

Protein S-Thiolation by Glutathionylspermidine (Gsp)

THE ROLE OF *ESCHERICHIA COLI* Gsp SYNTHETASE/AMIDASE IN REDOX REGULATION^{*[5]}

Received for publication, April 13, 2010, and in revised form, June 2, 2010. Published, JBC Papers in Press, June 8, 2010, DOI 10.1074/jbc.M110.133363

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Certain bacteria synthesize glutathionylspermidine (Gsp), from GSH and spermidine. *Escherichia coli* Gsp synthetase/amidase (GspSA) catalyzes both the synthesis and hydrolysis of Gsp. Prior to the work reported herein, the physiological role(s) of Gsp or how the two opposing GspSA activities are regulated had not been elucidated. We report that Gsp-modified proteins from *E. coli* contain mixed disulfides of Gsp and protein thiols, representing a new type of post-translational modification formerly undocumented. The level of these proteins is increased by oxidative stress. We attribute the accumulation of such proteins to the selective inactivation of GspSA amidase activity. X-ray crystallography and a chemical modification study indicated that the catalytic cysteine thiol of the GspSA amidase domain is transiently inactivated by H₂O₂ oxidation to sulfenic acid, which is stabilized by a very short hydrogen bond with a water molecule. We propose a set of reactions that explains how the levels of Gsp and Gsp S-thiolated proteins are modulated in response to oxidative stress. The hypersensitivities of GspSA and GspSA/glutaredoxin null mutants to H₂O₂ support the idea that GspSA and glutaredoxin act synergistically to regulate the redox environment of *E. coli*.

Protein thiols are readily oxidized and reduced to form sulfenates, sulfonates, sulfonates, and intra- and intermolecular disulfides. Most organisms have complex systems that regulate the intracellular redox states of thiols (1, 2). Small thiol-containing biomolecules (e.g. GSH and cysteine, form mixed-disulfides with protein thiols (S-thiolation). These post-translational modifications protect proteins from overoxidation and regulate certain protein functions (3, 4). For example, S-glutathionylation of *Escherichia coli* methionine synthase, which occurs when *E. coli* is oxidatively stressed, suppresses the synthase activity, thereby decreasing cellular methionine concentration

(5). Because GSH is abundant in most organisms (often existing at 1–10 mM), protein S-glutathionylation (GSH S-thiolation) is considered to be a reversible and universal cellular process. In *E. coli*, GSH and spermidine (Spd)⁴ form N¹-glutathionylspermidine (Gsp) via an ATP-dependent reaction catalyzed by the C-terminal Gsp synthetase domain (supplemental Fig. S1) (6–8). *E. coli* GspSA also hydrolyzes Gsp to GSH and Spd via the N-terminal amidase domain (supplemental Fig. S1) (6). Although GspSA was first found in *E. coli* more than 3 decades ago (9), it is not known what the physiological role of Gsp is or how the two opposing activities of GspSA are regulated *in vivo*.

Herein, we report that Gsp S-thiolated proteins (GspSSPs) have mixed disulfides of Gsp and protein thiols in *E. coli*. Intriguingly, we found that the level of GspSSPs increased when *E. coli* was treated with H₂O₂, indicating that this modification probably inhibits oxidation of protein thiols. The accumulation of GspSSPs probably occurred because, although Gsp amidase was inactivated by H₂O₂, Gsp synthetase was mostly unaffected. According to an x-ray crystallography study and a chemical modification study, we found that H₂O₂ oxidized the thiol of the amidase active-site nucleophile, Cys⁵⁹, to a sulfenic acid and that the sulfenic acid was stabilized by several hydrogen bonds, one of which involved a water molecule and was unusually short. We propose a set of reactions that explain how the transient inactivation of Gsp amidase leads to an accumulation of Gsp and an increased level of GspSSPs after oxidative stress. With elimination of the oxidative threat, Gsp amidase, GSH reductase, and glutaredoxin act in concert to convert oxidized Gsp (as the disulfide of Gsp ((GspS)₂), mixed disulfides of Gsp, and other small thiol-containing compounds and/or GspSSPs) to GSH. That GspSA and glutaredoxin act synergistically is supported by the hypersensitivity of *E. coli* mutants that lack both enzymes to H₂O₂.

EXPERIMENTAL PROCEDURES

The following experiments are described in the [supplemental material](#) due to space limitations: the construction of GspSA

* This work was supported by National Science Council of Taiwan Grant NSC97-2628-M-001-016-MY3.

[5] The on-line version of this article (available at <http://www.jbc.org>) contains supplemental Table S1 and Figs. S1–S10.

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⁴ The abbreviations used are: Spd, spermidine; (GspS)₂, disulfide of glutathionylspermidine; GSSG, disulfide form of GSH; GSSP, GSH S-thiolated protein; Gsp, glutathionylspermidine; GspSA, glutathionylspermidine synthetase/amidase; Gsp-SG, Gsp glutathione mixed disulfide; GspSSPs, Gsp S-thiolated proteins; Grx, glutaredoxin; mBBr, monobromobimane; 2-ME, β-mercaptoethanol; TSH, trypanothione; pNA, p-nitroanilide; MALDI, matrix-assisted laser desorption ionization; TOF, time-of-flight; MS, mass spectrometry.

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disrupted strain, protein crystallization and refinement, identification of sulfenic acid by dimedone, and the hydrolysis of GspSSPs by Gsp amidase.

Reagents and Chemicals—The chromogenic tripeptide γ -Glu-Ala-Gly-*p*-nitroanilide (γ -EAG-*p*NA), which was the amidase substrate, was synthesized as reported (10). The thiol-labeling reagent, monobromobimane (mBBr) and (GspS)₂ were purchased from Bachem and Invitrogen, respectively. Other chemicals were purchased from Sigma and Merck unless specified otherwise.

Protein Expression and Purification of GspSA—The genes, *GspSA*, *GspAF* (residues 1–197 of full-length *GspSA*), *GrxA* (coding for Grx1 (glutaredoxin 1)), and *GrxB* (coding for Grx2 (glutaredoxin 2)), were each subcloned into a pET28a plasmid (Novagen). Protein expression and purification procedures followed a previous report (11).

Detection of *E. coli* Gsp S-Thiolated Proteins—NR754 (wild type) and HA61002 (Δ *gspSA*) were each cultured in 1 ml of M9 minimal medium at 37 °C until the A₆₀₀ values of the cultures were 1.0. Then, 250 nmol of ¹⁴C-labeled spermidine (GE Healthcare) was added to each culture, and they were then incubated for an additional 10 h. Samples of the cells were treated with 0.5 mM H₂O₂ for 30 min, collected by centrifugation, mixed with SDS-loading buffer containing 0 or 50 mM 2-mercaptoethanol (2-ME), and then boiled for 15 min. After removing cell debris by centrifugation, the samples were subjected to SDS-PAGE. The separated proteins were stained with Coomassie Brilliant Blue or detected using a PhosphorImager system BAS-1500 (Fuji, Tokyo, Japan).

In Vitro and in Vivo Determination of Gsp Levels after H₂O₂ Treatment—For the *in vitro* assay, a 1.8 nM GspSA solution was first incubated with 500 μ M H₂O₂ for 5 min to inactivate the GspSA amidase activity and then treated with catalase (final concentration 1 mg/ml) for 20 min to remove any remaining H₂O₂. Omission of H₂O₂ served as the control. The samples were added to 250 mM Tris-HCl (pH 7.3), 2 mM GSH, 2 mM Spd, 1 mM ATP, 4 mM phosphoenolpyruvate, 10 mM MgCl₂, and 5 units/ml pyruvate kinase. Aliquots of 100 μ l were withdrawn periodically and heated at 95 °C for 10 min to inactivate the enzyme activities. Samples were then derivatized with mBBr, and Gsp and GSH contents were analyzed by HPLC (12).

For the *in vivo* assay, *E. coli* BL21(DE3) was cultured in M9 minimal medium until its A₆₀₀ was 1.5. Then the culture was treated with 1, 5, or 10 mM H₂O₂. After 10 min, the cells were centrifuged and lyophilized. Cells of suitable dry weight were lysed, and 800 μ M 2-ME (final concentration) was added. The lysates were derivatized with mBBr and then centrifuged at 8000 \times g for 30 min to remove cell debris. The resulting samples were subjected to HPLC to identify and quantify cellular thiol levels.

GspSA Activities Measured after H₂O₂ Treatment—To measure the degree to which Gsp amidase was inactivated by H₂O₂, γ -EAG-*p*NA was used as the substrate. The assay mixtures, at 25 °C, contained 0.45 nM GspSA, 125 mM Tris-HCl (pH 7.3), 1.25 mM γ -EAG-*p*NA, and various concentrations of H₂O₂. *p*-Nitroanilide formation was monitored as an increase in absorbance at 405 nm.

Gsp synthetase activity in the presence of H₂O₂ was assayed by a pyruvate kinase/lactate dehydrogenase-coupled assay that

used ADP (a product of Gsp synthetase) and consumed NADH. NADH consumption was monitored by fluorescence emission at 460 nm (excitation at 340 nm). The assay mixture contained 125 mM Tris-HCl (pH 7.3), 0.2 mM NADH, 1 mM phosphoenolpyruvate, 10 units/ml pyruvate kinase, 10 units/ml lactate dehydrogenase, 2 mM ATP, 10 mM GSH, 10 mM Spd, 10 mM MgCl₂, and various concentrations of H₂O₂. Control experiments indicated that H₂O₂ did not affect NADH consumption or the pyruvate kinase/lactate dehydrogenase couple.

The ability of GSH to restore amidase activity was assessed. GspSA (0.45 nM) was first inactivated with 500 μ M H₂O₂ for 5 min. Then catalase (final concentration 1 mg/ml) was added, and 4 mM GSH was incubated for 20 min. Inactivated Gsp amidase was then incubated with the aforementioned reagents to ascertain if they could reactivate Gsp amidase. The levels of recovered activity were measured using the γ -EAG-*p*NA assay. The control experiment used H₂O instead of H₂O₂, and its activity level was normalized to 100%.

The Viabilities of GspSA and Glutaredoxin Null Mutants after H₂O₂ Treatment—Overnight cultures (Δ *grxA*, Δ *grxB*, Δ *grxA* Δ *gspSA*, and Δ *grxB* Δ *gspSA*) were diluted with fresh M9 minimal medium containing 0.4% glucose and cultivated until A₆₀₀ of 1.0 were reached. Then different concentrations of H₂O₂ were added to the cultures, and they were incubated for an additional 1 h. The cultures were serially diluted with PBS buffer and plated onto LB agar plates. The survival percentage (survivability) was calculated as ((CFU in the presence of H₂O₂)/(CFU in the absence of H₂O₂))/100, where CFU represents colony-forming units. The survivability values (%) for each H₂O₂ concentration were calculated using those of at least three replicates and are presented as the means \pm S.D.

Conversion of Gsp-disulfide to GSH by a Gsp Amidase/GSH Reductase Couple—To determine if Gsp amidase could catalyze the hydrolysis of (GspS)₂, 5 mM Gsp-disulfide and 10 μ M GspSA (1 μ g) were incubated at 37 °C and then subjected to MALDI-TOF-MS. Similarly, to determine if (GspS)₂ could be converted to GSH by the Gsp amidase/GSH reductase couple, 0.23 unit/ml of GSH reductase (final concentration) was added to mixtures of 100 mM Tris-HCl (pH 7.3), 0.5 mM NADPH, 600 μ M (GspS)₂ at 25 °C with or without 28.7 μ M GspSA. NADPH consumption was measured by monitoring fluorescence emission at 460 nm (excitation at 340 nm). Replacement of (GspS)₂ with oxidized GSH (GSSG, the native substrate of GSH reductase) served as the positive control, whereas the negative control did not include (GspS)₂ and GSSG.

