

# S-Nitrosylation of Ascorbate Peroxidase Is Part of Programmed Cell Death Signaling in Tobacco Bright Yellow-2 Cells<sup>1</sup>[OPEN]

Maria Concetta de Pinto, Vittoria Locato, Alessandra Sgobba, Maria del Carmen Romero-Puertas, Cosimo Gadaleta, Massimo Delledonne, and Laura De Gara\*

Dipartimento Biologia, Università degli Studi di Bari, 70125 Bari, Italy (M.C.d.P., A.S., C.G.); Centro Integrato di Ricerca, Università Campus Bio-Medico di Roma, 00128 Rome, Italy (V.L., L.D.G.); Departamento de Bioquímica, Biología Celular y Molecular de Plantas, Estación Experimental del Zaidín, Consejo Superior de Investigaciones Científicas, 18080 Granada, Spain (M.d.C.R.-P.); and Dipartimento di Biotecnologie, Università degli Studi di Verona, 37134 Verona, Italy (M.D.)

ORCID IDs: 0000-0001-5938-7113 (L.D.G.); 0000-0002-2937-1935 (M.C.d.P.); 0000-0003-0267-5039 (V.L.).

Nitric oxide (NO) is a small redox molecule that acts as a signal in different physiological and stress-related processes in plants. Recent evidence suggests that the biological activity of NO is also mediated by S-nitrosylation, a well-known redox-based posttranslational protein modification. Here, we show that during programmed cell death (PCD), induced by both heat shock (HS) or hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) in tobacco (*Nicotiana tabacum*) Bright Yellow-2 cells, an increase in S-nitrosylating agents occurred. NO increased in both experimentally induced PCDs, although with different intensities. In H<sub>2</sub>O<sub>2</sub>-treated cells, the increase in NO was lower than in cells exposed to HS. However, a simultaneous increase in S-nitrosoglutathione (GSNO), another NO source for S-nitrosylation, occurred in H<sub>2</sub>O<sub>2</sub>-treated cells, while a decrease in this metabolite was evident after HS. Consistently, different levels of activity and expression of GSNO reductase, the enzyme responsible for GSNO removal, were found in cells subjected to the two different PCD-inducing stimuli: low in H<sub>2</sub>O<sub>2</sub>-treated cells and high in the heat-shocked ones. Irrespective of the type of S-nitrosylating agent, S-nitrosylated proteins formed upon exposure to both of the PCD-inducing stimuli. Interestingly, cytosolic ascorbate peroxidase (cAPX), a key enzyme controlling H<sub>2</sub>O<sub>2</sub> levels in plants, was found to be S-nitrosylated at the onset of both PCDs. In vivo and in vitro experiments showed that S-nitrosylation of cAPX was responsible for the rapid decrease in its activity. The possibility that S-nitrosylation induces cAPX ubiquitination and degradation and acts as part of the signaling pathway leading to PCD is discussed.

Nitric oxide (NO) is a gaseous and diffusible redox molecule that acts as a signaling compound in both animal and plant systems (Pacher et al., 2007; Besson-Bard et al., 2008). In plants, NO has been found to play a key role in several physiological processes, such as germination, lateral root development, flowering, senescence, stomatal closure, and growth of pollen tubes (Beligni and Lamattina, 2000; Neill et al., 2002; Correa-Aragunde et al., 2004; He et al., 2004; Prado et al., 2004; Carimi et al., 2005). In addition, NO has been reported to be involved in plant responses to both biotic and abiotic stresses (Leitner et al., 2009; Siddiqui et al., 2011) and in the signaling pathways leading to programmed cell death (PCD; Delledonne et al., 1998; de

Pinto et al., 2006; De Michele et al., 2009; Lin et al., 2012; Serrano et al., 2012).

The cellular environment may greatly influence the chemical reactivity of NO, giving rise to different biologically active NO-derived compounds, collectively named reactive nitrogen species, which amplify and differentiate its ability to activate physiological and stress-related processes. Many of the biological properties of NO are due to its high affinity with transition metals of metalloproteins as well as its reactivity with reactive oxygen species (ROS; Hill et al., 2010). However, recent evidence suggests that protein S-nitrosylation, due to the addition of NO to reactive Cys thiols, may act as a key mechanism of NO signaling in plants (Wang et al., 2006; Astier et al., 2011). NO is also able to react with reduced glutathione (GSH), the most abundant cellular thiol, thus producing S-nitrosoglutathione (GSNO), which also acts as an endogenous trans-nitrosylating agent. GSNO is also considered as a NO store and donor and, as it is more stable than NO, acts as a long-distance NO transporter through the floematic flux (Malik et al., 2011). S-Nitrosoglutathione reductase (GSNOR), which is an enzyme conserved from bacteria to humans, has been suggested to play a role in regulating S-nitrosothiols (SNO) and the turnover of S-nitrosylated proteins in plants (Liu et al., 2001; Rusterucci et al., 2007).

<sup>1</sup> This work was supported by the Italian Ministry of University and Research (grant nos. PRIN 20084XTFBC\_001 and FIRB 2010 RBFR1051LJ\_003).

\* Address correspondence to l.degara@unicampus.it.

The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors ([www.plantphysiol.org](http://www.plantphysiol.org)) is: Laura De Gara (l.degara@unicampus.it).

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[www.plantphysiol.org/cgi/doi/10.1104/pp.113.222703](http://www.plantphysiol.org/cgi/doi/10.1104/pp.113.222703)

A number of proteins involved in metabolism, stress responses, and redox homeostasis have been identified as potential targets for S-nitrosylation in *Arabidopsis* (*Arabidopsis thaliana*; Lindermayr et al., 2005). During the hypersensitive response (HR), 16 proteins were identified to be S-nitrosylated in the seedlings of the same species (Romero-Puertas et al., 2008); in *Citrus* species, S-nitrosylation of about 50 proteins occurred in the NO-mediated resistance to high salinity (Tanou et al., 2009).

However, while the number of candidate proteins for S-nitrosylation is increasing, the functional significance of protein S-nitrosylation has been explained only in a few cases, such as for nonsymbiotic hemoglobin (Perazzolli et al., 2004), glyceraldehyde 3-phosphate dehydrogenase (Lindermayr et al., 2005; Wawer et al., 2010), Met adenosyltransferase (Lindermayr et al., 2006), and metacaspase9 (Belenghi et al., 2007). Of particular interest are the cases in which S-nitrosylation involves enzymes controlling ROS homeostasis. For instance, it has been reported that S-nitrosylation of peroxiredoxin IIE regulates the antioxidant function of this enzyme and might contribute to the HR (Romero-Puertas et al., 2007). It has also been shown that in the immunity response, S-nitrosylation of NADPH oxidase inactivates the enzyme, thus reducing ROS production and controlling HR development (Yun et al., 2011).

