

Forum Review

Glutaredoxins: Glutathione-Dependent Redox Enzymes with Functions Far Beyond a Simple Thioredoxin Backup System

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ABSTRACT

Most cells contain high levels of glutathione and multiple glutaredoxins, which utilize the reducing power of glutathione to catalyze disulfide reductions in the presence of NADPH and glutathione reductase (the glutaredoxin system). Glutaredoxins, like thioredoxins, may operate as dithiol reductants and are involved as alternative pathways in cellular functions such as formation of deoxyribonucleotides for DNA synthesis (by reducing the essential enzyme ribonucleotide reductase), the generation of reduced sulfur (via 3'-phosphoadenylylsulfate reductase), signal transduction, and the defense against oxidative stress. The three dithiol glutaredoxins of *E. coli* with the active-site sequence CPYC and a glutathione binding site in a thioredoxin/glutaredoxin fold display surprisingly different properties. These include the inducible OxyR-regulated 10-kDa Grx1 or the highly abundant 24-kDa glutathione S-transferase-like Grx2 (with Grx3 it accounts for 1% of total protein). Glutaredoxins uniquely reduce mixed disulfides with glutathione via a monothiol mechanism where only an N-terminal low pK_a Cys residue is required, by using their glutathione binding site. Glutaredoxins also catalyze formation of mixed disulfides (glutathionylation), which is an important redox regulatory mechanism, particularly in mammalian cells under oxidative stress conditions, to sense cellular redox potential. *Antioxid. Redox Signal.* 6, 63–74.

INTRODUCTION

REVERSIBLE REDUCTIONS OF DISULFIDE BONDS can be mediated by a variety of thiol-redox enzymes, which contain an active site with the sequence motif CXXC. These proteins may perform fast and reversible thiol–disulfide exchange reactions between their active-site cysteine residue and half-cystines of their disulfide substrates. The pathways of the thioredoxin and glutaredoxin systems are responsible for the reduction of intracellular disulfides *in vivo* (39, 85, 90). Thioredoxins and glutaredoxins are abundant proteins with a number of isoforms in different species, which operate in essential biosynthetic reactions and regulate many biological functions.

Glutaredoxins are now known to exist in most living organisms, including prokaryotes (*e.g.*, *Escherichia coli*) (36), plants (*e.g.*, rice, spinach, poplar, *A. thaliana*) (17, 68, 71, 95),

viruses (*e.g.*, bacteriophage T4, vaccinia, human immunodeficiency virus) (1, 22, 23, 25), and eukaryotes (*e.g.*, yeast, *P. falciparum*, rabbit, calf, pig, and human) (30, 45, 62, 63, 80, 86, 118). The active sites of thioredoxin and glutaredoxin (the CXXC motif) have been found in a growing number of redox-active enzymes. These include, *e.g.*, T4 glutaredoxin (101), protein disulfide isomerases (24), DsbA (7, 90), and NrdH redoxin (48).

The glutaredoxin system was first discovered in 1976 as a dithiol hydrogen donor system for ribonucleotide reductase, in a mutant lacking thioredoxin 1 (Trx1) in *E. coli* (36). In the glutaredoxin system, electrons are transferred from NADPH, to glutathione reductase (GR), then to glutathione (GSH), and finally to one of the three today known glutaredoxins (Grx1, Grx2, and Grx3) (Fig. 1) (41). Glutaredoxins were later shown to be general thiol–disulfide oxidoreductases (37, 38) that can reduce protein disulfides (by a dithiol mechanism) or

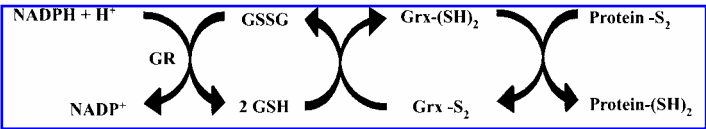


FIG. 1. General mechanism of the glutaredoxin system. In the glutaredoxin system, electrons are transferred from NADPH to glutathione reductase (GR), glutathione (GSH), and finally to the glutaredoxins. Glutaredoxins will in turn reduce disulfides in target proteins like ribonucleotide reductase.

mixed disulfides forming between GSH and proteins or low-molecular-weight thiols (by a dithiol and/or monothiol mechanism) (11).

Glutaredoxin isoforms

The glutaredoxin family has grown during the last years, and there are today numerous isoforms known in different organisms with quite different structures and catalytic activities. In terms of their structure and catalytic properties, glutaredoxins can today be classified in three categories (110).