RESULTS

Identification of *E. coli* Gsp S-Thiolated Proteins—To investigate if Gsp S-thiolates *E. coli* proteins, ¹⁴C-labeled spermidine (Spd*) was added to cultures of NR754 (wild type) and HA61002 (Δ *gspSA*). NR754 has an endogenous GspSA that can conjugate GSH and Spd* to form ¹⁴C-labeled Gsp (Gsp*; Fig. 1A). After uptake of Spd*, Gsp*-labeled proteins were detected in lysates of NR754 by phosphorimaging after SDS-PAGE (Fig. 1B, right). The proteins were Gsp S-thiolated was confirmed by treatment of the Gsp*-labeled cell lysates with 2-ME (Fig. 1B, right), which decreased the amount of radiolabeled proteins observed and was attributed to disulfide

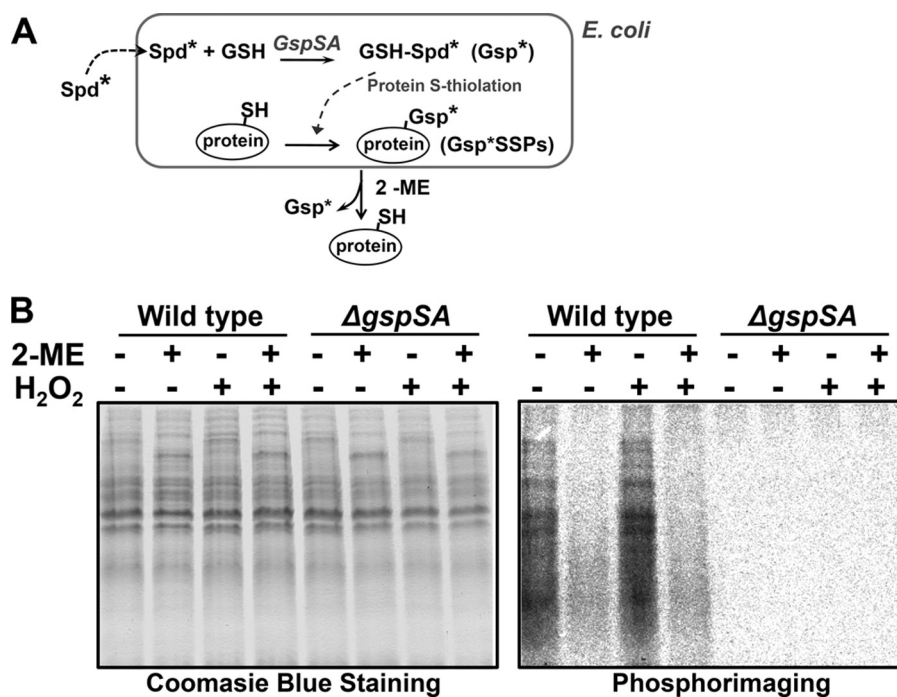


FIGURE 1. Detection of GspSSPs in *E. coli*. *A*, a schematic diagramming how Gsp S-thiolation of *E. coli* proteins was detected. ^{14}C -Labeled spermidine (Spd^*) was added into an *E. coli* culture and was then conjugated with GSH by Gsp synthetase activity in GspSA to form radiolabeled Gsp (Gsp^*). Gsp^* SSPs were detected by phosphorimaging after SDS-PAGE. The levels of radiolabeled proteins were reduced when extracts were treated with 2-ME. *B*, SDS-PAGE analysis of *E. coli* proteins in NR754 (wild type) and HA61002 (ΔgspSA). *Left*, Coomassie Brilliant Blue-stained proteins. *Right*, phosphorimaging of radiolabeled proteins.

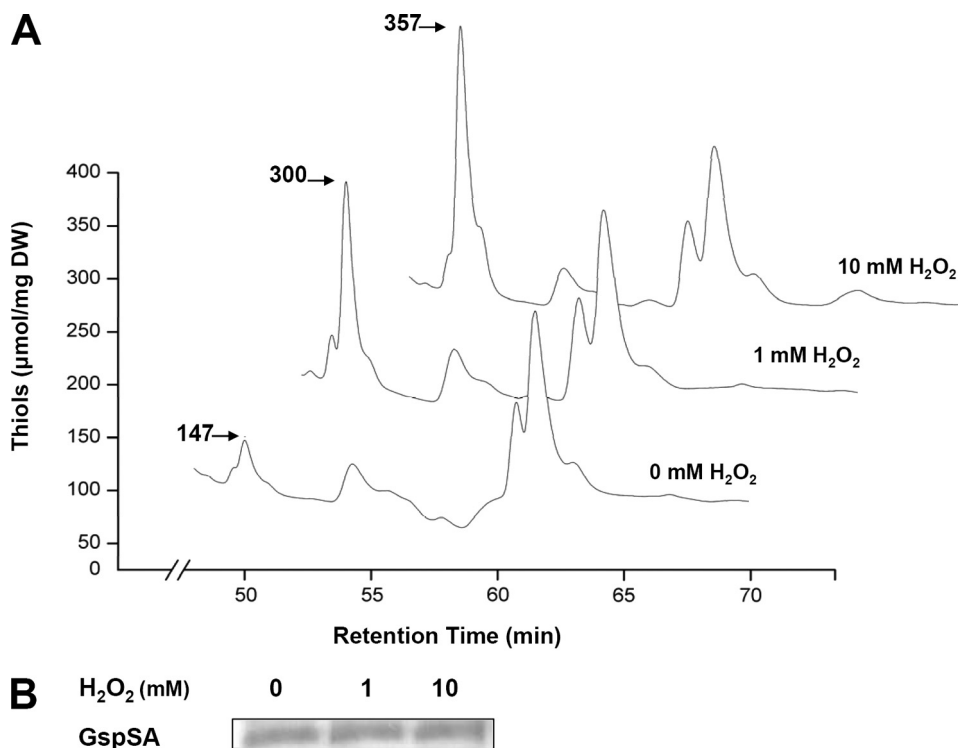


FIGURE 2. Gsp accumulation in *E. coli* after H_2O_2 treatment. The levels of Gsp and GspSA in *E. coli* were measured after the bacteria had been cultured in M9 minimal medium, treated with H_2O_2 , lysed, and treated with mBBr. *A*, HPLC chromatograms of mBBr-derivatized thiol compounds detected using fluorescence spectroscopy. The arrows indicate the elution position of Gsp. The numbers above the arrows are the amounts (μmol) of Gsp obtained from 1 mg, dry weight, of cells. *B*, SDS-PAGE of GspSA shows that its expression level was unaffected by H_2O_2 .

cleavage by 2-ME. Proteins of HA61002 (ΔgspSA) were not radiolabeled because Gsp could not be synthesized in HA61002 (Fig. 1*B*, right). Interestingly, the enhanced level of GspSSPs after H_2O_2 treatment was reminiscent of the protective effects offered by GSH S-thiolation (13), which implied that Gsp might also protect protein thiols against irreversible oxidation. Various Gsp-protein conjugates were formed (Fig. 1*B*, right), suggesting that Gsp S-thiolation of proteins may be involved in diverse types of biological processes.

Rapid Accumulation of Gsp *In Vivo* in the Presence of H_2O_2 —To measure the intracellular Gsp level after treatment with H_2O_2 , M9 minimal medium cultures of *E. coli* BL21(DE3) that were in stationary phase ($A_{600} = 1.2$) were treated with 1, 5, or 10 mM H_2O_2 and then incubated for an additional 10 min. The cells were collected by centrifugation and then lysed. Monobromobimane (mBBr) was added into the lysates to derivatize thiol-containing compounds (12), and after HPLC analysis, mBBr-modified Gsp in the eluates was quantified (fluorescence emission at 480 nm, excitation at 375 nm). The addition of 1 or 10 mM H_2O_2 led to a 2.2- or 3.6-fold increase in Gsp concentration, respectively, within 10 min (Fig. 2*A*). Expression of GspSA was not altered by H_2O_2 treatment (Fig. 2*B*), indicating that the observed increase in Gsp was not linked to the level of GspSA.

Selective Inactivation of Gsp Amidase by H_2O_2 —To determine how the GspSA in *E. coli* is affected by oxidative damage, the enzyme was treated with 50, 100, and 500 μM H_2O_2 , and the synthetase and amidase activities were determined. In all cases, the Gsp amidase activity decreased as functions of time and dose (Fig. 3*A*) with 50% inhibitory concentration of 250 μM (data not shown). Inactivation was >95% when GspSA was incubated with 500 μM H_2O_2 for 5 min. Conversely, the synthetase activity remained almost completely active under the

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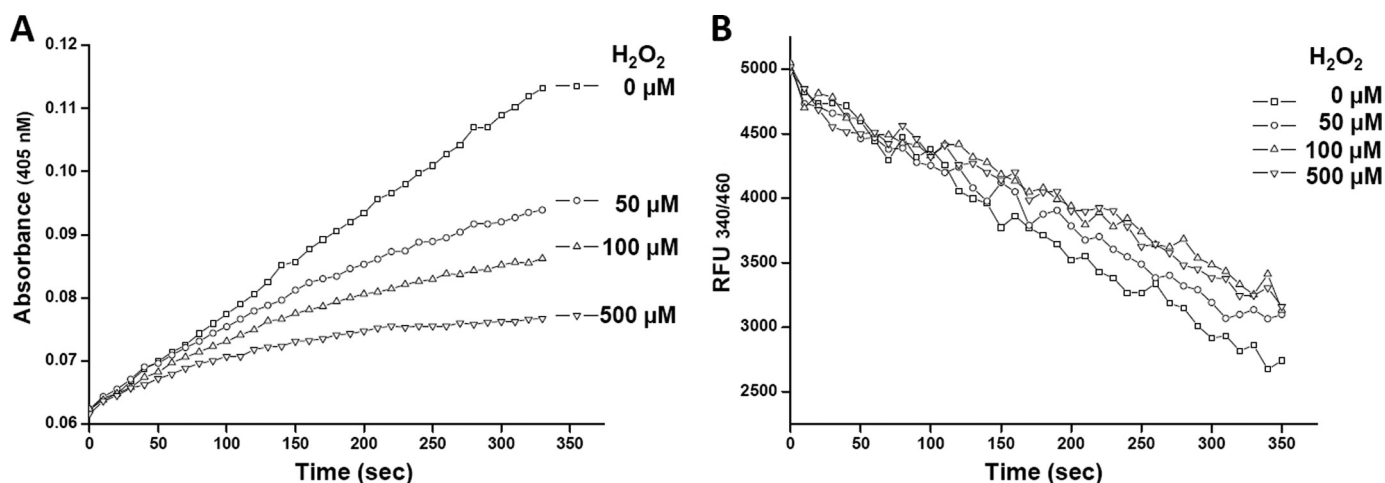


FIGURE 3. **Effects of H_2O_2 on GspSA amidase and synthetase activities.** *A*, plots of Gsp amidase activity that remained after treatment with four different concentrations of H_2O_2 . Activity was measured using the chromogenic substrate γ -EAG-*p*NA. *B*, plots of Gsp synthetase activity that remained after treatment with four different concentrations of H_2O_2 . At worst, there was only a 10% reduction in synthetase activity compared with that of the negative control (0 M H_2O_2). Synthetase activity was measured as the consumption of NADH by the pyruvate kinase/lactate dehydrogenase couple, which also used ADP generated by Gsp synthetase.

same conditions (Fig. 3*B*). The finding that H_2O_2 affects the two activities differently is supported by the structural information described below.