Recently, S-nitrosylation has also been shown to be involved in PCD of *nitric oxide excess1* (*noe1*) rice (*Oryza sativa*) plants, which are mutated in the *OscATC* gene coding for catalase (Lin et al., 2012). In these plants, which show PCD-like phenotypes under high-light conditions, glyceraldehyde 3-phosphate dehydrogenase and thioredoxin are S-nitrosylated. This suggests that the NO-dependent regulation of these proteins is involved in plant PCD, similar to what occurs in animal apoptosis (Sumbayev, 2003; Hara et al., 2005; Lin et al., 2012). The increase in hydrogen peroxide ( $H_2O_2$ ) after exposure to high light in *noe1* plants is responsible for the production of NO required for leaf cell death induction (Lin et al., 2012). There is a strict relationship between  $H_2O_2$  and NO in PCD activation (Delledonne et al., 2001; de Pinto et al., 2002); however, the mechanism of this interplay is largely still unknown (for review, see Zaninotto et al., 2006; Zhao, 2007; Yoshioka et al., 2011). NO can induce ROS production and vice versa, and their reciprocal modulation in terms of intensity and timing seems to be crucial in determining PCD activation and in controlling HR development (Delledonne et al., 2001; Zhao, 2007; Yun et al., 2011).

In previous papers, we demonstrated that heat shock (HS) at 55°C and treatment with 50 mM  $H_2O_2$  promote PCD in tobacco (*Nicotiana tabacum*) Bright Yellow-2 (BY-2) cells (Vacca et al., 2004; de Pinto et al., 2006; Locato et al., 2008). In both experimental conditions, NO production and decrease in cytosolic ascorbate peroxidase (cAPX) were observed as early events in the PCD pathway, and cAPX decrease has been suggested to contribute to determining the redox environment required for PCD (de Pinto et al., 2006; Locato et al., 2008).

In this study, the production of nitrosylating agents (NO and GSNO) in the first hours of PCD induction by HS or  $H_2O_2$  treatment in tobacco BY-2 cells and their role in PCD were studied. The possibility that S-nitrosylation could be a first step in regulating cAPX activity and turnover as part of the signaling pathway leading to PCD was also investigated.

## RESULTS

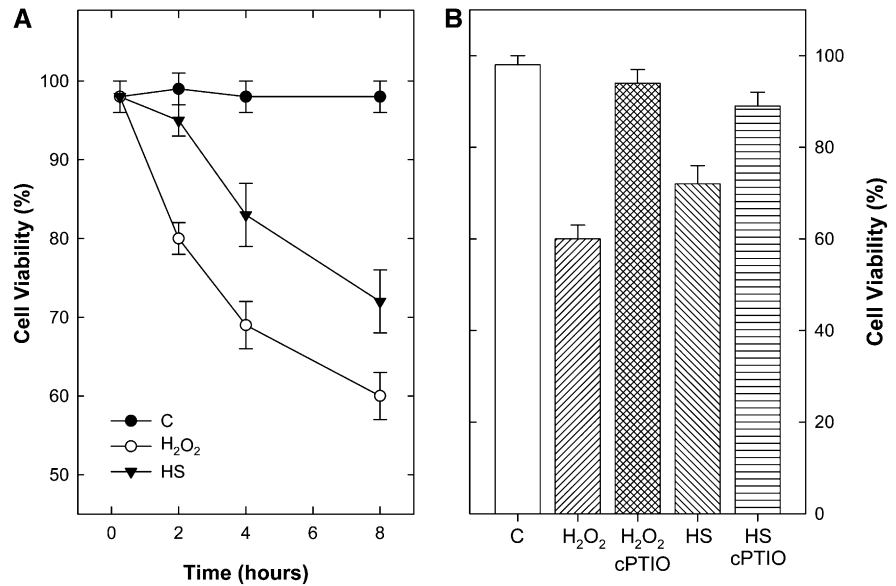
PCD was induced in tobacco BY-2 cell suspensions by 10 min of HS at 55°C or treatment with 50 mM  $H_2O_2$  as reported previously (Vacca et al., 2004; de Pinto et al., 2006). The time-dependent viability of cells in the first 8 h after PCD induction is reported in Figure 1A. In both experimental conditions, cell death increased over time, although it was faster in  $H_2O_2$ -treated cells than in heat-shocked cells. The addition of the NO scavenger 2-(4-Carboxyphenyl)-4,4,5,5-tetramethylimidazole-1-oxyl-3-oxide (cPTIO) in the culture medium of tobacco BY-2 cells, before exposure to the PCD-inducing stimulus ( $H_2O_2$  or HS), significantly blocked cell death (Fig. 1B), thus confirming the key role of NO in the induction of these two types of PCD (de Pinto et al., 2006; Locato et al., 2008). Therefore, NO level was measured during the first 8 h after PCD induction (Fig. 2A). Both PCD-inducing stimuli led to an increase in NO, which was already evident after 15 min. A further increase occurred in the subsequent hours, although it was much higher in the heat-shocked cells than in  $H_2O_2$ -treated cells.

Since it is known that NO strongly reacts with thiol groups, the levels of GSNO and the glutathione pool were determined in the HS- and  $H_2O_2$ -treated cells. In  $H_2O_2$ -treated cells, GSNO increased very rapidly after the treatment and progressively decreased, with values comparable to the controls, after 8 h (Fig. 2B). On the other hand, in heat-shocked cells, GSNO levels rapidly decreased and remained very low at all the analyzed times (Fig. 2B). The glutathione pool also changed as a consequence of PCD induction: in  $H_2O_2$ -treated cells, the glutathione pool decreased notably 15 min after the treatment; a further decrease occurred in the following hours. In heat-shocked cells, the first decrease in the glutathione pool was observed 4 h after the treatment and was always less marked than in  $H_2O_2$ -treated cells (Fig. 2C).

The difference in GSNO content in the two PCD conditions was in line with the behavior of GSNOR, the enzyme responsible for GSNO removal. Indeed, the activity of GSNOR decreased in  $H_2O_2$ -treated cells, whereas it increased in heat-shocked cells (Fig. 3A). The changes in GSNOR activity depended on changes in its expression, as shown by reverse transcription (RT)-PCR analysis (Fig. 3B).