The first is exemplified by the classical glutaredoxins, which are 10-kDa proteins with the CXXC motif (usually CPYC) as their active site (Fig. 2) and with the thioredoxin/glutaredoxin fold (Fig. 3). Grx1 and Grx3 of *E. coli* belong to this first classical category. Both are ~10-kDa proteins with similar structure (the thioredoxin/glutaredoxin fold), and they have 33% sequence identity (4, 12, 66). These enzymes are electron donors for reductive enzymes like ribonucleotide reductase.

The second category is structurally related to the glutathione *S*-transferases (GSTs), but with glutaredoxin oxidoreductase activity. Common structural characteristics are a two-domain structure, the first domain having a thioredoxin/glutaredoxin fold containing the active-site residues and the second domain having an α -helical structure. This class of glutaredoxins is defined by *E. coli* Grx2, which has a three-dimensional structure (Fig. 3), highly similar to GSTs (116). It mainly differs from the GSTs in that it contains the

dithiol active-site sequence CPYC in the glutaredoxin domain, and thus has glutaredoxin activity. Other proteins that are structurally related to this category, even though they have no significant amino acid homology and only one active-site cysteine, are the human θ class GST, the human GST ω 1 (GSTO1), the mouse GST θ -like stress response protein (p28), and the human chloride intracellular channel 1 (CLIC1) (9, 34, 56, 94). All these proteins are detoxifying or stress response proteins.

The third category of glutaredoxins is defined by having a monothiol active site (normally CGFS). Monothiol glutaredoxins have so far been identified in yeast (yGrx3, yGrx4, and yGrx5) and man [protein kinase C-interacting cousin of thioredoxin (PICOT)] (92, 115). The yeast monothiol glutaredoxins have a protective role against oxidative stress, with the mutant lacking Grx5 being very sensitive to both menandione and hydrogen peroxide and containing high amounts of carbonylated proteins compared with the parental strain. The mutant also showed increased sensitivity (>10-fold) to high concentrations of KCl. A yeast null mutant for the three-monothiol glutaredoxins is not viable, suggesting that monothiol glutaredoxins are very specific for their substrates and their functions cannot be replaced by their dithiol counterparts (92). Moreover, yeast Grx5 has been shown to be part of the mitochondrial machinery involved in the synthesis and assembly of iron-sulfur clusters (93). The human monothiol, PICOT, is expressed in various tissues, and overexpression in T cells inhibits the activation of c-Jun N-terminal kinase (JNK) and the transcription factors activator protein 1 (AP-1) and nuclear factor- κ B (NF- κ B) (115). Monothiol glutaredox-

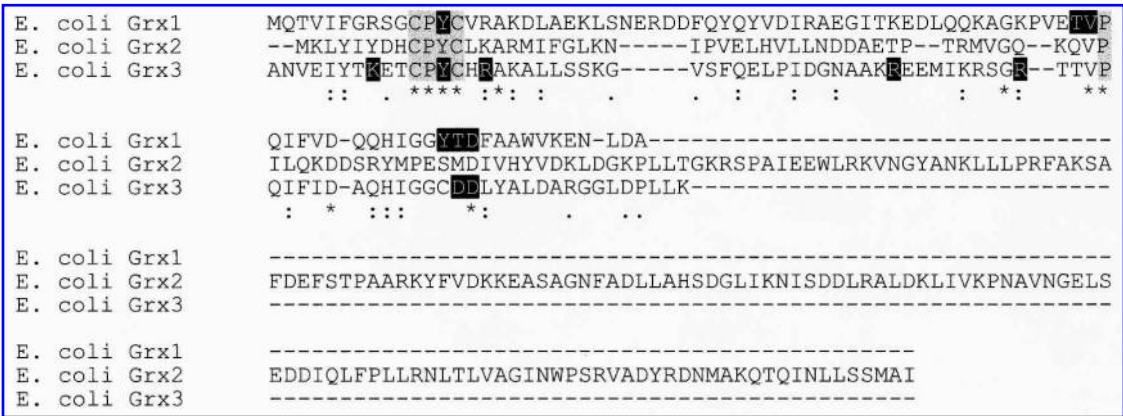


FIG. 2. Sequence alignment of the *E. coli* glutaredoxins. The active-site sequence is shown as gray boxes, as is the consensus proline residue. Residues involved in the binding of GSH in *E. coli* Grx1 and Grx3 are marked with black boxes (74, 117).