To determine whether H_2O_2 -mediated amidase inactivation could be rescued by a biological reducing agent, inactivated GspSA (treated with 500 μM H_2O_2 for 5 min and then incubated with catalase for 20 min to remove excess H_2O_2) was exposed to GSH. The addition of 4 mM GSH (physiological concentration) recovered $\sim 80\%$ of the amidase activity (supplemental Fig. S2). To examine how selectively inactivated Gsp amidase affected the level of Gsp, GspSA was treated with GSH, Spd, ATP, phosphoenolpyruvate, and pyruvate kinase with or without prior exposure to H_2O_2 . The mixtures were then treated with mBBr and analyzed by HPLC. Whether H_2O_2 -treated or not, the Gsp concentrations initially increased and then declined (supplemental Fig. S3); therefore, the level of Gsp was tightly regulated. After pretreatment with H_2O_2 , Gsp accumulated to a greater extent than it did otherwise (no treatment). Additionally, less GSH was present at all times longer than the initial stage (~ 25 min). Both of these observations suggested that H_2O_2 selectively inactivates Gsp amidase, but the amidase activity recovers at a later stage. More Gsp was produced as a consequence of oxidative damage.

Identification of Cys⁵⁹-Sulfenic Acid by X-ray Crystallography and a Chemical Modification Study—The structure of the H_2O_2 -treated Gsp amidase fragment (GspAF- H_2O_2 ; supplemental Table S1) was obtained by soaking a GspAF crystal in crystallization buffer containing 1 mM H_2O_2 for 3 days before x-ray crystallography. The electron density map of GspAF- H_2O_2 (Protein Data Bank entry 3A2Z) at 1.5 Å resolution has a density not seen in untreated GspAF that extends from Cys⁵⁹ S^γ and corresponds to two adjacent oxygen atoms (Fig. 4*A*). The distance between the S and O1 is 2.1 Å, the C-S-O1 angle is 96.0°, and the S-O1-O2 angle is 94.2°. The second oxygen atom (O2) is unusually close to O1 (2.2 Å). Using the structural and other information (see below), we suggest that the Cys⁵⁹ thiol was oxidized to sulfenic acid and that its oxygen atom forms a very short hydrogen bond (< 2.3 Å) (14) with a water molecule

($\text{H}_2\text{O}_{\text{trid}}$; Fig. 4*B* and supplemental Table S1); therefore, the extra electron density probably arose as a consequence of an S-O1 \cdots H \cdots O2-H hydrogen bond. Partial negative charges could be present at O1 and O2 because such hydrogen bonds have partial ionic character. Conversely, we do not believe that a hydroperoxide-derivatized cysteine ($-\text{S}-\text{O}-\text{O}-\text{H}$) was present because the S-O and O-O distances are not compatible with such a compound, and it would be less stable than a sulfenic acid (15).

The sulfenic acid that was produced when a GspAF crystal was soaked with 1 mM H_2O_2 for 20 min was reduced to a free thiol when subsequently treated with 1 mM GSH (data not shown). Interestingly, the sulfenic acid was not further oxidized by either prolonged incubation with H_2O_2 or by a greater concentration of H_2O_2 (10 mM). To our surprise, Cys⁵⁹ was covalently bonded to an acetate oxygen in the GspAF-acetate crystal structure (Protein Data Bank code 3A30; supplemental Fig. S4). This S-modification was probably caused by a nucleophilic attack of an acetate ion on the sulfenic acid, which was favorable because of the large acetate concentration (100 mM) and the prolonged exposure.

Although Cys⁵⁹, which is the catalytic nucleophile for GspSA amidase, was oxidized by H_2O_2 , other GspSA cysteines, including Cys³³⁸ and Cys⁵³⁹, which form part of the synthetase binding site (9), were not oxidized when crystals of GspSA were treated with H_2O_2 (data not shown).

To further corroborate that the Cys⁵⁹ thiol was oxidized to a sulfenic acid (16), GspAF was first treated with 100 μM H_2O_2 for 10 min, which fully inactivated GspAF, and then reacted with 100 μM 5,5-dimethyl-1,3-cyclohexanedione (dimedone), which specifically reacts with sulfenic acid (16), at 25 °C for 12 h. After removing excess reagents, derivatized GspAF was digested with trypsin, and its hydrolytic products were analyzed by MALDI-TOF-MS (Fig. 4*C*). The signal $(\text{M} + \text{H})^+$ at m/z 1176.8 is expected for the adduct formed by the GspSA sequence ⁵⁷WQCVEFAR⁶⁴ ($M_r = 1037$) and dimedone ($M_r = 140$). The presence of b- and γ-series ions confirmed that dimedone modified the Cys⁵⁹ sulfenic acid. Therefore, the thiol of Cys⁵⁹ was oxidized to the sulfenic acid by H_2O_2 .

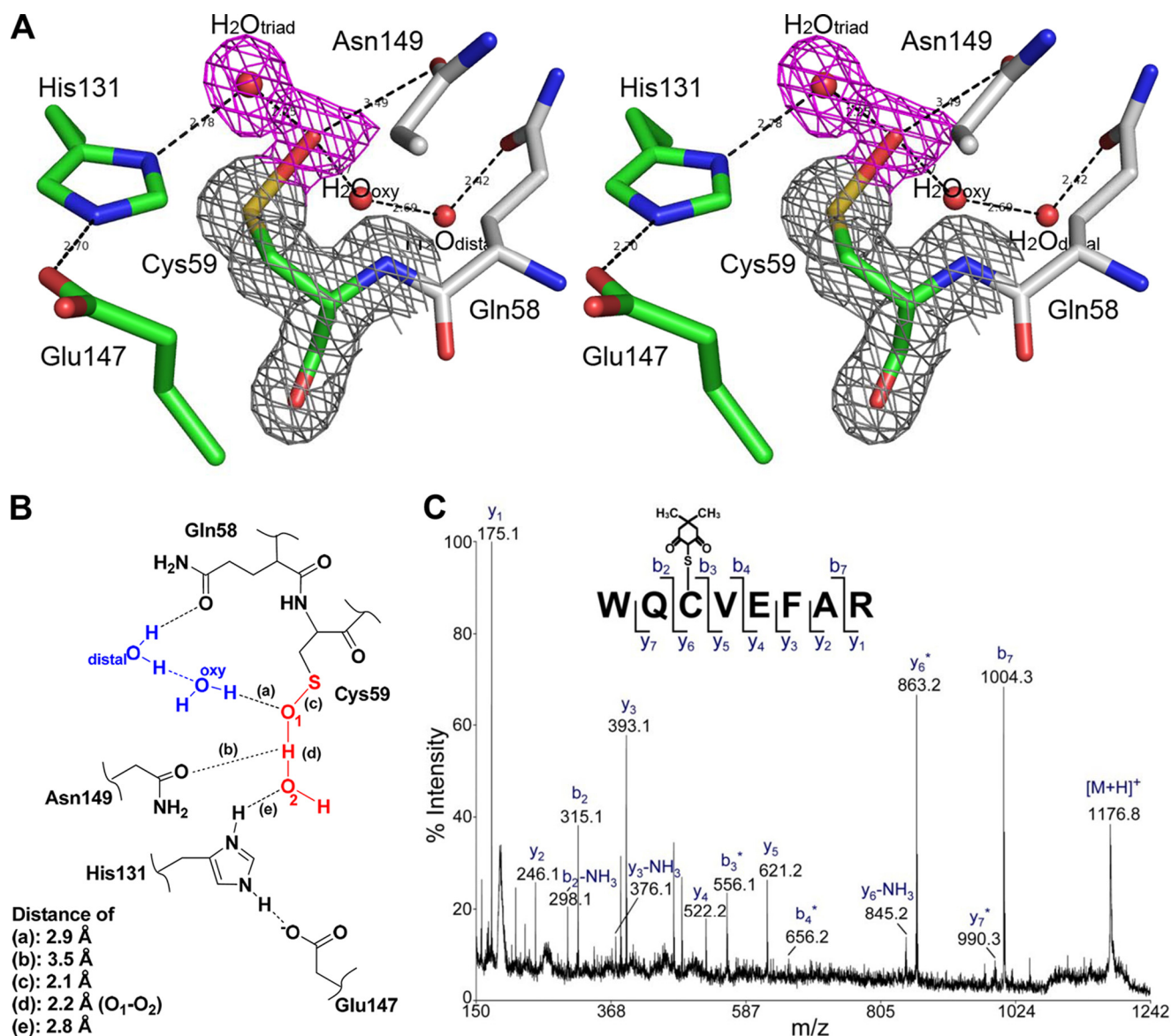


FIGURE 4. Identification of the Cys⁵⁹ sulfenic acid by x-ray crystallography and chemical modification/mass spectrometry. *A*, stereo view of the $2F_o - F_c$ electron density map at the active site of GspAF- H_2O_2 . The electron density map, drawn at a contour level of 1σ , shows continuous density (in red) connected to the S γ atom of Cys⁵⁹. This density was fitted with the oxygen atom of a sulfenic acid (-SOH) and the oxygen of a tightly hydrogen-bonded water molecule. Limited by the structure resolution, it is possible that the Asn¹⁴⁹ side chain can be flipped. *B*, schematic of the hydrogen bond network associated with the Cys⁵⁹ sulfenic acid in GspAF- H_2O_2 . The sulfenic acid/water hydrogen bond is shown in red. Two other water molecules that contribute to the stability of the sulfenic acid are shown in blue. *C*, MALDI-MS-MS spectrum of the tryptic peptides that contained the Cys⁵⁹-dimedone adduct. Gsp amidase, after oxidation by H_2O_2 , was treated with dimedone, digested with trypsin, and subjected to MALDI-MS. The dimedone-modified Cys⁵⁹-containing peptide (⁵⁷WQCVVEFAR⁶⁴) has a molecular weight of 1176.6. That covalent dimedone modification of Cys⁵⁹ had occurred is evidenced by the y- and b-ions identified with asterisks.

Hydrolysis of Gsp-disulfide and Gsp S-Thiolated Proteins and Peptides by Gsp Amidase—*E. coli* lacks an enzyme that can reduce (GspS)₂ (17). If (GspS)₂ is involved in *E. coli* redox regulation, then there must be a way to convert (GspS)₂ to Gsp. We next showed that it is possible to convert (GspS)₂ to GSH by coupling Gsp amidase and GSH reductase activities. (GspS)₂ could be hydrolyzed by Gsp amidase, as shown by MALDI-TOF-MS analysis. After a 10-min or 4-h incubation (GspS)₂ with GspSA, Spd, Gsp-GSH mixed disulfide (Gsp-SG), and GSH disulfide (GSSG) were generated, as indicated by the presence of MS peaks at m/z 740.6 ((M + H)⁺, Gsp-SG), at m/z 613.3 ((M + H)⁺, GSSG), and at m/z 635.3, ((M + Na)⁺, GSSG) (Fig. 5A). A second assay was per-

formed to determine if (GspS)₂ was a substrate for GSH reductase. GSH reductase activity was detected as NADPH consumption, which was monitored by NADPH absorption at 340 nm (Fig. 5B). GSH reductase alone (without the addition of GSSG) served as the negative control (*open circles* in Fig. 5B). No activity was observed when (GspS)₂ was incubated with only GSH reductase and NADPH (*filled squares*), in contrast to the result found for GSSG (*filled circles*). Activity was also observed when (GspS)₂ was treated with GspSA and GSH reductase (*open triangles*). The experimental results presented in Fig. 5B suggested that both (GspS)₂ and Gsp-SG were converted to GSH and Spd via consecutive reactions by Gsp amidase and GSH reductase (Fig. 5C).