Despite the different contents of NO and GSNO, S-nitrosylated proteins quickly increased after exposure to both the PCD-inducing stimuli and remained higher than the controls for all the analyzed times (Fig. 4A). Immunoblotting with a monoclonal antibody that

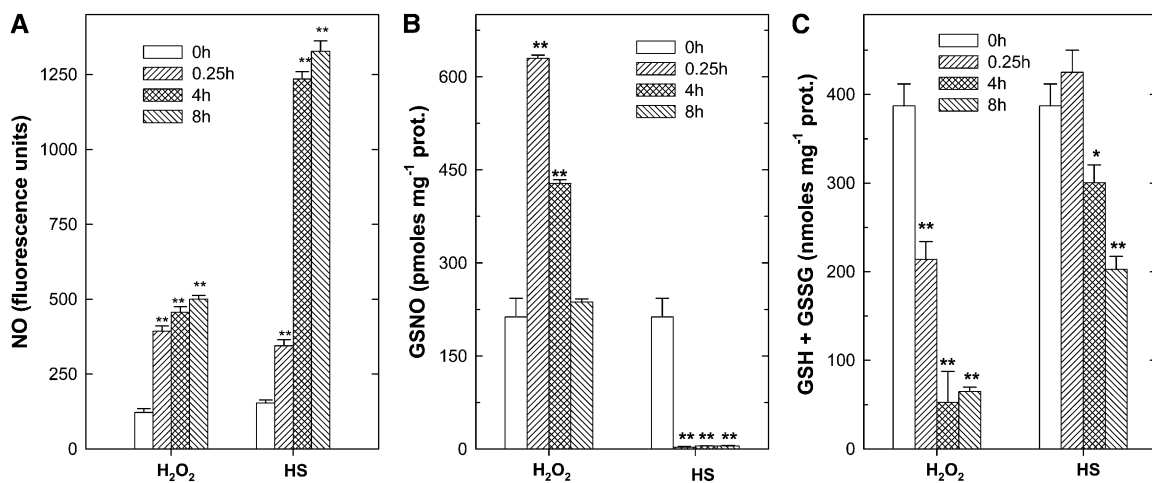
**Figure 1.** Effects of HS and H<sub>2</sub>O<sub>2</sub> on cell viability of tobacco BY-2 cells. A, Time-dependent viability of cells treated with 50 mM H<sub>2</sub>O<sub>2</sub> or exposed for 10 min to 55°C (HS). B, Cell viability 8 h after exposure to the PCD-inducing stimuli. Where indicated, cells were preincubated for 10 min with 500 μM cPTIO. The viability of cells was measured by trypan blue staining and examination by phase-contrast microscopy. The reported results are means ± SE of five independent experiments. C, Control.



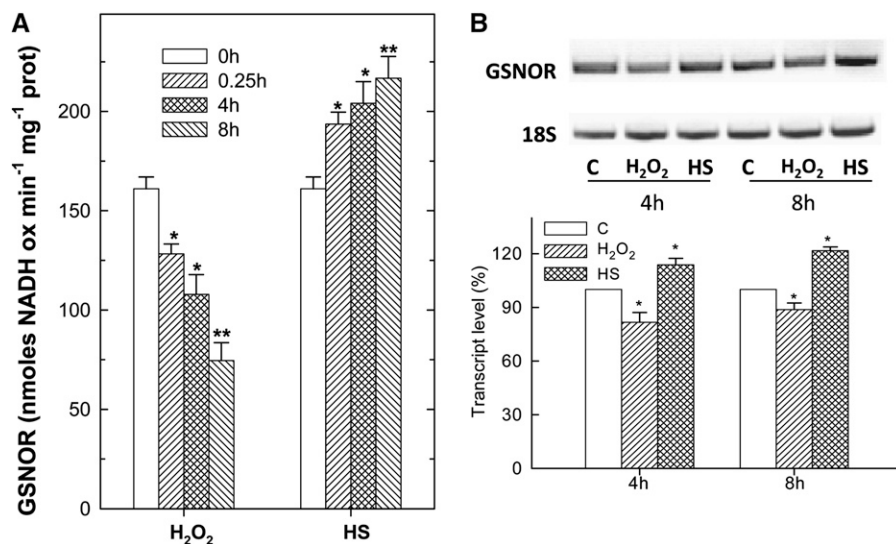
recognizes cAPX on S-nitrosylated proteins, isolated by the biotin-switch method (Jaffrey and Snyder, 2001) and purified with neutravidin-agarose beads, confirmed that S-nitrosylation of cAPX happened in both experimental conditions (Fig. 4B). Densitometric analysis showed that S-nitrosylation of cAPX occurred faster during the H<sub>2</sub>O<sub>2</sub>-induced PCD than during the HS one (Fig. 4B). Interestingly, a decrease in cAPX activity was found in parallel with its S-nitrosylation (Fig. 4C). The activity of cAPX decreased 15 min after exposure of the cells to both PCD-inducing stimuli and further declined in the following hours. However, this decrease was stronger in H<sub>2</sub>O<sub>2</sub>-treated cells than in HS-treated cells. The decrease in cAPX was a precocious event in the PCD signaling pathway, since it occurred when no

cellular death hallmarks (cell shrinkage, micronuclei formation, and DNA laddering) were evident (data not shown).

In order to confirm that S-nitrosylation was responsible for cAPX inhibition, in vitro experiments were performed. Partial purification of cAPX was obtained from nontreated tobacco BY-2 cells (Table I). The purified cAPX was exposed to a range of GSNO concentrations typically used for in vitro S-nitrosylation, and the formation of SNO-APX was monitored by the biotin-switch method. Figure 5A shows that cAPX was S-nitrosylated by GSNO in a concentration-dependent manner. Dithiothreitol (DTT) addition markedly reduced the concentration of SNO-APX formation, which was consistent with the presence of a reversible thiol



**Figure 2.** Time-dependent changes in NO, GSNO, and the glutathione pool during HS- and H<sub>2</sub>O<sub>2</sub>-induced PCD. A, NO fluorescence emission of tobacco BY-2 cells was measured at the indicated times in cells loaded with 4,5-diaminofluorescein 2-diacetate before exposure to H<sub>2</sub>O<sub>2</sub> or HS. B and C, GSNO (B) and the glutathione pool (GSH + oxidized glutathione [GSSG]); C) in tobacco BY-2 cells collected at the indicated times after exposure to PCD-inducing stimuli. The values represent means ± SE of three independent experiments. \**P* < 0.05, \*\**P* < 0.01 (Student's *t* test).