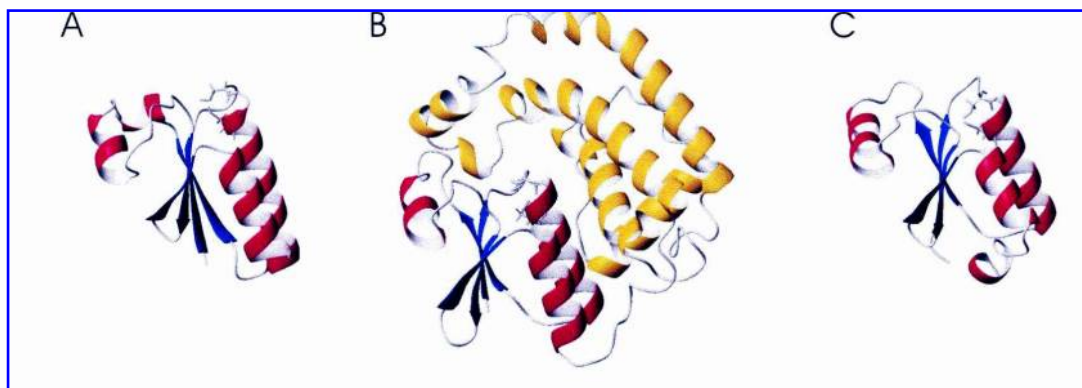


FIG. 3. Three-dimensional structures of the *E. coli* glutaredoxins. (A) Oxidized *E. coli* Grx1 (1EGO) (117). (B) Reduced *E. coli* Grx2 (1G7O) (116). (C) Oxidized *E. coli* Grx3 (1FOV) (75). The active-site cysteines are displayed as sticks. The structures are from the protein Data Bank, and the figures were generated using the program MOLMOL (57). β -sheets are displayed in blue, α -helices belonging to the thioredoxin/glutaredoxin fold in red, and the α -helices of the C-terminal domain of Grx2 in yellow.

ins have been identified in many different species, through genome databank searches (29, 47).

The glutaredoxin fold

The thioredoxin/glutaredoxin fold was first identified in 1975 (42) from the crystal structure of oxidized *E. coli* Trx1, and is characterized by a central core of a four to five stranded mixed β -sheet, flanked by three to four α -helices. In glutaredoxins, the fold consists of a four stranded mixed β -sheet surrounded by three α -helices (Fig. 3) (25, 66, 101). In addition, several other proteins apart from the thioredoxins and glutaredoxins share the common structural fold, and thus belong to the thioredoxin superfamily, despite the low sequence identity (18). Proteins belonging to the thioredoxin superfamily of enzymes include DsbA, NrdH redoxin, protein disulfide isomerases, chaperones, GSTs, and glutathione peroxidases (18, 25, 26, 51, 67, 88, 102, 104). In contrast to the relatively low homologies among different thioredoxins, glutaredoxins exhibit rather high amino acid sequence homology, particularly in the area of the active site. The three-dimensional structures of a number of glutaredoxins from different species, including bacteriophage T4, vaccinia Grx1, *E. coli* Grx1, Grx2, and Grx3, pig Grx1, and human Grx1, have been determined (25, 49, 50, 102, 106, 116). The three-dimensional structures of *E. coli* Grx1 (12, 102, 117) and Grx3 (28, 74, 75) have been obtained by NMR (Fig. 3), in the oxidized, reduced, and mixed-disulfide forms. Structural studies have revealed three characteristic regions within the dithiol glutaredoxins. First is the active-site CXXC motif (usually CPYC), second a solvent-accessible hydrophobic area, and finally a well defined binding site for GSH. The latter involves two intermolecular backbone-backbone hydrogen bonds forming an antiparallel intermolecular β -bridge between the protein and GSH (12, 74). In *E. coli* Grx3, these interactions involve residue Lys8, Tyr13, Arg16, Arg40, Arg49, Asp66, and Asp67. The binding of GSH to *E. coli* Grx1 and Grx3 is overall very similar. The conformation of the active site of oxidized glutaredoxins is also conserved. Moreover, local interactions and small, but significant, conformational changes in the active site modulate the redox po-