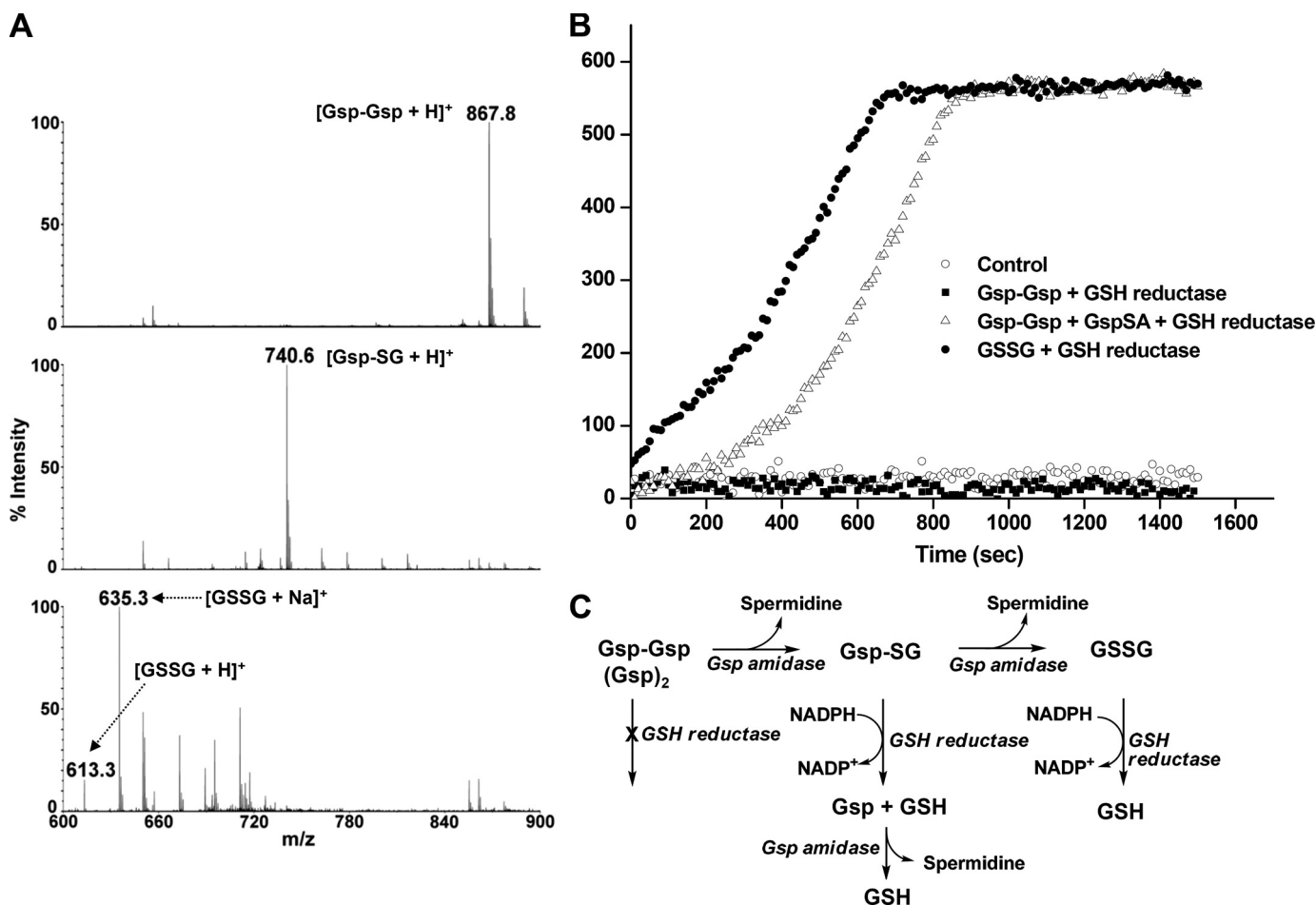


FIGURE 5. Conversion of $(\text{GspS})_2$ to GSH and Spd by the Gsp amidase/GSH reductase couple. A, a MALDI-TOF spectrum that shows the molecular weights of the hydrolysis products after $(\text{GspS})_2$ was treated with GspSA for 0 min (top), 10 min (middle), or 4 h (bottom). GSSG was the end product. B, the Gsp amidase/GSH reductase coupled assay. $(\text{GspS})_2$ cannot be reduced by GSH reductase alone (■), but it is reduced when both GspSA and GSH reductase are present (Δ). GSSG plus GSH reductase served as the positive control (●). GSH reductase alone served as the negative control (○). C, reaction scheme for the enzymatic conversion of $(\text{GspS})_2$ to GSH and Spd by the Gsp amidase/GSH reductase couple.

We next tested whether Gsp S-thiolated peptides and proteins were substrates for Gsp amidase. Lysates of *E. coli* proteins were treated with disulfide of biotinylated Gsp (*Biotin-GspS*)₂ (Fig. 6A) to generate biotin-labeled GspSSPs (biotin-GspSSPs), which could be detected with an anti-biotin antibody (Fig. 6B). Treatment of these proteins with GspSA removed Spd-biotin moieties because biotin-GspSSPs were no longer observed after staining with the anti-biotin antibody (Fig. 6C, left panel, lane 3). Treatment with 2-ME also produced the same result, presumably because 2-ME cleaved Gsp-protein disulfides (Fig. 6C, left panel, lane 2). A synthetic Gsp-containing peptide (T28-Gsp) was also incubated with GspSA, and a MALDI-TOF-MS spectrum of that incubation mixture indicated that T28-Gsp was a substrate for Gsp amidase (supplemental Fig. S5). Therefore, Gsp amidase can hydrolyze a variety of Gsp-derivatized substrates, yielding Spd and GSH S-thiolated proteins/peptides.

Sensitivities of Different *E. coli* Strains to Oxidative Stress—To characterize how Gsp and GspSA protect against oxidative stress, cultures of NR754 (wild type) and HA61002 (ΔgspSA) were treated with various concentrations of H_2O_2 , and the viabilities of the cells were examined after treatment. The strains were cultured in M9 minimal medium until the cells

reached mid-exponential phases, at which point they were treated with H_2O_2 , incubated for 1 h, serially diluted with PBS buffer, and then transferred to LB plates. The viabilities of NR754 and HA61002 under oxidative stress were similar (supplemental Fig. S6), which is consistent with a previous report that an *E. coli* strain lacking the ability to synthesize GSH was as resistant to H_2O_2 as the corresponding wild-type strain was (18).

Because glutaredoxins can reduce GSH S-thiolated proteins (GSSPs) (19), we wanted to determine if these enzymes are part of a redox cycle involving Gsp S-thiolation. The viabilities of two glutaredoxin null strains (ΔgrxA and ΔgrxB) and two double mutant strains ($\Delta\text{grxA}\Delta\text{gspSA}$ and $\Delta\text{grxB}\Delta\text{gspSA}$) were examined after they were treated with H_2O_2 . When preincubated with 1 or 5 mM H_2O_2 for 1 h, ΔgrxA and ΔgrxB had survivability values of 60 and 30%, respectively (Fig. 7). The double mutant strains were even more susceptible to oxidative damage because their survivabilities were reduced by 70 and 99% after exposure to 1 and 5 mM H_2O_2 , respectively. Therefore, there is a synergistic protective effect by GspSA and Grx against oxidative damage. Moreover, in a separate experiment, the levels of GspSSPs were substantially decreased when recombinant glutaredoxin (Grx1 or Grx2) was added to *E. coli*

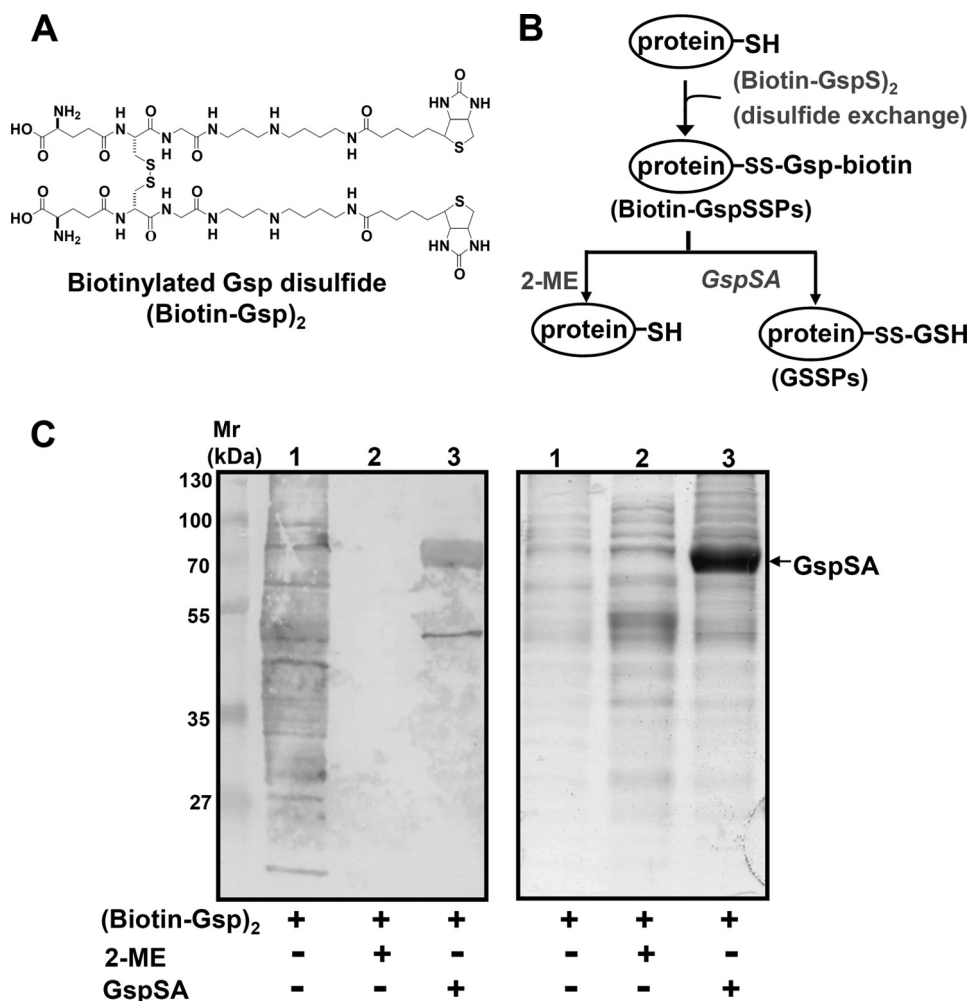


FIGURE 6. Conversion of GspSSPs to GSSPs by Gsp amidase-catalyzed hydrolysis. *A*, the (biotin-Gsp)₂ structure. *B*, schematic showing the preparation of biotinylated Gsp S-thiolated proteins (biotin-GspSSPs). Treatment of biotin-GspSSPs with GspSA generated GSH S-thiolated proteins. Treatment of biotin-GspSSPs with 2-ME generated unlabeled proteins. *C*, SDS-PAGE of biotin-GspSSPs. *Left*, Western blot using an alkaline phosphatase-conjugated anti-biotin antibody. *Mr*, molecular weight markers. *Lane 1*, biotin-GspSSPs from an *E. coli* lysate. *Lane 2*, biotin-GspSSPs as in *lane 1* that were treated with 20 mM 2-ME before SDS-PAGE. *Lane 3*, biotin-GspSSPs as in *lane 1* that were treated with 5 μg of GspSA before SDS-PAGE.

lysates that contained Gsp*SSPs (supplemental Fig. S7). These results strengthen the idea that Grxs participate in the reduction of Gsp S-thiolated proteins.