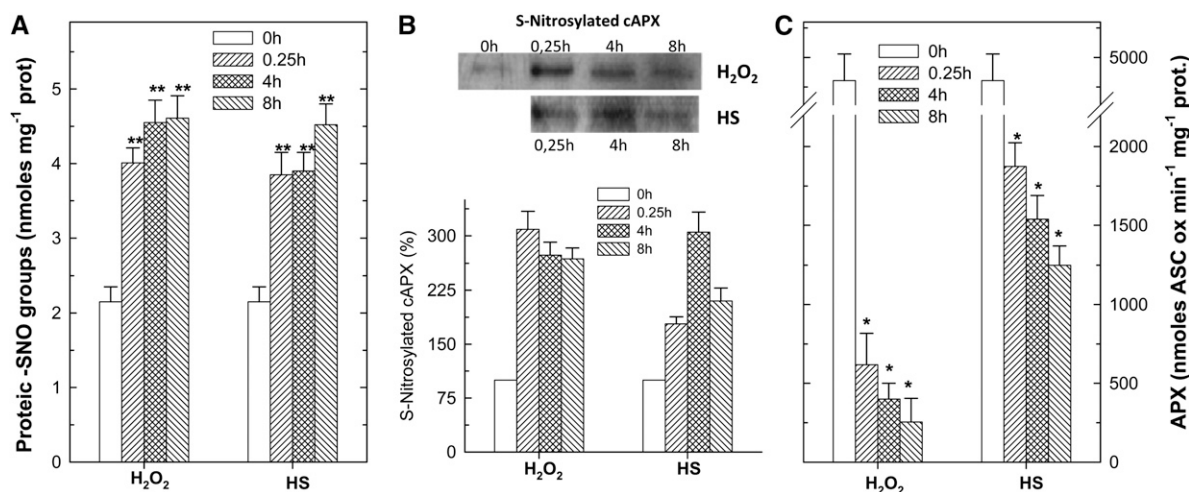
**Figure 3.** Changes in GSNOR activity and expression during HS- and H<sub>2</sub>O<sub>2</sub>-induced PCD. A, GSNOR activity was measured at the indicated times after exposure to PCD-inducing stimuli. B, Representative image and densitometric analyses of semi-quantitative RT-PCR results for GSNOR at 4 and 8 h after PCD induction. Densitometric values of GSNOR transcript level are expressed as a percentage considering the values obtained for control as 100%. rRNA was used to normalize the results. The values represent means  $\pm$  SE of three independent experiments. \* $P < 0.05$ , \*\* $P < 0.01$  (Student's *t* test). C, Control.

modification (Fig. 5B). The absence of an effect following exposure to GSH confirmed the specificity of this posttranslational modification (Fig. 5B). The exposure to GSNO also significantly reduced the activity of the enzyme in a concentration-dependent manner (Fig. 5C). Interestingly, *in vitro* S-nitrosylation of partially purified cAPX from control BY-2 cells was also responsible for the alteration of enzyme kinetics from sigmoidal to hyperbolic (Fig. 5D), with a Hill coefficient changing from  $1.6 \pm 0.08$  in control cAPX to  $0.95 \pm 0.07$  in the S-nitrosylated enzyme.

Since S-nitrosylation could be a signal for protein degradation via the ubiquitin-proteasome pathway (Kim et al., 2004; Kwak et al., 2010), we also investigated whether cAPX was ubiquitinated during PCD in tobacco BY-2 cells. Immunoblotting with anti-cAPX on enriched fractions of ubiquitinated proteins highlighted

that ubiquitination of cAPX occurred during the PCD induced by the two stimuli, although not at the same time (Fig. 6A). Indeed, ubiquitinated cAPX appeared 15 min after PCD induction in both kinds of PCD but was higher in H<sub>2</sub>O<sub>2</sub> cells. In addition, the appearance over time of bands with a higher  $M_r$ , indicative of poly-ubiquitinated cAPX, clearly demonstrated that ubiquitination of cAPX occurred faster in H<sub>2</sub>O<sub>2</sub> cells than in HS cells. (Fig. 6A). In line with this, a decrease in the total level of cAPX was observed during both types of PCD but was faster in H<sub>2</sub>O<sub>2</sub> cells than in HS cells (Fig. 6B).



Finally, in order to verify whether cAPX ubiquitination and degradation were NO-dependent events, these analyses were performed in cells subjected to PCD stimuli in the presence of cPTIO. The cPTIO ability to scavenge NO produced during H<sub>2</sub>O<sub>2</sub>-induced PCD has been confirmed by using the specific fluorescent probe



**Figure 4.** S-Nitrosylation of cAPX during PCD. A, Total protein SNO groups at different times after HS and H<sub>2</sub>O<sub>2</sub> treatment. B, Representative image and densitometric analyses of S-nitrosylated cAPX. Densitometric values of S-nitrosylated cAPX are expressed as a percentage considering the values obtained for control as 100%. In each well, 5  $\mu$ g of total nitrosylated proteins was loaded. The gels are representative of five different experiments. C, Specific activities of cAPX during H<sub>2</sub>O<sub>2</sub>- and HS-induced PCD. The values represent means  $\pm$  SE of five independent replicates. \* $P < 0.05$ , \*\* $P < 0.01$  (Student's *t* test).

**Table 1.** Partial purification of cAPX from tobacco BY-2 cells

The enrichment in cAPX was determined by the increase in its specific activity and protein level observed by western blotting.

Sample	Protein Content	cAPX Activity	cAPX $\mu\text{g}^{-1}$ Protein
	$\text{mg mL}^{-1}$	$\text{nmol min}^{-1} \text{mg}^{-1} \text{protein}$	
Crude extract	$4.92 \pm 0.5$	$4,859 \pm 325$	
cAPX-enriched extract	$0.153 \pm 0.04$	$22,600 \pm 3,250$	