tential by affecting the stability of each of the reduced, oxidized, and mixed disulfide forms (75). Comparison of the reduced and oxidized forms of *E. coli* Grx1 revealed that the solvent-accessible surface of the conserved hydrophobic area increases upon reduction. This should favor binding interactions with substrate proteins. After reduction of the substrate, the decrease of the hydrophobic interaction area of the now oxidized glutaredoxin could facilitate the release of the substrate (117). In contrast to *E. coli* Grx1 and Grx3 (both ~10 kDa), *E. coli* Grx2 is a much larger enzyme (24.3 kDa) with the N-terminal, residue 1–72, forming a glutaredoxin domain, connected by an 11-residue linker to the highly helical C-terminal domain, residue 84–215 (Fig. 3) (116). The structure of Grx2 is similar to that of GSTs, although they lack an obvious sequence homology. The structural similarity is interesting, because a relatively new class of mammalian GST-like protein, the single cysteine ω class, has glutathione oxidoreductase activity, rather than the GST activity (9).

Catalytic mechanism of glutaredoxin

Thiol redox control predicts that thiols that are oxidized to disulfides may affect protein structure and activity (39). Generally, disulfide bonds stabilize protein structure (*e.g.*, bovine serum albumin), while biological activity of proteins may also be affected (*e.g.*, OxyR). In some oxidoreductases, formation and reduction of disulfides are essential for enzymatic activity as part of a catalytic mechanism [*e.g.*, ribonucleotide reductase and 3'-phosphoadenylylsulfate (PAPS) reductase].

Glutaredoxins catalyze GSH-disulfide oxidoreductions usually via the two redox-active cysteines separated by two other amino acids (typically CPYC) (39, 41). The oxidoreductions are either dithiol reactions reducing protein disulfides or monothiol reductions of mixed disulfides with GSH. In comparison, the structurally and functionally related thioredoxins reduce a wide range of protein disulfides, but have low or no activity with mixed disulfides.

In the dithiol reduction, the solvent-exposed N-terminal cysteine of the active-site sequence of the glutaredoxin initiates a nucleophilic attack on one of the sulfur atoms of the disulfide target (Fig. 4A). This results in the formation of a

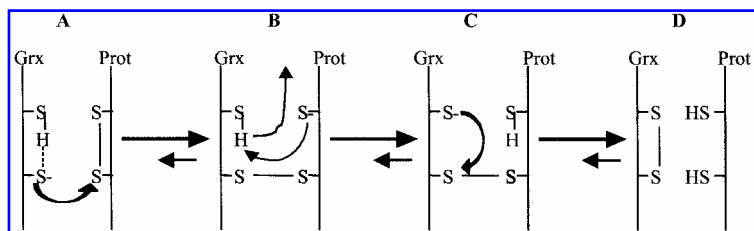


FIG. 4. The glutaredoxin dithiol oxidoreductase mechanism. Glutaredoxin-mediated oxidoreductions of disulfide bonds in target proteins are shown.

mixed disulfide between the glutaredoxin and the target protein (Fig. 4B). The free second C-terminal cysteine of the active site becomes deprotonated and attacks the N-terminal glutaredoxin sulfur atom participating in the mixed disulfide with the target protein (Fig. 4C). As a consequence, oxidized glutaredoxin (Grx-S_2) and reduced target [Prot-(SH)_2] are generated (Fig. 4D).

In the monothiol mechanism concerning the reduction of protein-SG mixed disulfides, glutaredoxins utilize only the N-terminal cysteine thiol (Fig. 5) (11). In this reaction, glutaredoxins specifically interact with the GSH moiety of the GSH-mixed disulfide target, and not the protein substrate, due to the glutaredoxin affinity for GSH (12, 74). This results in the formation of a covalent Grx-SG GSH mixed intermediate and release of the non-GSH moiety in its reduced form. The Grx-SG mixed intermediate is reduced by a second GSH molecule, generating glutathione disulfide (GSSG). Finally, GR regenerates GSH by reducing the GSSG.

