of NO (Fig. 2; Dordas *et al.*, 2003b, 2004; Perazzolli *et al.*, 2004).

NO is an effective inhibitor of cytochrome oxidase in the mitochondrial electron transport chain (Zottini *et al.*, 2002) and may further reduce cell respiration and energy production. Under hypoxia, nsHbs scavenge NO and may also help in maintaining the energy status of plant cells by an alternative mechanism to the classic fermentation pathways (Igamberdiev and Hill, 2004; Igamberdiev *et al.*, 2005). The NR-dependent production of NO and its subsequent oxidation by nsHb seems to be a NAD(P)H-consuming mechanism. The overall system oxidizes 2.5 moles of NADH per 1 mol of nitrate recycled, leading to the maintenance of redox status during hypoxia (Dordas *et al.*, 2003a; Igamberdiev and Hill, 2004). The lower NADH/NAD⁺ and NADPH/NADP⁺ ratios in alfalfa root cultures expressing barley nsHb compared with control cells, and the higher ratios in nsHb silenced lines upon low O₂ and

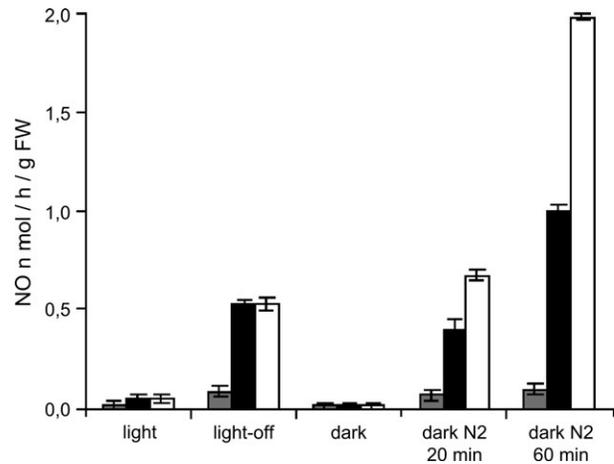


Fig. 2. Gas phase NO emission pattern of *Arabidopsis* wild-type plants (black bars) and transgenic *Arabidopsis* lines expressing the *Arabidopsis* class-1 nsHb gene in sense (grey bars) or antisense (white bars) orientation, 30 min after light exposure (light), after transfer of light-adapted plants to darkness (light-off), 30 min after dark adaptation (dark), and 20 min or 60 min after hypoxic stress by flushing with N₂ in the dark (dark N₂ 20 min and 60 min; Perazzolli *et al.*, 2004).

antimycin treatment, support the existence of this alternative fermentation mechanism (Igamberdiev *et al.*, 2004). Since alfalfa root cultures expressing barley nsHb (Dordas *et al.*, 2003a) and maize-cultured cells expressing barley nsHb (Sowa *et al.*, 1998) have lower alcohol dehydrogenase activity than control cultures under hypoxia, alternative fermentation based on nsHb could substitute alcohol dehydrogenase for recycling NADH. Furthermore, this nsHb cycle sustains glycolysis and the energy status of plant cells, maintaining a higher level of ATP in nsHb overexpressing lines under hypoxia (Sowa *et al.*, 1998; Dordas *et al.*, 2003a; Igamberdiev *et al.*, 2005).

Haemoglobin-based NO modulation during plant growth conditions

NO accumulates under normal growth conditions as it is produced from nitrite either through light-mediated non-enzymatic conversion by carotenoids or by the action of NR (Klepper, 1990). In *Arabidopsis* lines overexpressing the class-1 nsHb, the NR-mediated emission of NO resulting from the accumulation of nitrite on transfer of light-adapted plants to darkness (Kaiser *et al.*, 2002) is significantly lower compared with control plants (Fig. 2; Perazzolli *et al.*, 2004), suggesting a function of nsHbs in the constant control of NO accumulation.

Arabidopsis class-1 nsHb is induced by nitrate (Wang *et al.*, 2000), a class-1 nsHb of the *Lotus japonicus* is strongly induced by NO (Shimoda *et al.*, 2005), and both rice class-1 nsHbs are strongly up-regulated by nitrite, nitrate, and NO (Ohwaki *et al.*, 2005). Furthermore, treatment with

nitrate and nitrite failed to induce nsHbs in rice mutants defective in NR expression (Ohwaki *et al.*, 2005) indicating that the induction of nsHb is closely associated with NR-dependent NO production. Since NR-derived NO is potentially dangerous, these data indicate that nsHbs may well protect against NO generated following nitrogen fertilization (Klepper, 1990) and during normal growth condition (Ohwaki *et al.*, 2005). The effect of nsHbs in defence against nitrosative stress is observed during treatment with NO donors (Dordas *et al.*, 2003a; Seregelyes *et al.*, 2003). NO treatment causes a decline in the ATP levels and ATP/ADP ratios in transgenic alfalfa cultures underexpressing the nsHbs, whereas lines overexpressing the class-1 barley nsHb show protection against this nitrosative stress (Dordas *et al.*, 2003a). Similarly, tobacco seedlings and leaves of transgenic lines overexpressing the alfalfa class-1 nsHb are less sensitive to NO than wild-type plants (Seregelyes *et al.*, 2003).