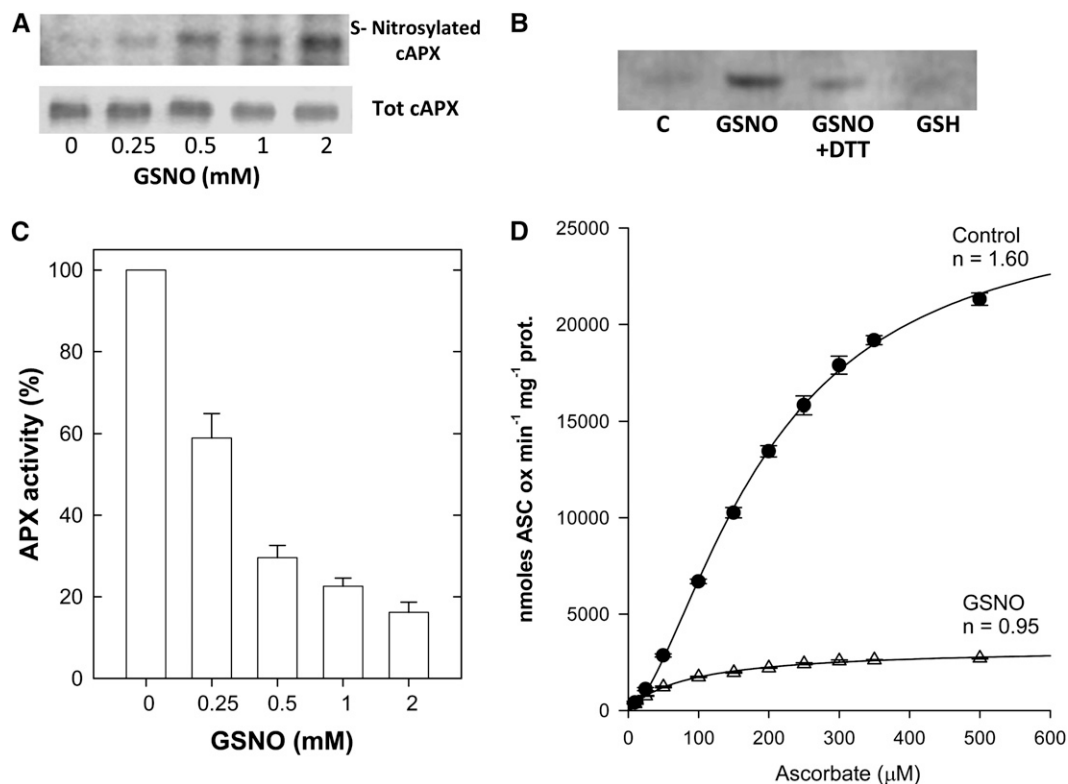
4,5-diaminofluorescein 2-diacetate (Fig. 7A). Consistently, in the presence of cPTIO, the levels of cAPX ubiquitination and degradation were also remarkably decreased (Fig. 7, B and C). Similar results were obtained in cells undergoing PCD after HS exposure (data not shown).

## DISCUSSION

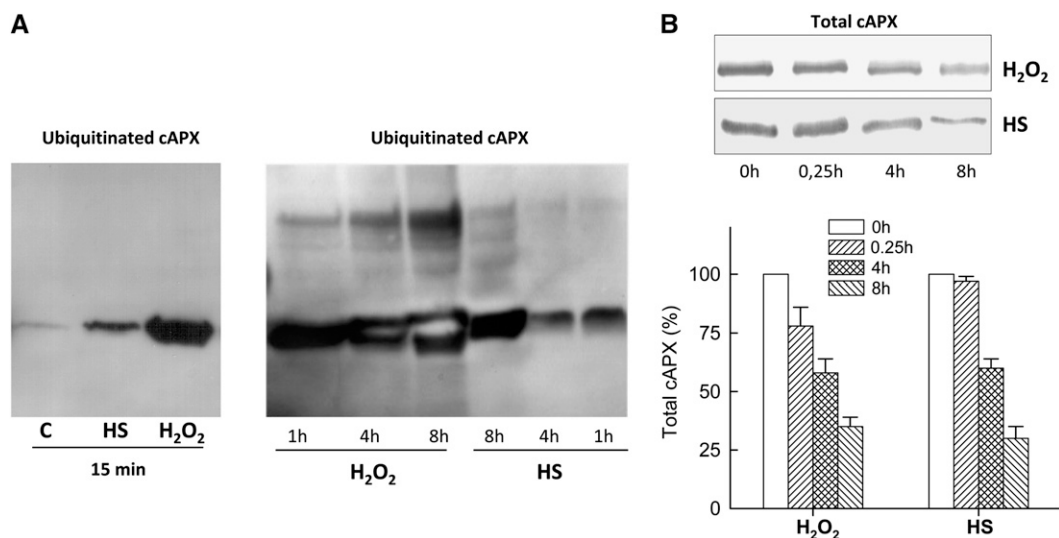
The production of a NO burst is a common event in the induction of PCD due to different stimuli. In fact,

NO performs a pivotal role in HR induction (Delledonne et al., 1998; Zaninotto et al., 2006), leaf senescence (Carimi et al., 2005),  $\text{Cd}^{2+}$ -induced PCD in suspension cell cultures (De Michele et al., 2009), and PCD induced by high light in leaves of *noe1* rice lacking catalase activity (Lin et al., 2012).

We confirmed that NO plays a key role in  $\text{H}_2\text{O}_2$ - and HS-dependent PCD induction in tobacco BY-2 cells (de Pinto et al., 2006; Locato et al., 2008), since treatment of cells with the NO scavenger cPTIO, before exposure to the PCD-inducing stimuli, significantly blocked cell death (Fig. 1B). Our data show that the accumulation of NO occurs rapidly (within 15 min) in the PCDs induced by  $\text{H}_2\text{O}_2$  and HS. However, higher levels of this molecule subsequently accumulated in heat-shocked cells over a period of 8 h (Fig. 2A). In  $\text{H}_2\text{O}_2$ -treated cells, the lower increase in NO was accompanied by a simultaneous increase in GSNO, while in heat-shocked cells, the level of GSNO was lower than that observed in the control cells (Fig. 2B). The decrease in GSNO observed in heat-shocked cells does not seem to be due to a temperature-dependent degradation, since very low amounts of this molecule were found at all the analyzed times, even when the cells were maintained



**Figure 5.** In vitro S-nitrosylation of cAPX is responsible for its activity inhibition and kinetic changes. A, Representative images of S-nitrosylated and total cAPX after treatment with increasing GSNO concentration. B, cAPX S-nitrosylation obtained with 2 mM GSNO was reverted in the presence of 5 mM DTT and did not occur in the presence of GSH. C, Control. The gels in A and B are representative of three different experiments. C, Inhibition of cAPX activity in the presence of increasing GSNO concentrations; cAPX activity was expressed as a percentage of the activity of nontreated extracts considered as 100%. D, Changes in kinetic behavior of cAPX after in vitro S-nitrosylation. The analysis was performed on partially purified cAPX before and 30 min after treatment with 2 mM GSNO. ASC, Ascorbate. The values represent means  $\pm$  SE of three independent experiments. The n values are Hill coefficients.



**Figure 6.** Ubiquitin-dependent degradation of cAPX during H<sub>2</sub>O<sub>2</sub>- and HS-induced PCD. A, Representative images of ubiquitinated cAPX at various times after PCD induction by H<sub>2</sub>O<sub>2</sub> and HS. C, Control. B, Representative image and densitometric analysis of total cAPX during PCD. Densitometric values of total cAPX are expressed as a percentage considering the values obtained for control as 100%. All gels are representative of three different experiments. The values represent means  $\pm$  SE of three independent experiments.