As the reduction of glutathionylated proteins seems to require the recognition of only the GSH moiety of the substrate, and not the substrate itself, the monothiol mechanism resulting in deglutathionylation can thus be seen as a more general function of the glutaredoxins. Contrary to what was originally believed, glutathionylation of proteins may not only occur due to increased GSSG levels as the formation of protein GSH conjugates has been reported without an increase of GSSG levels (64). Protein glutathionylation has been realized as an increasingly important regulatory mechanism in biochemical processes, by reversible modification of protein thiols (19). Several proteins have been detected to undergo glutathionylation due to changes in the intracellular redox environment. These include protein chaperones, cytoskeletal proteins, cell cycle regulators, and enzymes of the intermediate metabolism (61). Furthermore, these types of posttranslational modification are involved in the regulation of specific transcriptional events vital to the adaptation seen in cells during oxidative stress (53). For instance, glutathionylation of Cys62 of eukaryotic NF- κ B subunit p50 and Cys269 of c-Jun result in loss of DNA binding activity (54, 81). Tyrosine hydroxylase, protein phosphatase 2A, tyrosine phosphatase 1B, and α -ketoglutarate dehydrogenase are all inhibited by re-

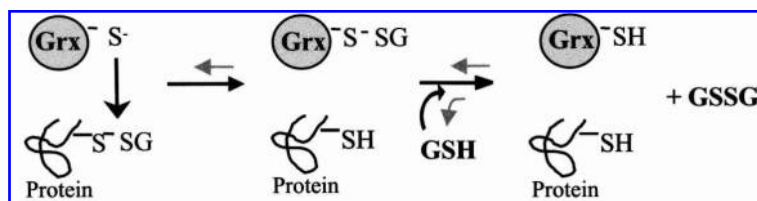
versible glutathionylation (8, 10, 76, 87). Recently, retinal pigment epithelium cells were shown to be glutathionylated and the reversible glutathionylation of these proteins was mediated by glutaredoxin (16). G-actin has also been reported to be glutathionylated at Cys374 and to undergo deglutathionylation by glutaredoxin. It has been further shown that human Grx1 knockdown cells affected G-actin in terms of polymerization, translocation, and reorganization near the cell periphery (113, 114).

Even though there are many reports about posttranscriptional regulation via *S*-glutathionylation in eukaryotic cells, only the transcription factor OxyR and PAPS reductase have so far been reported to be regulated in this manner in *E. coli* (52, 60). Recent studies showed that the OxyR protein can exist in an *S*-nitrosylated (S-NO), *S*-glutathionylated (S-SG), and hydroxylated (S-OH) state *in vivo*. The posttranslational modification of the protein's regulatory thiol (Cys199) is transcriptionally active, but differs in structure, cooperative properties, DNA binding affinity, and promoter activity, with glutathionylated OxyR having the highest transcriptional activity (52). Glutathionylated PAPS reductase is completely inactive, and was observed *in vivo* in poorly growing *gor-grxA-grxB-grxC*⁻ expressing inactive Grx2-C9S/C12S. However, expression of monothiol Grx2-C12S or wild-type Grx2 (known not to be electron donors for PAPS reductase) in the *gor-grxA-grxB-grxC*⁻ strain, the protein mixed disulfide species was absent. Glutaredoxins were further able to reduce glutathionylated PAPS reductase *in vitro*. Reversible glutathionylation may thus regulate the activity of PAPS reductase (60). Formation of protein-GSH mixed disulfides is of physiological relevance for *E. coli*, because up to 2% of the total GSH content (10–20 μM) is in the form of protein-mixed disulfides in a wild-type cell and can be even higher, as for example in *trxAgrxA* null mutants (5–7%) (70).

THE GLUTAREDOXIN SYSTEM OF *ESCHERICHIA COLI*

Three glutaredoxins (Grx1, Grx2, and Grx3) have so far been described in *E. coli* (Fig. 2) (3, 36). The first (Grx1, en-

FIG. 5. The monothiol mechanism of the glutaredoxins. Reduction of protein GSH-mixed disulfides (black arrows) and the generation of glutathionylated protein (gray arrows) by the reversed reaction are shown.



coded by *grxA*) was discovered as a GSH-dependent electron donor for ribonucleotide reductase 1a, in a mutant lacking the first isolated electron donor, Trx1 (36). The other two glutaredoxins, Grx2 (encoded by *grxB*) and Grx3 (encoded by *grxC*), were purified from an *E. coli* null mutant for Grx1 and Trx1 (3). Because of the strong preference of glutaredoxins for GSH-mixed disulfides, they have been proposed to participate in enzyme regulation, particularly under oxidative conditions (31, 33).