Transient NO generation observed after symbiotic bacteria inoculation in *Lotus japonicus* roots indicates that NO also accumulates during beneficial plant–microbe interactions (Shimoda *et al.*, 2005). NO could be produced in the infected cells of root nodules due to their high metabolic activity during the infection process, or in the release of NO by nitrogen-fixing bacteroids (Vieweg *et al.*, 2005). Thus, NO may be involved in symbiotic interactions, either as a messenger molecule or as a by-product of the altered metabolism in root nodules (Herouart *et al.*, 2002). Symbiotic rhizobium infection causes the up-regulation of a class-1 nsHb in *Lotus japonicus* (Shimoda *et al.*, 2005) and the induction of the two truncated Hbs in root nodules and in roots of *Medicago truncatula* colonized by arbuscular mycorrhizal fungi (Vieweg *et al.*, 2005). It is assumed that these Hbs could be involved in NO detoxification in specific root tissues during symbiosis (Shimoda *et al.*, 2005; Vieweg *et al.*, 2005), since it can inactivate nitrogenase (Cueto *et al.*, 1996).

In other detrimental plant–microbe interactions, NO exerts a number of fundamental functions, such as those occurring during plant defence against pathogen attack, by contributing together with ROS to trigger hypersensitive cell death and induce defence genes (Delledonne *et al.*, 1998). The observation that challenge of *Arabidopsis* plants overexpressing the *Arabidopsis* class-1 nsHb with an avirulent strain of the bacterial pathogen *Pseudomonas syringae* causes normal accumulation of NO and hypersensitive cell death, indicates that nsHbs do not interfere with NO bursts originated by acute responses when NO signalling functions through the hypersensitive resistance response are needed (Perazzoli *et al.*, 2004). However, further experimentation is required to elucidate the role of nsHb during disease resistance, since the overexpression of alfalfa nsHb in tobacco results in fewer lesions in leaves when challenged with incompatible bacteria or tobacco necrosis virus compared with control plants (Seregelyes

et al., 2003). Moreover, these lines have higher ROS, salicylic acid (SA), and pathogenesis-related protein 1 levels after pathogen infection (Seregelyes *et al.*, 2003, 2004). The differences of nsHb expressing plants during plant–pathogen interactions might be explicable by the different rates of catalytic NO detoxification. The expression of *Escherichia coli* flavoHb, which possesses strong NO detoxification activity (Gardner *et al.*, 1998), is able to attenuate the pathogen-induced NO burst when expressed in plants and reduces the development of hypersensitive cell death and the expression of defence genes (Zeier *et al.*, 2004).

Further NO modulation mechanisms in plant

In addition to Hb-based NO detoxification and non-enzymatic NO scavenging by O_2^- or through thiols, plants may possess additional NO metabolizing mechanisms to control the levels of NO under different conditions. For example, some enzymes such as xanthine oxidase, glutathione peroxidase, and GSNO reductase (GSNOR) are reported to break down NO-related species (Sies *et al.*, 1997; Trujillo *et al.*, 1998; Díaz *et al.*, 2003). GSNO has been shown to induce systemic resistance against TMV infection in tobacco (Song and Goodman, 2001) and to be a powerful inducer of plant defence genes (Durner *et al.*, 1998). An enzyme that metabolizes GSNO has been identified in *E. coli* (Liu *et al.*, 2001a) and the characterization of GSNOR-deficient yeast showed enhanced susceptibility to nitrosative stress (Liu *et al.*, 2001b). A similar gene has also been identified in both pea and *Arabidopsis* (Shafqat *et al.*, 1996; Sakamoto *et al.*, 2002), suggesting that plants may be able to modulate the bioactivity and signalling function of this stabilized form of NO. A recent study has shown that mutation in *AtGSNOR1*, an *Arabidopsis thaliana* GSNOR, modifies cellular levels of SNO under both physiological and pathophysiological conditions (Feechan *et al.*, 2005) indicating the existence of cross-reactions between free NO and GSNO that could control the level of NO and its signalling capacity. In the absence of GSNOR activity, the cellular level of SNO is higher compared with control *Arabidopsis* lines and the plant resistance response against avirulent pathogens and virulent pathogens are compromised. This suggests that whereas a reduction of NO accumulation leads to pathogen susceptibility, a decrease in the concentration of SNO promotes protection against microbial infection (Feechan *et al.*, 2005). *AtGSNOR* is also required to maintain the non-host resistance to the wheat powdery mildew pathogen in *Arabidopsis* and is a positive regulator of the SA signalling network since *AtGSNOR* is required for normal *PR1* expression in pathogen-infiltrated and in SA-treated plants (Feechan *et al.*, 2005). *Arabidopsis* plants overexpressing *AtGSNOR* show a reduced SNO level, accelerated

kinetics of *PR1* expression, and enhanced basal resistance against bacterial and oomycete pathogens (Feechan *et al.*, 2005). These results confirm that an additional regulatory system depending on GSNO formation and AtGSNOR activity is involved in the control of NO signalling functions (Feechan *et al.*, 2005). However, the physiological relevance of these enzymes in plant NO metabolism should be more thoroughly investigated under different stress conditions.