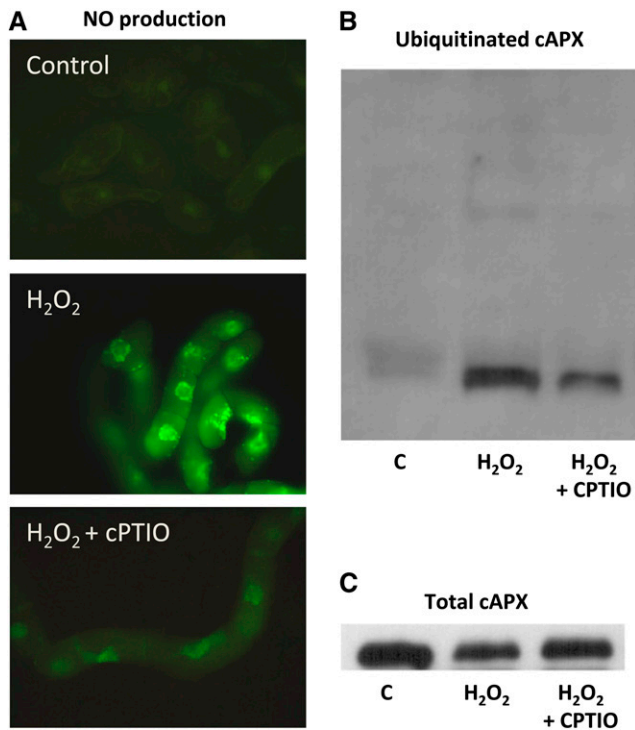
for 8 h at their optimal temperature. The different levels of GSNO observed in the two experimentally induced PCDs may in part be explained by the changes observed in GSNOR activity and expression (Fig. 3). In fact, in heat-shocked cells, the increase in GSNOR could induce GSNO removal, whereas in H<sub>2</sub>O<sub>2</sub>-treated cells, the decrease in GSNOR could favor the accumulation of GSNO. Accordingly, an opposite correlation between GSNO content and GSNOR has been demonstrated previously in different pepper (*Capsicum annuum*) plant organs (Airaki et al., 2011). In addition, the different levels of NO and GSNO in the two experimentally induced PCDs are also in line with a different behavior of the glutathione pool. It is not surprising that in tobacco BY-2 cells, the glutathione pool is much higher than GSNO (Fig. 2, B and C), since the range of the two metabolites in tobacco BY-2 cells concurs with the literature (Singh et al., 1996; Airaki et al., 2011). It is known that NO release from GSNO is stimulated by high GSH concentrations (Singh et al., 1996). In heat-shocked cells, the maintenance of a high content of the glutathione pool after PCD induction might promote the decomposition of GSNO and thus contribute to the strong increase in NO occurring in cells undergoing PCD after HS exposure. On the other hand, in H<sub>2</sub>O<sub>2</sub> cells, the more rapid and marked decrease in the glutathione pool could be a factor favoring GSNO accumulation.

It has been suggested that an increase in NO and GSNO and a decrease in NO removal are part of NO signaling (Diaz et al., 2003; Rusterucci et al., 2007). GSNO can act as a NO donor by directly transferring a NO group to a target Cys residue, thus playing a key role in regulating the biological activity of NO (Pawloski et al., 2001). However, S-nitrosylation may also be due to the

direct reaction of ROS with Cys residues. Thus, despite the different contents in NO and GSNO, observed in H<sub>2</sub>O<sub>2</sub> and HS cells, protein S-nitrosylation promptly occurs in both kinds of PCD (Fig. 4A).

S-Nitrosylation is considered to be one of the most important functional forms of NO-dependent post-translational modification and is involved in regulating various signaling processes (Astier et al., 2011). In plants, several proteome-wide analyses show that protein S-nitrosylation might affect a large spectrum of cellular functions (Lindermayr et al., 2005; Romero-Puertas et al., 2008; Tanou et al., 2009). It has also been reported that protein S-nitrosylation occurs during abiotic stress (Ortega-Galisteo et al., 2012; Camejo et al., 2013) and is an important mediator of H<sub>2</sub>O<sub>2</sub>-induced cell death in rice leaves (Lin et al., 2012), even if this does not exclude a direct role of H<sub>2</sub>O<sub>2</sub> in activating specific pathways leading to PCD or to stress responses.

Our data show that cAPX, a key enzyme for H<sub>2</sub>O<sub>2</sub> removal in plant cells (Shigeoka et al., 2002; De Gara 2004), is S-nitrosylated in both H<sub>2</sub>O<sub>2</sub>- and HS-induced PCD (Fig. 4B). In fact, Lin et al. (2012) reported ascorbate peroxidase among S-nitrosylated proteins in the H<sub>2</sub>O<sub>2</sub>-induced cell death in *noe1* plants. It is worth noting that S-nitrosylation of cAPX seems to be responsible for the immediate decrease in the enzyme activity observed in both HS- and H<sub>2</sub>O<sub>2</sub>-induced PCD (Fig. 4C). This is supported by in vitro results showing that the GSNO-dose-dependent S-nitrosylation of cAPX causes a parallel decrease in enzyme activity (Fig. 5). The faster S-nitrosylation of cAPX observed during H<sub>2</sub>O<sub>2</sub>-induced PCD compared with that observed in HS-induced PCD is also consistent with the more rapid and stronger decrease in cAPX activity observed in H<sub>2</sub>O<sub>2</sub>-treated cells (Fig. 4) and, as a consequence, with the



**Figure 7.** NO-dependent ubiquitination and degradation of cAPX during  $H_2O_2$ -induced PCD. A, NO production in  $H_2O_2$ -treated cells; where indicated, cells were preincubated for 10 min with 500  $\mu M$  cPTIO. B, cAPX ubiquitination in  $H_2O_2$ -treated cells in the absence and presence of cPTIO. C, Total cAPX during  $H_2O_2$ -induced PCD in the absence and presence of cPTIO. All gels are representative of three different experiments. C, Control.

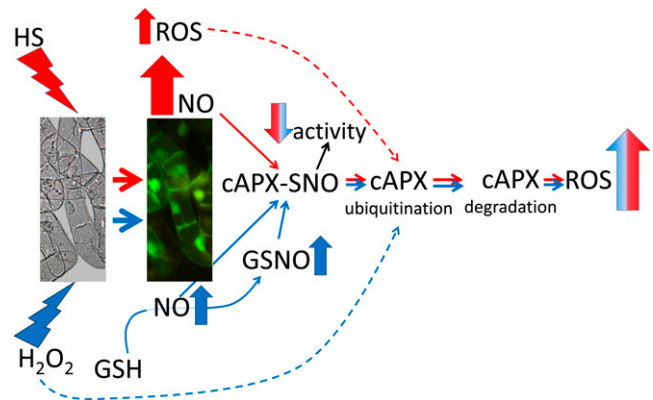
different rates of PCD occurrence in the two different conditions (Fig. 1A).  $H_2O_2$  itself could also contribute to cAPX inactivation (Hiner et al., 2000), further explaining the timing of PCD occurrence faster in  $H_2O_2$ -treated cells than in the HS-exposed ones. A decrease in antioxidants has also been reported as part of the strategies that cells exploit to activate the oxidative burst that characterizes PCDs triggered by various stimuli (for review, see de Pinto et al., 2012).