DISCUSSION

Redox Regulation of Gsp and Gsp S-Thiolated Proteins—Most organisms use GSH to regulate their intracellular thiol and disulfide levels. Gsp is a GSH derivative found only in some bacteria and parasitic protozoa. As reported herein, we showed that Gsp forms mixed disulfides with the thiols of *E. coli* proteins *in vivo* and that the amounts of these Gsp derivatives are linked to intracellular redox conditions. *In vivo* Gsp S-thiolation of *E. coli* proteins is affected by several factors, including the intracellular Gsp concentration. We demonstrated that the Gsp level increases when *E. coli* is oxidatively stressed. The selective inactivation of Gsp amidase provides a rational explanation for this event. When *E. coli* is exposed to reactive oxygen species, the thiol of Cys⁵⁹ of the active-site amidase domain is oxidized to sulfenic acid, which inactivates Gsp amidase and

consequently causes Gsp to accumulate (Fig. 8). Accumulated Gsp possibly scavenges oxidants directly or forms mixed disulfides with protein thiols. Once the source of the oxidative stress has been eliminated, Gsp amidase activity can be rescued by reaction of the sulfenic acid with a reducing reagent (e.g. GSH or Gsp). Sulfenic acid is a reactive electrophile and reacts with thiol reagents, such as GSH, to generate mixed disulfides. The amidase active site is solvent-exposed, which should allow GSH or other small thiol-containing molecules to react with the sulfenic acid. After formation of a mixed disulfide, an additional thiol exchange may continue regenerating the thiol of Cys⁵⁹ and thereby recovering amidase activity (supplemental Fig. S8). The reactivated amidase may then hydrolyze either excessive Gsp to GSH and Spd and/or GspSSPs to GSSPs and Spd. Gsp could also be oxidized to produce (GspS)₂ and/or other mixed disulfides upon reaction with reactive oxygens. We showed that GSH reductase alone cannot reduce (GspS)₂ but that Gsp amidase must first remove the spermidine moiety. The conversion of (GspS)₂ to Spd and GSH by the Gsp amidase/GSH reductase couple suggests that Gsp may be part of an oxidative defense mechanism that does not require a Gsp-specific reductase. Such a reductase has not been found in *E. coli* (17).

The results allow us to propose a reaction scheme (Fig. 8) that explains how Gsp amidase activity is modulated *in vivo* so that the Gsp level reflects the intracellular redox condition.

Glutaredoxins reduce mixed disulfide bonds between GSH and GSSPs by forming a GrxSSG intermediate that can be subsequently reduced by a molecule of GSH (20). The protein expression level of Grx1 is enhanced under oxidative stress in *E. coli*, whereas Grx2 is constitutively produced (21). We found that the amounts of GspSSPs decreased in the presence of Grx1 or Grx2 (supplemental Fig. S7), suggesting that Grxs can reduce mixed disulfides. As mentioned, Gsp amidase catalyzes the hydrolytic removal of Spd from GspSSPs, leading to the formation of GSSPs. A Grx can then reduce the GSSPs to generate free protein thiol(s) (supplemental Fig. S9). However, we cannot exclude the possibility that glutaredoxin directly reduces GspSSPs, with the resulting Grx-Gsp mixed disulfide intermediate subsequently reduced via thiol-disulfide exchange (supplemental Fig. S9). Because Δ*grxA*Δ*gspSA* and Δ*grxB*Δ*gspSA* were more easily killed by H₂O₂ than were

Glutathionylspermidine, a Redox Regulator

$\Delta grxA$ and $\Delta grxB$, it appears that the activities of Grx and GspSA can provide a coordinated defense against oxidative damage in *E. coli*.

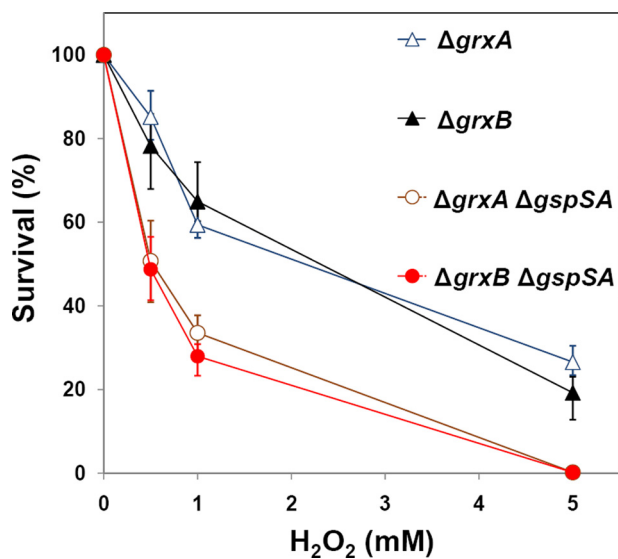


FIGURE 7. Glutaredoxin- and GspSA/glutaredoxin-null mutants exhibit hypersensitivities to exogenous H₂O₂. All strains were grown in M9 minimal medium until the cell densities reached 1.0 A₆₀₀. Then the cultures were treated with various concentrations of H₂O₂ for 1 h, and then 0.1 ml of each culture was transferred onto LB plates. The numbers of viable cells were then determined. Survival percentages (survivabilities) of $\Delta grxA$ (Δ , blue), $\Delta grxB$ (\blacktriangle , black), $\Delta grxA \Delta gspSA$ (\circ , brown), and $\Delta grxB \Delta gspSA$ (\bullet , red) were calculated as ((CFU in the presence of H₂O₂)/(CFU in the absence of H₂O₂))/100. Survivability values (%) are the means of three replicates \pm S.D. (error bars).

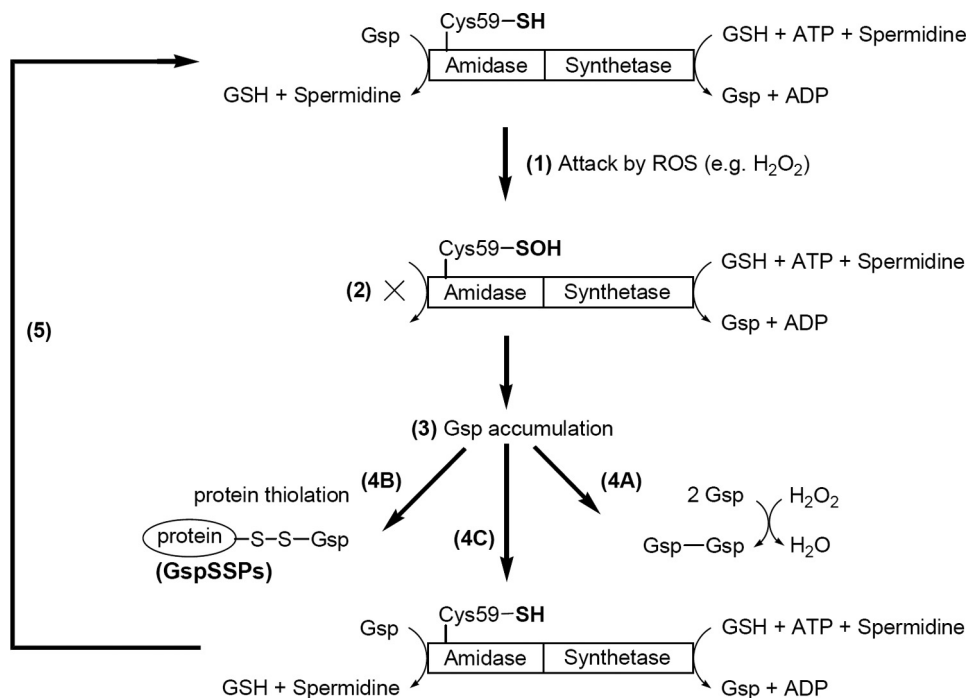


FIGURE 8. The roles of Gsp and glutathionylspermidine synthetase/amidase in the intracellular redox regulation of *E. coli*. When exposed to reactive oxygen species (ROS), the active-site Cys⁵⁹ thiol of Gsp amidase is oxidized to sulfenic acid (1), which causes the inactivation of Gsp amidase (X) (2). Because Gsp synthetase is not affected by ROS, intracellular Gsp accumulates (3). Gsp may then scavenge harmful oxidants by forming Gsp-disulfides and other small molecule disulfide compounds (4A) and/or protecting protein thiols from oxidation by Gsp S-thiolation (4B). With the removal of the oxidative stresses, intracellular GSH and/or Gsp may rescue oxidized Gsp amidase, restoring amidase activity (4C). Reactivated Gsp amidase may hydrolyze Gsp to GSH and Spd or hydrolytically remove Spd from Gsp-disulfide or Gsp-modified proteins. Finally, the amount of Gsp returns to its basal level (5).

To date, most studies concerning protein S-thiolation have focused on GSH, because GSH is abundant in cells (4). However, protein S-thiolation by other thiol-containing molecules, such as cysteine or Gsp, may have different effects. For example, a previous study demonstrated that GSH S-thiolation of Ca²⁺-dependent protein kinase C α inhibits the activity of Ca²⁺-dependent protein kinase C α and its isozymes, whereas cysteine S-thiolation does not (22). Both trypanothione (TSH) and Gsp are more efficient reducing agents than is GSH. The non-enzymatic reductions of dehydroascorbate and H₂O₂ by Gsp and TSH are several times faster than those by GSH (23, 24). It has also been found that Gsp was a more efficient S-thiolating agent than was GSH (25). GSH is negatively charged (-1) at physiological pH, whereas Gsp is positively charged (+2). Gsp and GSH therefore introduce opposite charges into the proteins that they thiolate. Protein thiols are deprotonated to form thiolates that interact more readily with (Gsp)₂ at pH >6, rather than GSSG (25). Although GSH and Gsp have distinct physical and chemical properties, it is still difficult to elucidate how GSH and Gsp function *in vivo* because of the involvement of the GspSA amidase-catalyzed conversion of GspSSPs to GSSPs.

Dissimilar Amidase Active Sites Linked to Differential Redox Regulation—Parasitic protozoa use TSH, which is synthesized by TSH synthetase/amidase to defend against oxidative damage. Like GspSA, TSH synthetase/amidase has an amidase activity that can hydrolyze the amide bond of Gsp. There-

fore, it would be interesting to know if TSH amidase can be selectively and reversibly inactivated. In the x-ray structure of *Leishmania major* TSH synthetase/amidase, the C-terminal segment partially obstructs accessibility to the catalytic Cys⁵⁹ nucleophile (26). Consequently, the active site of TSH amidase is substantially blocked, in contrast with that of GspSA, which is part of a large, solvent-accessible cleft. Even if the TSH amidase Cys⁵⁹ thiol could be oxidized to sulfenic acid and/or form a mixed disulfide with GSH or TSH, the restricted access almost certainly would impede subsequent thiol exchange (supplemental Figs. S8 and S10). Because access to the TSH amidase active site is partially obscured, TSH reductase and TSH trypanothione may compensate as a defense mechanism against reactive oxygen in parasitic protozoa. It is also possible that, with the evolutionary emergence of TSH reductase and TSH trypanothione, TSH amidase degenerates and no longer participates in redox regulation.