Conclusions

During the last two years large advances have been made in the field of NO regulation and metabolism. Recent publications have reported a crucial involvement of nsHbs in NO modulation during different plant growth and stress conditions, indicating that, in plants as well, the primordial function of Hbs is the detoxification of NO catalysing an O₂ and NAD(P)H-dependent nitrate-forming reaction. The *in vivo* results have demonstrated that the Hb-based NO detoxification plays a crucial role to protect plant cells against nitrosative stress and modulation of NO signalling functions. Furthermore, the existence of different NO modulation reactions indicates that specific NO detoxification mechanisms may be involved in specific plant conditions in the fine control of the level and functions of NO. However, the identification of the precise source of NO, depending on the physiological process and the associated NO modulation system that prevent unregulated NO accumulation, needs further investigation. In particular, the involvement of nsHb and truncated Hbs in NO modulation during pathogenic and symbiotic plant–microbe interactions needs clarification. Moreover, nsHb interactions with NO have been demonstrated only for the class-1 molecule and the function of the strongly different class-2 nsHb has not yet been investigated. While the low O₂ affinity of the class-2 nsHbs suggests their involvement in O₂ storage or transport, their possible activity in NO biosynthesis at low O₂ levels has recently been hypothesized. Furthermore, the reaction of NO with thiols and the subsequent SNO interaction with nsHb and other target proteins demonstrated in plants are a promising starting point to characterize enzymatic and non-enzymatic NO control more fully and the possible signal cascade by which NO operates in plant cells through protein *S*-nitrosylation.

Future prospectives

NO participates in the regulation of several physiological processes, and the identification of mechanisms controlling its level in plant cells indicates a fine-tuning between NO synthesis and detoxification. Recent reports suggest a crucial role of plant Hbs in NO metabolism, and these findings now raise questions about their main physiological func-

tions. Whereas the role of high oxygen affinity class-1 nsHbs has been largely demonstrated in NO detoxification during plant growth and hypoxic stress (Dordas *et al.*, 2003b, 2004; Igamberdiev *et al.*, 2004; Perazzolli *et al.*, 2004), other studies suggest a function in H₂O₂ metabolism (Sakamoto *et al.*, 2004; Yang *et al.*, 2005). Since during hypoxia copious amounts of H₂O₂ are generated, it has been proposed that the nsHb-dependent protection to hypoxia may be a result of the decreased cellular level of H₂O₂ (Yang *et al.*, 2005). However, other evidence suggests that class-1 nsHbs overexpressing plants produce increased levels of H₂O₂ upon bacterial infection (Serégelyes *et al.*, 2003). Further investigation of the balance between NO and ROS during hypoxia, together with a detailed characterization of the interaction between nsHb with H₂O₂ is expected to lead to a better understanding of the activities of nsHbs in ROS homeostasis. In addition a better biochemical characterization of plant Hbs can be expected. The structural features of haem iron coordination recently reported for tomato nsHb (Ioanitescu *et al.*, 2005), and the kinetic binding properties of rice class-1 nsHb (Hargrove, 2000) have the potential to provide further information about the enzymatic properties of nsHbs. In particular, the effect of hexacoordination in the increase of the rate of iron reduction, reported for human and rice hexacoordinated Hbs (Weiland *et al.*, 2005), could deepen the biochemical knowledge regarding mechanisms of nsHbs reduction through direct NAD(P)H processes (Perazzolli *et al.*, 2004; Serégelyes *et al.*, 2004) and through mediation of a specific reductase (Igamberdiev *et al.*, 2004).

The evidence that bacterial flavoHbs (Zeier *et al.*, 2004) and alfalfa class-1 nsHb (Serégelyes *et al.*, 2003) affect SA accumulation in pathogen-infected plants, and the recent demonstration that the barley class-1 nsHb affects ethylene accumulation in NO- and hypoxia-treated maize cells (Manac'h-Little *et al.*, 2005) indicates a role of nsHbs in controlling NO-dependent hormone-mediated signalling that deserves further investigation. The recent identification of *S*-nitrosylation of *Arabidopsis* class-1 nsHb (Perazzolli *et al.*, 2004) and other plant proteins (Sokolovski and Blatt, 2004; Lindermayr *et al.*, 2005), together with the evidence that *Arabidopsis* class-1 nsHb can mediate tyrosine nitration of itself and other proteins (Sakamoto *et al.*, 2004), are important starting points from which to characterize the signal cascade by which NO operates in plant cells.

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