In previous papers (Vacca et al., 2004; de Pinto et al., 2006), we showed that the immediate decrease in cAPX activity, observed during PCD induced by exposure to HS or  $H_2O_2$ , is due to a change in the kinetics of the enzyme from sigmoidal to hyperbolic. The data from this work prove that this kinetic change is due to cAPX S-nitrosylation, since it occurs when the partially purified enzyme is in vitro trans-nitrosylated by GSNO treatment (Fig. 5D). The loss of cooperativity in the S-nitrosylated cAPX, evident from the change in the Hill coefficient (Fig. 5D), suggests that one of the two ascorbate-binding sites in the catalytic domain of the enzyme has been lost. It has been reported that pea (*Pisum sativum*) cAPX possesses two binding sites for ascorbate, with different affinities for the substrate (Lad et al., 2002). The high-affinity site is located in the vicinity of the Cys-32 residue (Mandelman et al., 1998).

Since the Cys-32 residue is well conserved in the cAPX of various species, including tobacco, we can speculate that the NO- or GSNO-dependent S-nitrosylation of this residue could be responsible for the changes in enzyme kinetics and catalytic turnover. In Arabidopsis, for example, APX1, a cytosolic isoenzyme of ascorbate peroxidase, has been identified among S-nitrosylable proteins, with Cys-32 recognized as the site of S-nitrosylation (Fares et al., 2011).

Some evidence suggests that S-nitrosylation could represent a signal for protein degradation through the ubiquitin-proteasome pathway in animal cells (Kim et al., 2004; Kwak et al., 2010; Dunne et al., 2013). Our data show that cAPX is also promptly ubiquitinated in cells undergoing  $H_2O_2$ - and HS-induced PCDs (Fig. 6A). Consistently, we found that the proteasome is involved in HS-induced PCD in tobacco BY-2 cells (Vacca et al., 2007). Moreover, the faster ubiquitination of cAPX in  $H_2O_2$ -treated cells also correlates with the faster decrease in cAPX protein level occurring under this experimental condition in comparison with HS (Fig. 6B). Interestingly, when NO production is reduced by treatment with the NO scavenger cPTIO, cAPX ubiquitination and degradation are remarkably prevented (Fig. 7), thus indicating, to our knowledge for the first time, that also in plants S-nitrosylation acts as a signal for ubiquitin-dependent protein degradation. Further studies are required in order to verify whether the oxidative environment activating PCD in  $H_2O_2$ -treated cells induces other alterations in cAPX that contribute to its ubiquitination.

In conclusion, our results suggest that S-nitrosylation of cAPX, which takes place when no markers of cell death are evident, is part of the early signaling pathway leading to NO-dependent PCD. In vitro and in vivo



**Figure 8.** S-Nitrosylation of cAPX is a part of PCD signaling in tobacco BY-2 cells. The diagram summarizes the results described in this paper.  $H_2O_2$  treatment induces an increase of both NO and GSNO in cells; on the other hand, the HS-mediated oxidative stress determines only a high production of NO. In both cases, an increase in S-nitrosylation of cAPX occurs. S-Nitrosylation of cAPX, possibly in association with other oxidative mechanisms (dotted lines), affects cAPX activity and makes cAPX a target for ubiquitination and consequent degradation. The decrease in cAPX activity and protein level determines the high ROS production involved in PCD.



evidence suggests that S-nitrosylation of cAPX is pivotal for the rapid decrease in enzyme activity, since it affects its kinetic properties. As summarized in Figure 8, the rapid decrease in cAPX activity, due to an immediate posttranslational modification, supports the hypothesis that alterations in both ROS production and ROS scavengers are critical for the oxidative burst to occur as a precocious event of plant PCD. Our data also further underline the tight relationship between NO and ROS in the control of PCD.

## MATERIALS AND METHODS

### Cell Treatments and Analyses of Cell Viability

The tobacco (*Nicotiana tabacum*) 'Bright-Yellow 2' cell suspensions were routinely propagated and cultured according to Nagata et al. (1992). For the experiments, a stationary culture (7 d) was diluted 4:100 (v/v). On day 4 of culture, cells were treated with 50 mM H<sub>2</sub>O<sub>2</sub> (de Pinto et al., 2006) or subjected to HS by transferring to 55°C for 10 min (Vacca et al., 2004). At the indicated times, 1 mL of cell suspension was collected for cell viability and NO analyses. Cell viability was determined by trypan blue staining as described previously (de Pinto et al., 1999). For each sample 1,000 cells were scored.

For other analyses, cells were separated from the culture medium by vacuum filtration on Whatman 3MM paper (Whatman International).

### NO, SNO, and Glutathione

NO was measured with the fluorescent probe 4,5-diaminofluorescein 2-diacetate according to Locato et al. (2008).

SNO groups were assayed following the method of Saville (1958) after separation of the extracts on the basis of molecular mass. Briefly, cells were homogenized in 0.1 M Tris-HCl, pH 6.8, at 4°C and centrifuged at 20,000g for 15 min. The supernatants were successively separated with Amicon Ultra 5K tubes (Millipore) in two fractions: low molecular mass (less than 5 kD) and high molecular mass (more than 5 kD). The two fractions were incubated for 5 min with an equivalent volume of 1% (w/v) sulfanilamide dissolved in 0.5 M HCl in the presence or absence of 0.2% (w/v) HgCl<sub>2</sub>. Samples were then incubated for 5 min with an equivalent volume of 0.02% (w/v) N-(1-naphthyl)-ethylenediamine dihydrochloride dissolved in 0.5 M HCl, and the absorbance of azo-dye products was read at 550 nm. SNO levels were quantified as the difference of absorbance in samples incubated in the presence and absence of HgCl<sub>2</sub> and comparing the values with a standard curve made with GSNO (Sigma-Aldrich). SNO of the low-molecular-mass fraction were considered as GSNO. The results were normalized against the whole-cell lysate protein content measured according to Bradford (1976).

Glutathione content was measured as described by de Pinto et al. (1999).

### GSNOR and cAPX Activities

Cells (0.3 g) were homogenized in liquid N<sub>2</sub> with 4 volumes of buffer containing 50 mM Tris-HCl, pH 7.8, 0.05% (w/v) Cys, and 0.1% (w/v) bovine serum albumin. The homogenates were then centrifuged at 20,000g for 15 min, and the supernatants were used for the determination of enzymatic activities.