*Cys*⁵⁹ Sulfenic Acid of GspSA Is Primarily Stabilized by a Very Short Hydrogen Bond—Sulfenic acid is an unstable compound and is highly reactive; therefore, it usually acts as an intermediate *en route* to other more stable oxidized sulfur compounds (e.g. sulfinic and sulfonic acids) (27). Nature has used different strategies to stabilize sulfenic acids. For example, the sulfur of sulfenic acid and an amide nitrogen can form a cyclic sulfonamide, which has been found in the crystal structure of protein-tyrosine phosphatase (Protein Data Bank entry 1OEM) (28). The sulfenic acid of an archaeal 2-Cys peroxiredoxin (Protein Data Bank entry 2ZCT) is hypervalent with an S–N covalent bond (2.2 Å) between S^γ of Cys⁵⁰ and N^{δ1} of His⁴² (29). Other sulfenic acids derived from cysteines exist in solvent-inaccessible and nonpolar microenvironments. Their limited solvent accessibilities prevent further oxidation to a sulfinic or sulfonic acid, which are not reducible. Conversely, Cys⁵⁹ of Gsp amidase is solvent-accessible because it is located on the surface. We did not observe formation of Cys⁵⁹ sulfinic acid or sulfonic acid even when GspAF was exposed to 10 mM H₂O₂. The sulfenic acid of GspAF–H₂O₂ is most likely stabilized by hydrogen bonds formed with water oxygens. In the GspAF–H₂O₂ structure, the S–O1 bond (2.1 Å) is longer than those S–O bonds commonly observed in proteins (~1.7 Å) (e.g. NAD(P)H oxidase (Protein Data Bank entry 2CDU)) (30). The S–O1 of GspAF–H₂O₂ is thus polarized, which probably causes the sulfur to be partially positively charged and thereby prevents further oxidation. The very short hydrogen bond between O1 and O2 (O1···H···O2) also stabilizes the sulfenic acid (Fig. 4, A and B). Because both O1 and O2 should be partially negatively charged, the repulsion between them might be compensated for by three hydrogen bonds (hydrogen bonds of *a*, *b*, and *e* in Fig. 4B) found in the GspAF crystal structure. Two of the three hydrogen bonds involving O1 are the hydrogen bonds with a water molecule (H₂O_{oxy}) and with the side-chain O of Asn¹⁴⁹, which is an oxyanion binding site residue, with distances of 2.9 and 3.5 Å, respectively. Interestingly, the N^ε of Gln⁵⁸, which is also the other residue in the oxyanion hole, forms a hydrogen bond network with two water molecules (H₂O_{oxy} and H₂O_{distal}) (Fig. 4, A and B). The third hydrogen bond is formed between a hydrogen of O2 and an imidazole nitrogen of His¹³¹. These observations are consistent with the suggestion of Salsbury *et al.* (31) that surrounding hydrogen bond networks stabilize the sulfenic acids found in proteins.

In summary, Gsp formed mixed disulfides with the thiols of a variety of *E. coli* proteins. These mixed disulfides represent a previously uncharacterized type of post-translational modification. The *E. coli* GspSA amidase activity was selectively inhibited *in vivo* by oxidation of its Cys⁵⁹ thiol to sulfenic acid. This inhibition led to a rapid increase in the amounts of intracellular Gsp and GspSSPs. Basal levels of Gsp and GspSSPs were recovered once the oxidative threat was eliminated, and at that time, the amidase activity was restored. Moreover, the hypersensitivities of the GspSA/Grx null mutants to H₂O₂ support the idea that GspSA and Grx synergistically defend against oxidative damage.

Acknowledgments—Some *E. coli* strains were obtained from the National Bioresource Project, Japan. We thank the National Synchrotron Radiation Research Center of Taiwan and the National Core Facility of Proteomics for mass spectrometry analysis.

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Supplemental Information

PROTEIN S-THIOLATION BY GLUTATHIONYLSPERMIDINE (GSP): THE ROLE OF *ESCHERICHIA COLI* GSP SYNTHETASE/AMIDASE IN REDOX REGULATION

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Running head: Glutathionylspermidine, a redox regulator

Supplemental Materials and Methods:

Construction of the gspSA disrupted strain, HA61002—The strain, HA61002, carrying *gspSA* was derived from the *E. coli* strain NR754 (wild type), an *araD* revertant of MC4100 (genotype: F⁻*araD139Δ(argF-lac)* U169*rpsL150relA1fibB5301 deoC1ptsF25rbsR*)(1). A *gspSA*-disrupted strain was constructed by homologous recombination experiments. Primers 5*gspSbla* (5'-*CAGACGGAAGAT ACTGAATACAGCTTACCGCAGCCGGAATTGCAGTATATATGAGTAAACTT* GGTCTG) and 3*gspSbla* (5'-*GCCTTTGTTTTCCAGGCGCGCTCCGCTGATTTTC AGCAGCTCGCCCA TTTTTATAACCTCCTTAGAGC*) were used to amplify a region encompassing the *bla* resistance gene in pKD46. The resulting PCR product with ends (italicized portion of primers) homologous to the chromosomal region of *gspSA* was used for inserting *bla* into the chromosome of DY330 *gspSA*. The *gspSA*-disrupted strain was selected at 30 °C on media containing ampicillin and confirmed by the colony PCR, which is adopted to amplify the inserted gene as contrasted to the wild-type *gspSA* gene. Alleles were transferred by P1 transduction; the *gspSA::bla* insertion was introduced into NR754 to a corresponding HA61002 strain. This construct was again verified by colony PCR using primers as the above involved in an insertion region. RT-PCR with primers at start codon of *gspSA* and the downstream of *bla*-inserted region on *gspSA* also confirmed that this *gspSA*-disrupted strain did not generate a transcript of the wild-type mRNA. The double mutants were constructed by introducing *grxA* or *grxB* allele (2) to Δ *gspSA* mutant (HA61002) with P1 transduction. The resulting transductants Δ *grxA* Δ *gspSA* and Δ *grxB* Δ *gspSA* were designated as HA61011 and HA61012, respectively.

Protein crystallization, structure determination, and crystallographic refinement—Purified GspAF was found to be >95% homogeneous according to SDS-PAGE and its purity was confirmed by mass spectrometry. For sitting-drop crystallization, 2 μ l of a GspAF solution (20 mg/ml) was mixed in a reservoir with one volume of 0.1 M acetate (pH 4.5), 0.8 M NaH₂PO₄, 1.2 M K₂HPO₄, 0.1 M imidazole. Crystals of GspAF treated with H₂O₂ (GspAF_H₂O₂) were obtained under similar conditions with slight modifications.

All crystals were soaked in the crystallization solution described above that was modified to contain 20% glycerol before data collection. All data were collected using ADSC Quantum315 or Quantum210 CCD detectors at the Synchrotron Protein Crystallography Facility BL13B1 and BL13C1 beamlines, National Synchrotron

Radiation Research Center, Hsin-Chu, Taiwan. Data were processed and integrated using the program *HKL2000* (3).

The structures of the GspAF_H₂O₂ and GspAF_acetate (a crystal that had been exposed to H₂O₂ for 1 month) were determined by molecular replacement using the program *CNS* (4) and a known GspSA structure as the template (5). The coordinates, the topology, and the parameter files for acetate and Gsp (that were required for *CNS* calculations) were taken from the HIC-UP server (6). Refinement and data-collection statistics are listed in Table S1.

Identification of the sulfenic acid of Cys59 by dimedone-labeling and subsequent mass spectrometry—GspSA (0.37 nM) was treated with 100 μM H₂O₂ for 10 min and the incubated with 100 μM dimedone at 25 °C for 12 h. After removing excess H₂O₂ and dimedone by HiTrap desalting chromatography (GE Healthcare), the sample was digested with trypsin (10 μg/ml) and subjected to MALDI-TOF-MS.

Gsp amidase-catalyzed removal of Spd from Gsp-thiolated proteins—Biotinylated Gsp-disulfide [(biotin-GspS)₂] was prepared by reacting 200 mM (GspS)₂ with 400 mM biotin-*N*-hydroxysuccinimide ester for 8 h at 37 °C. MALDI-TOF MS of the reaction mixture gave a signal at *m/z* = 1320.2 that corresponded to that of (biotin-GspS)₂. An *E. coli* lysate was treated with 1 mM (biotin-GspS)₂ in 100 mM Tris buffer (pH 7.3) for 3 h at 37 °C, so that the lysate proteins were biotinylated after disulfide exchange with (biotin-GspS)₂. After dialysis removed unreacted (biotin-GspS)₂, half of the mixture was treated with 10 μg GspSA to hydrolyze the Spd moiety and produce GSH-thiolated proteins, while the other half of the mixture was treated with 20 mM 2-ME to generate free protein thiols. Both reactions were run for 8 h at 37 °C, then subjected to 10% non-reducing SDS-PAGE and western blotting using an anti-biotin antibody that was conjugated to alkaline phosphatase.

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Supplemental Figures

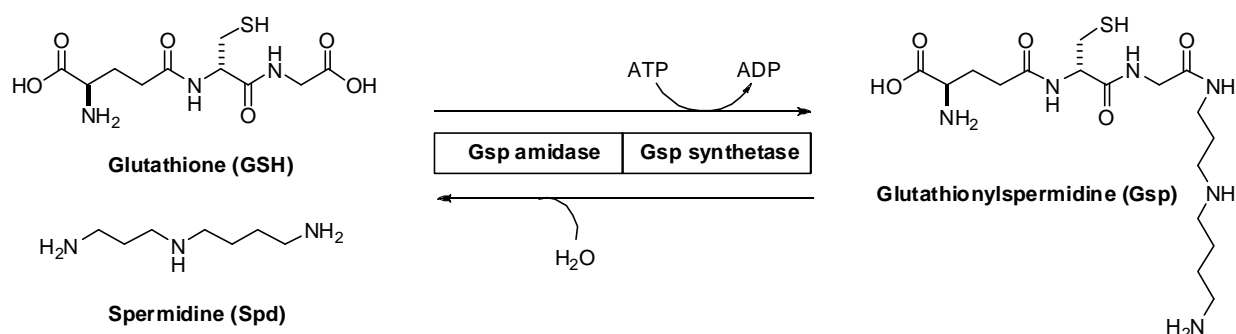


Figure S1. The reactions catalyzed by *E. coli* glutathionylspermidine synthetase/amidase (GspSA).

GspSA from *E. coli* is a bifunctional protein that contains an N-terminal amidase domain and a C-terminal synthetase domain. The two catalyzed reactions are shown at the molecular level.

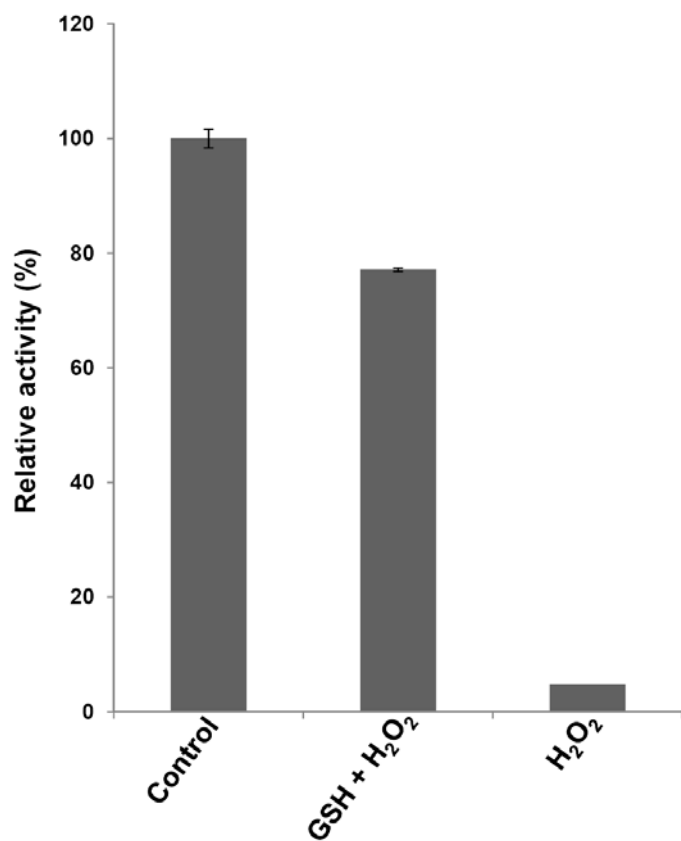


Figure S2. The recovery of H₂O₂-inactivated Gsp amidase by GSH

Bar graphs diagramming the effect of the GSH (4 mM) on the recovery of H₂O₂-inactivated Gsp amidase activity. For the negative control, water replaced H₂O₂, and its measured Gsp amidase activity was normalized to 100%. Each reported value is the mean of values obtained from at least three replicates. Uncertainties are reported as standard deviations.