In comparison with thioredoxins, little is still known about the actual function of these glutaredoxins (Table 1). However, apart from PAPS reductase and ribonucleotide reductase, glutaredoxins are required for the reduction of arsenate reductase (ArsC) and OxyR in *E. coli* (6, 32, 119). ArsC catalyzes the reduction of arsenate [As(V)] to arsenite [As(III)]. ArsC has a single catalytic cysteine residue, Cys12, that can form a covalent thiolate-As(V) intermediate (72). The reduction of the enzyme-bound As(V) intermediate to an enzyme-bound As(III) intermediate requires glutaredoxin. Glutaredoxin mutants lacking the N-terminal cysteine in the active site, leading to an inactive enzyme, could not catalyze the ArsC-As(V) reduction, whereas mutants lacking the C-terminal cysteine could still support the activity of ArsC (100). This finding led to the conclusion that the ArsC intermediate is not formed during the catalytic cycle, but instead an ArsC-S-SG complex, which subsequently is reduced by glutaredoxins via a monothiol mechanism. From the *E. coli* glutaredoxins, Grx2 has the highest catalytic activity (100-fold higher than Grx1) in reducing ArsC (100).

Oxidative stress occurs when cells are exposed to elevated levels of reactive oxygen species, such as superoxide ($O_2^{\cdot-}$), hydrogen peroxide (H_2O_2), and alkyl hydroperoxides (ROOH). Oxidative stress can lead to DNA damage and thus mutations, as well as lipid peroxidation, disassembly of iron-sulfur clusters, disulfide bond formation, protein carbonylation, and other potentially lethal effects. To protect cells against the oxidative damage, cells produce a number of antioxidant enzymes. Both thioredoxins and glutaredoxins have been shown to have a protective role against oxidative stress (for reviews, see 13, 40, 90). *E. coli* glutaredoxins contributed to the defense against hydrogen peroxide, with *gshA*⁻ and *grxB*⁻ cells

being more sensitive to hydrogen peroxide as shown by increased carbonylation of intracellular proteins of the relevant mutants, particularly in the stationary phase (112). Furthermore, Grx1 (as well as Trx2 and GR) has been shown to be regulated by the transcription factor OxyR, which is known to activate the expression of several antioxidant defensive genes in response to elevated levels of hydrogen peroxide (13). Significant up-regulation of catalase activity has been observed in null mutants for Trx1 and the three glutaredoxins, whereas up-regulation of glutaredoxin activity was observed in catalase-deficient strains especially with additional defects in the thioredoxin pathway (112). In addition, elevation of all glutaredoxin species has been reported in catalase-deficient strains, particularly when combined with null mutants from the thioredoxin or glutaredoxin system (82). This shows an interconnection between the glutaredoxin and catalase antioxidant defenses.

It is generally believed that aging results from oxidative damage of macromolecules as a result of fluctuations in the balance between oxidants and antioxidants (65, 89). There is, for instance, an age-related decline in GSH levels that has been reported for a number of organisms. Overexpression of GSH in transgenic *Drosophila* results in an increased life span (103). Similar to eukaryotic cells, stationary phase *E. coli* becomes increasingly oxidized. This is despite their enhanced capacity to manage oxidative stress by the global regulator σ^s [*rpoS*-encoded sigma factor S (RpoS)], OxyR, and SoxRS (for more information, see reviews 77–79). The oxidative stress theory on aging thus opens the possibility of a pivotal potential function for the thioredoxin and the glutaredoxin systems.

Grx1

Grx1 was discovered and named as a small GSH-dependent donor for ribonucleotide reductase (36). Grx1 has close homologues in most living organisms (66). Trx1 is normally more abundant in the cell (10 μM) compared with Grx1 (1 μM), but Grx1 has a 10-fold lower K_m value for ribonucleotide reductase (38, 43). Measurements of thymidine incorporation in newly synthesized DNA further suggest that

TABLE 1. SUMMARY OF THE *E. COLI* GLUTAREDOXIN SYSTEM

Gene	Protein	Molecular mass (kDa)	Regulation	Sensitivity	Substrate specificity	
					Protein disulfides	Mixed disulfides
<i>gor</i>	Glutathione reductase (GR)		OxyR, ppGpp	H_2O_2 , CHP, tBHP, diamide		GSH
<i>grxA</i>	Glutaredoxin 1 (Grx1)	9.7	OxyR	Diamide, H_2O_2	RR, OxyR, PAPS reductase, ArsC, (MSR)	ArsC, PAPS reductase
<i>grxB</i>	Glutaredoxin 2 (Grx2)	24.3	Acid stress, osmosis, RpoS, ppGpp, cyclic AMP	Diamide, H_2O_2	ArsC	ArsC, PAPS reductase
<i>grxC</i>	Glutaredoxin 3 (Grx3)	9		Menandione, CHP	(RR), ArsC	ArsC, PAPS reductase