GSNOR (EC 1.1.1.284) activity was measured following the decrease in A<sub>340</sub> due to the oxidation of NADH occurring for GSNO consumption. The reaction mixture contained 0.05 M Tris-HCl, pH 8.0, 0.5 mM EDTA, 0.2 mM NADH, and 0.4 mM GSNO. An extinction coefficient of 6.2 mM<sup>-1</sup> cm<sup>-1</sup> was used, and the activity was expressed as nmoles of NADH oxidized per minute per milligram of protein.

cAPX (EC 1.1.1.11) activity was determined following the H<sub>2</sub>O<sub>2</sub>-dependent oxidation of ascorbate at 290 nm, as described by Paradiso et al. (2012).

### Semiquantitative RT-PCR

Total RNA was isolated from tobacco BY-2 cells using the RNeasy plant minikit (Qiagen) according to the supplier's recommendation. Residual DNA was removed from the RNA samples using a DNA-free kit (Ambion). Synthesis

of complementary DNA was performed from 2 mg of total RNA with 10-μM random primers (Amersham Biosciences Europe), utilizing an Omniscript Reverse Transcriptase kit (Qiagen) according to the supplier's recommendation. PCR was performed with specific primers for GSNOR (5'-GCAAGTTC-TGCAAATCAGGA-3' and 5'-GCTCTTTGGGGTTGATGAAT-3'; accession number HQ830156.1) and 18S ribosomal RNA (rRNA; AJ236016; 5'-CATGAT-AACTCGACGGATCG-3' and 5'-GAAGGCCAACGTAATAGGAC-3'). The 18S rRNA was used as an internal control in order to normalize each sample for variations in the amount of initial RNA. The products of PCR amplification produced a single band at the predicted sizes of 441 and 594 bp for GSNOR and 18S rRNA, respectively. These were analyzed on 1.5% (w/v) agarose gels containing 0.5 mg mL<sup>-1</sup> ethidium bromide.

### Immunodetection of S-Nitrosylated cAPX

Cells were homogenized in liquid N<sub>2</sub> with four volumes of buffer containing 50 mM HEPES, pH 7.5, 5 mM EDTA, and 1 mM phenylmethylsulfonyl fluoride. The homogenates were centrifuged at 20,000g for 15 min and the supernatants subjected to biotin switch (Jaffrey and Snyder, 2001). Briefly, Cys-free residues were blocked by incubating 2 mg of proteins with 5 μL of 20 mM methyl-methaniosulfate (Pierce) and 25 μL of 25% (w/v) SDS for 30 min at 50°C, with frequently vortexing. Samples were subsequently precipitated with 2 volumes of ice-cold acetone and resuspended in 100 μL of buffer containing 25 mM HEPES, pH 7.7, 1 mM EDTA, and 1% (w/v) SDS. The resuspended samples were incubated for 1.5 h in the dark with 1 mM ascorbate and 1 mM N-(6-(biotinamido)hexyl-3'-(2'-pyridylidithio)propionamide (Pierce) and frequently vortexed. Purification of biotinylated proteins was obtained as described by Belenghi et al. (2007). Biotinylated samples were diluted with 2 volumes of neutralization buffer (25 mM HEPES, 1 mM EDTA, 100 mM NaCl, and 0.8% (v/v) Triton X-100, pH 7.7) supplemented with 140 μL of neuroavidin-agarose (Pierce) and incubated overnight, at 4°C, with continuous shaking. Beads were washed three times with 2 mL of buffer containing 25 mM HEPES, pH 7.7, 1 mM EDTA, 600 mM NaCl, and 0.8% (v/v) Triton X-100 and resuspended in 40 μL of SDS-PAGE loading buffer (0.225 M Tris-HCl, pH 6.8, 7.5% (w/v) SDS, 30% (v/v) glycerol, 1.5% (w/v) dithioerythritol, and 0.03% (w/v) bromophenol blue). After 5 min of incubation at 100°C and subsequent cooling, samples were centrifuged at 20,000g for 5 min. The supernatants were separated by 12.5% (w/v) SDS-PAGE and subjected to immunoblotting with the anti-cAPX monoclonal antibody as described previously (de Pinto et al., 2002).

### Immunodetection of Ubiquitinated cAPX

Cells were homogenized in liquid N<sub>2</sub> with 2 volumes of buffer containing 50 mM HEPES, pH 7.5, 5 mM EDTA, 150 mM NaCl, 1 mM phenylmethylsulfonyl fluoride, and 10 mM N-Ethylmaleimide. The homogenates were centrifuged at 20,000g for 15 min and the supernatants used for the analysis. In particular, ubiquitinated proteins were obtained using the Ubiquitinated Protein Enrichment Kit (Calbiochem), following the manufacturer's instructions. The obtained extracts, enriched in ubiquitinated proteins, were separated by 12.5% (w/v) SDS-PAGE and subjected to immunoblotting with the anti-cAPX monoclonal antibody as described previously (de Pinto et al., 2002). In order to detect total cAPX level, crude extracts were also subjected to immunoblotting with cAPX antibody.

### In Vitro Studies of Partially Purified cAPX

cAPX was partially purified by electroelution as described by De Gara et al. (1997). Briefly, proteins were separated by native PAGE, and a gel lane was cut and stained for ascorbate peroxidase activity in order to identify the ascorbate peroxidase position on the gel (De Gara et al., 1997). The area containing cAPX isoenzymes on the remaining gel was then electroeluted with a GE 200 SixPac Gel Eluter (Hoefer Scientific Instruments) following the experimental conditions recommended by the supplier.

Aliquots of semipurified cAPX were incubated in the dark at room temperature for 30 min with different concentrations of GSNO (ranging from 0.25 to 2 mM) or with 2 mM GSH in MES buffer (pH 7.5). A cAPX aliquot treated with 2 mM GSNO was then incubated with 10 mM of the reducing agent DTT. Excess of reagents were eliminated by protein precipitation with 2 volumes of cold acetone. Proteins were then subjected to biotin switch, resuspended in SDS-PAGE loading buffer, and loaded on 12.5% (w/v) SDS-PAGE gels. S-Nitrosylated cAPX was detected with an anti-biotin antibody (Pierce).

The kinetics of control and GSNO-treated cAPX were obtained by determining its activity with 170 μM H<sub>2</sub>O<sub>2</sub> and increasing ascorbate concentrations



(10–500  $\mu\text{M}$ ). The value for the Hill coefficient was obtained by analysis with the Enzyme Kinetics software (SPSS).

Sequence data from this article can be found in the GenBank/EMBL data libraries under accession number HQ830156.1 (GSNOR).

Received June 6, 2013; accepted October 23, 2013; published October 24, 2013.

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