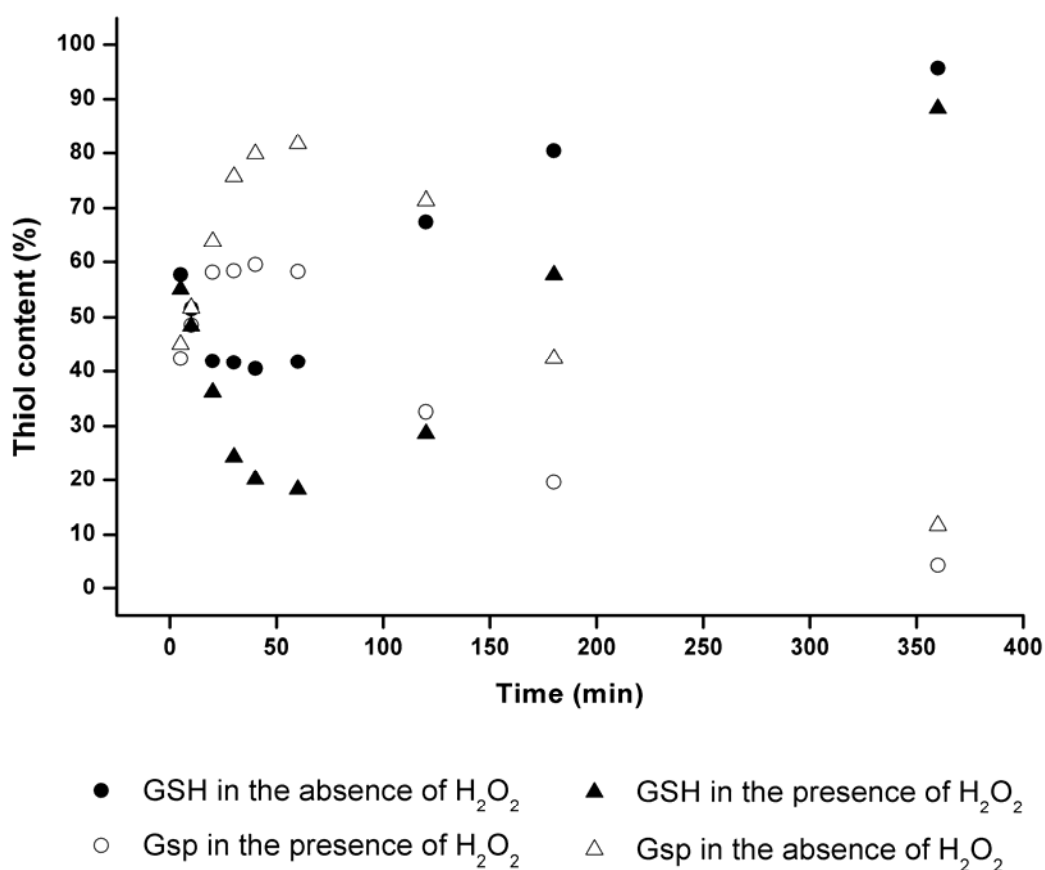


Figure S3. H₂O₂-induced Gsp accumulation *in vitro*. The levels of mBBR-derivatized GSH and Gsp were measured by fluorescence spectroscopy (excitation at 360 nm, emission at 480 nm) after HPLC separation. Experiments were carried out in the presence of ATP, Spd, GSH, GspSA with or without preincubation 500 μ M H₂O₂ for 5 min. Initially (0~50 min), Gsp accumulated. Once ATP was depleted (ca. 50 min), synthesis of Gsp was terminated and production of GSH by Gsp amidase was observed. Because H₂O₂ selectively inactivated Gsp amidase without affecting Gsp synthetase, the amount of Gsp that accumulated was greater in the presence of H₂O₂ (Δ) than in its absence (\circ). Conversely, the amount of GSH consumed in the presence of H₂O₂ (\blacktriangle) was greater than in its absence (\bullet).

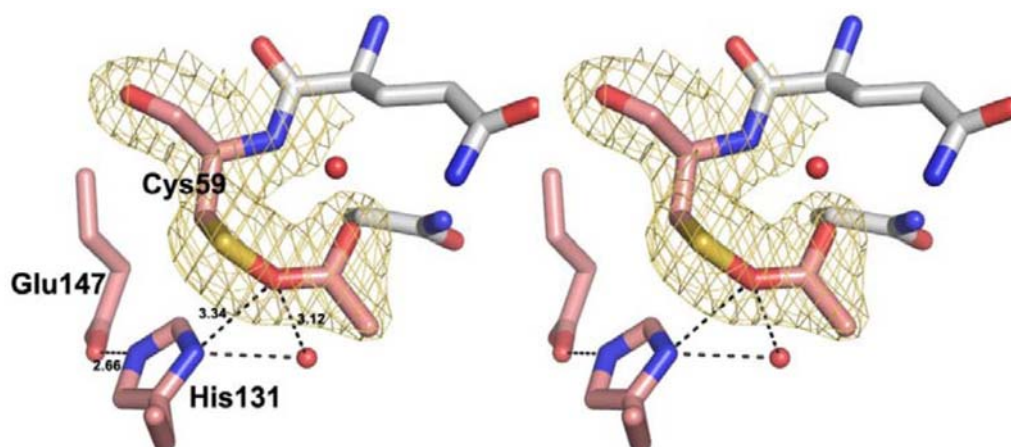


Figure S4. Stereo view of the GspAF_acetate active site in which an acetate is covalently bound to Cys59.

Crystallization conditions were the same as those reported in Fig. 4A, except that the crystals were grown for 1 month in the presence of H₂O₂. The electron density map is drawn at a contour level of 1σ to show the continuous density between the Cys59 S_γ atom and an oxygen atom of the acetate.

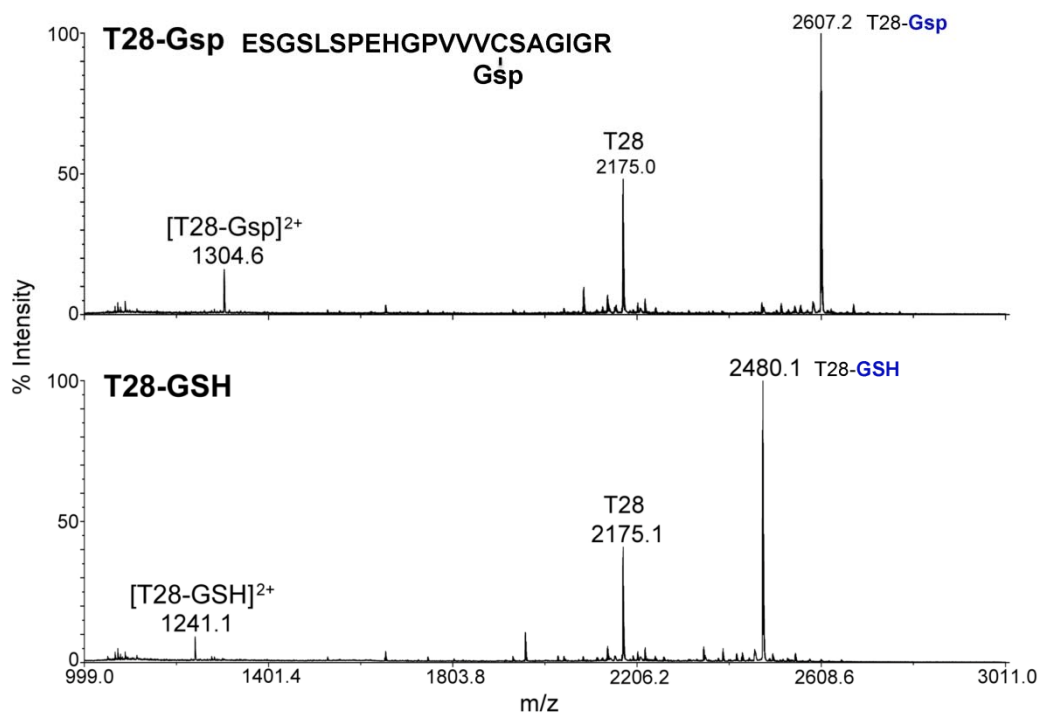


Figure S5. The Spd moiety of the Gsp *S*-thiolated peptide, T28-Gsp, can be hydrolyzed by Gsp amidase. The synthetic peptide, $^{200}\text{ESGSLSP EHG P V V C V H C S A G I G R}^{221}$ (T28), derived from protein tyrosine phosphatase-1B, was reacted with $(\text{GspS})_2$ to give T28-Gsp with a mixed disulfide bond between Cys215 of T28 and Gsp. T28-Gsp was hydrolyzed by GspSA, and the products were identified using MALDI-TOF-MS. The spectrum of T28-Gsp (top) has the expected signals at m/z 2607.2 and m/z 1304.6; whereas, the spectrum of T28-Gsp after hydrolysis (bottom) has signals at m/z 2480.1 and 1241.1, indicating that T28-Gsp was hydrolyzed to T28-GSH.

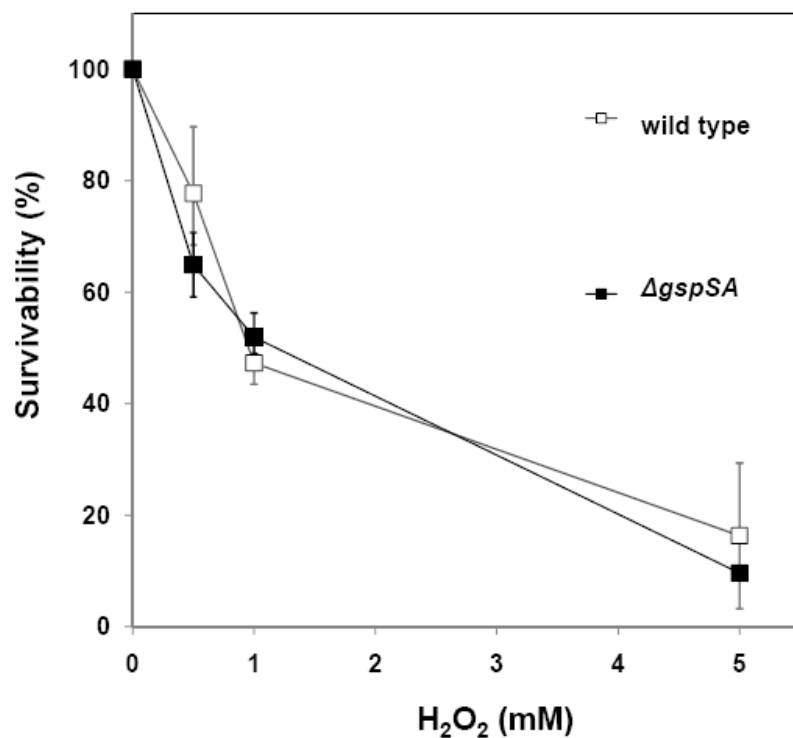


Figure S6. The viabilities of HA6001 ($\Delta gspSA$) and NR754 (wild type) after H₂O₂ treatment. HA6001 (■) and NR754 (□), were cultured in M9 minimal media until each culture reached an OD₆₀₀ of 1.0. Then 0, 0.5, 1, or 5 mM H₂O₂ was added to a culture and the cells were incubated for an additional 1 h, after 0.1 mL of each culture was plated on an LB plate and the number of viable cells counted. Survival percentage (survivability) was calculated as [(CFU in the presence of H₂O₂)/(CFU in the absence of H₂O₂)] / 100. Each survivability value is mean of at least three replicates \pm SD

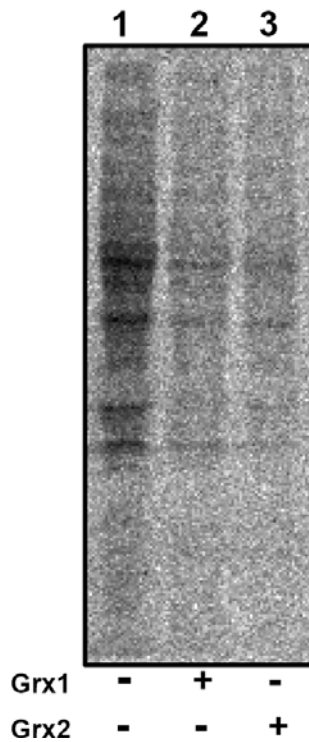
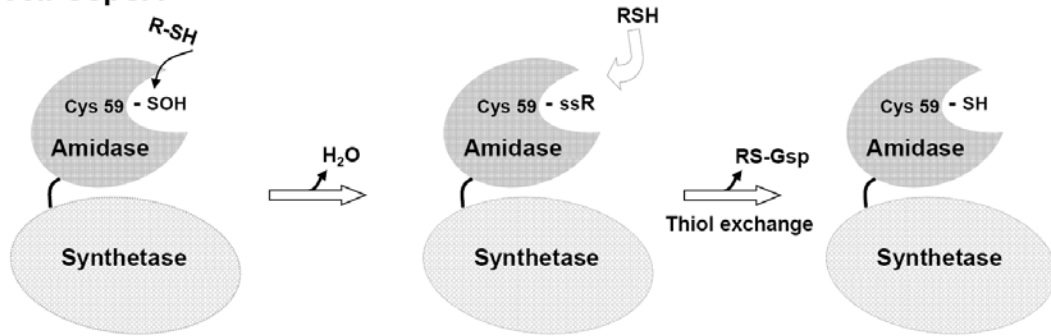


Figure S7. Reduction of Gsp S-thiolated proteins by glutaredoxins. The *E. coli* recombinant glutaredoxins, Grx1 and Grx2, were added individually into *E. coli* lysates that contained (Gsp*SSPs) (see Fig. 1). After 1 h, the mixtures were separated by SDS-PAGE and the radiolabeled proteins were detected by phosphorimaging. In comparison with the negative control (lane 1), the amounts of radiolabeled proteins decreased significantly when Grx1 or Grx2 was present (lanes 2 and 3, respectively).

E. coli GspSA



L. major TSH-SA

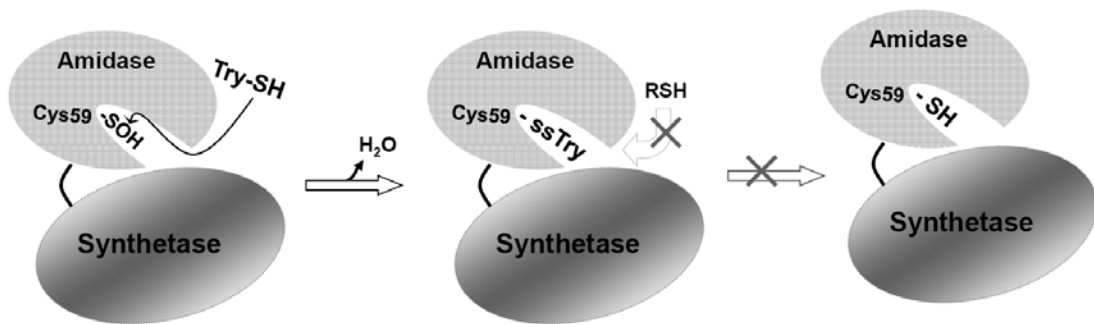


Figure S8. Schematics illustrating the different redox regulation mechanisms for *E. coli* GspSA and parasitic protozoa TSH-SA.

The recovery of Gsp amidase activity in *E. coli* may occur via nucleophilic attack by Gsp or GSH (or other small thiol compounds) to form a cysteine-mixed disulfide. Because Cys59 is accessible to solvent, the disulfide can then be reduced via thiol-exchange with a GSH or Gsp. Conversely, the TSH amidase substrate-binding channel is narrow and solvent inaccessible, because it is blocked by the C terminal region of the synthetase domain (residues 634~652).

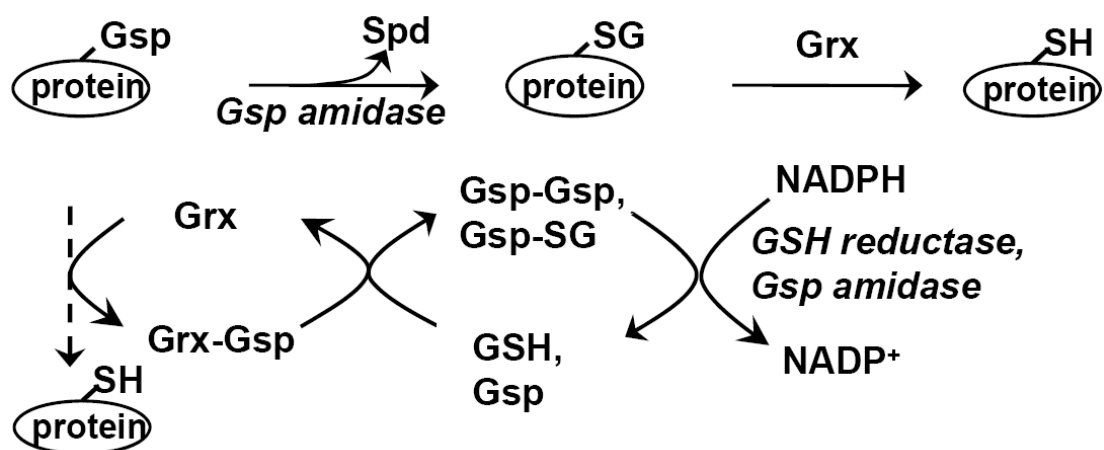


Figure S9. Two possible metabolic pathways involving Gsp S-thiolated proteins.

Spermidine (Spd) is removed from glutathionylspermidine (Gsp) S-thiolated proteins by Gsp amidase to generate glutathione (GSH) S-thiolated proteins that are further reduced by reaction with glutaredoxin (Grx). Alternatively, Gsp S-thiolated proteins may undergo a thiol-disulfide exchange with glutaredoxin to form a Grx-Gsp intermediate. Grx and GSH are regenerated by thiol-disulfide exchange, followed by reaction with the GSH reductase/Gsp amidase couple.

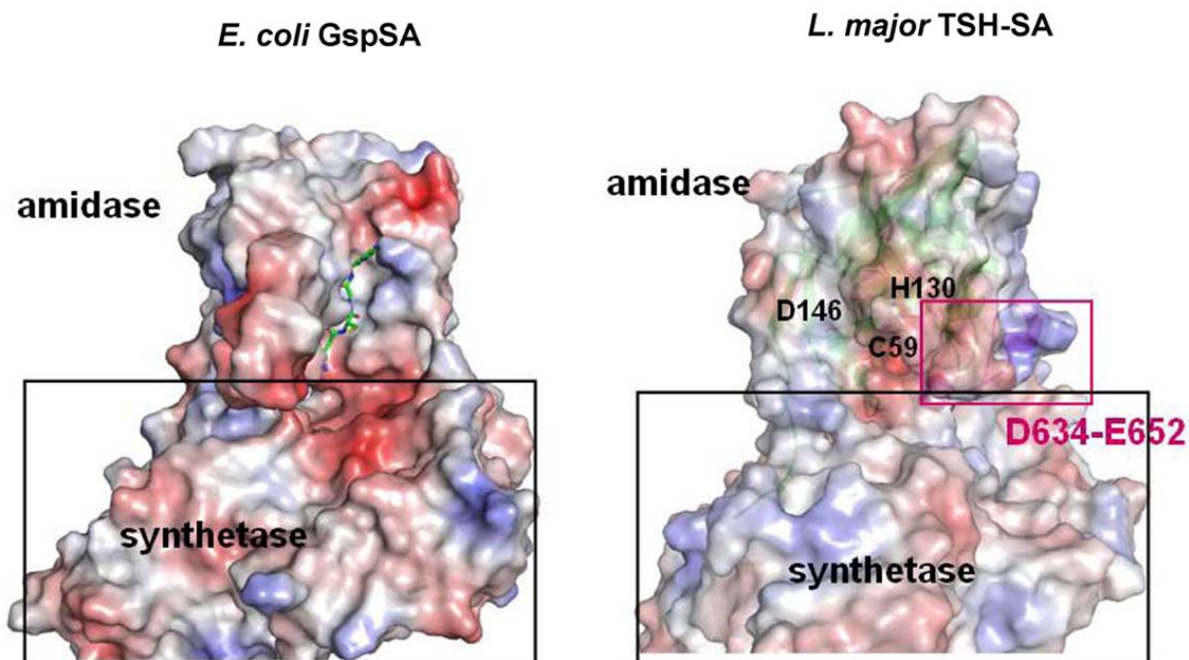


Figure S10. Comparison of the *E. coli* GspSA and *L. major* TSH-SA amidase active-sites. *E. coli* GspSA with Gsp (in green) bound in the amidase active site. The amidase binding site is accessible in comparison with that of *L. major* TSH-SA, which is partially blocked by residues 634-652 (framed in magenta) of the synthetase domain. The *L. major* TSH-SA catalytic triad residues (H130, C59, and D149) are buried.

Supplementary Table

Table S1. Data collection and refinement statistics

	GspAF_H ₂ O ₂	GspAF_acetate
Space group	<i>P6₄22</i>	<i>P6₄22</i>
No. of molecules per asymmetric unit	1	1
Unit cell parameters (Å)	83.9 83.9 106.5	83.51 83.51 105.84
Resolution, Å	25 – 1.5 (1.55 – 1.50)	30-2.2 (2.28-2.20)
Total no. of reflections	609744	116621
No. of unique reflections	35956	11604
Completeness, %	99.8 (100.0)	100 (99.9)
Redundancy	17.0 (15.1)	10.1 (10.3)
I/sigma	77.6 (5.3)	34.8 (5.9)
R_{merge}^a	5.1 (59.7)	9.2 (60.9)
Refinement statistics		
Resolution, Å^b	25 – 1.5 (1.55 – 1.50)	30-2.2 (2.28-2.20)
R_{working}	18.0 (27.4)	19.97 (23.14)
R_{free}^c	20.4 (22.4)	24.87 (32.05)
rmsd bond length, Å	0.0201	0.0052
rmsd angles	1.8658	1.2390
Ramachandran plot, %		
Most favored/allowed regions	89/99.4	88.1/100
Average B factor (Å²)	26.47	31.41
Waters	43.54	31.15
Acetate		28.59

$$^aR_{\text{merge}} = \text{SUM} (\text{ABS} (I - \langle I \rangle)) / \text{SUM} (I)$$

^bValues in parentheses are for the highest-resolution shell.

^cR_{free} = R factor calculated using 5% of the reflection data chosen randomly and omitted from the start of refinement.