CHP, Cumene hydroperoxide; MSR, methionine sulfoxide; RR, ribonucleotide reductase; tBHP, *tert*-butyl hydroperoxide.

mainly Grx1 and to a lesser extent Trx1 contribute to the reduction of ribonucleotides in *E. coli* (82). Grx1 is also an alternate electron donor to thioredoxin for the reduction of PAPS reductase (108, 109). When Grx1 was overexpressed to levels similar Trx1, Grx1 was able to rescue the growth defects of a *trxAmetE* null mutant, and could reduce methionine sulfoxide reductase (105).

Grx1 has 85 amino acid residues, including the active-site sequence CPYC (Fig. 2), and a molecular mass of 10 kDa. The protein level of Grx1 in the cell varies from ~600 ng/mg at the exponential phase to ~285 ng/mg at the stationary phase (82). Thermodynamic stability experiments showed that oxidized and reduced Grx1 are very similar in stability. In heat-induced denaturation, monitored by circular dichroism, the T_m was 55 and 57°C for the oxidized and reduced form, respectively. In guanidine hydrochloride solutions, the midpoint denaturation concentrations were 2 M for both the oxidized and reduced forms. This differs greatly from the thioredoxin in *E. coli*, where the oxidized form is far more stable than the reduced (98).

Grx1 is induced by hydrogen peroxide in an OxyR-dependent fashion (107). The transcriptional regulator OxyR is sensitive to oxidation and activates the expression of antioxidant genes (there among Grx1) in response to hydrogen peroxide. Grx1 catalyzes the reduction, and thus the inactivation, of OxyR *in vivo*, and as OxyR regulates Grx1, the response is autoregulated (6, 119). However, the role of Grx1 as a reductant of disulfide bonds can be reversed to that of an oxidant in very oxidizing environments (112).

The first null mutant for Grx1 was constructed in 1988, and showed no significant phenotype (96). The combined null mutant for *trxAgrxA* was viable in rich media, but showed no viability in minimal media unless supplemented with reduced cysteine. This finding led to the conclusion that either Trx1 or Grx1 is essential for the reduction of PAPS reductase. However, the null mutant for *trxAgrxA* maintained deoxyribonucleotide synthesis, with an increase of ribonucleotide reductase activity of up to 23-fold, implying that a third hydrogen donor must exist in the cell (later found to be Trx2 and Grx3) (69, 97). Lack of Trx1 or Grx1 leads to an increased level of the other enzyme (as determined by enzyme-linked immunosorbent assay), most probably in order to maintain a balanced supply of deoxyribonucleotides. Grx1 is 10-fold induced in the absence of thioredoxin reductase, and the effect is even more pronounced in null mutants for *trxAtxC* and *trxAtxBtrxC* (20–30-fold) (44, 82). An extremely high (70-fold) increase has also been observed for Grx1 in null mutants for *gshAtxA* (70).

Grx2

Grx2 was purified from an *E. coli* null mutant lacking Trx1 and Grx1 (3). Characterization of Grx2 shows that it is highly different from the other known glutaredoxins in terms of molecular mass (24.3 kDa), amino acid sequence, and catalytic activity (111). Grx2 cannot reduce ribonucleotide reductase or PAPS reductase, but has the highest catalytic activity using the mixed disulfide between GSH and β -hydroxyethyl disulfide (HED) as substrate with a turnover of 554 s⁻¹ (HED assay) (3, 59, 111). *E. coli* Grx2 has

close homologues in *Actinobacillus actinomycetemcomitans* (87% amino acid identity), *Neisseria meningitidis* (58%), and *Vibrio cholerae* (42%), all known pathogens, but it is not a ubiquitous protein.

Grx2 was found to contribute to 80% of the total glutaredoxin activity measured by the HED assay. Null mutants for *grxB* and all three glutaredoxin genes (*grxA-grxB-grxC*) are viable in rich and minimal media. However, the null mutant for *grxB* has been prone to lysis under starvation conditions and exhibits a distorted morphology (83).

The levels of Grx2 are growth phase-dependent, and are elevated at stationary phase of growth (up to 10 μ g/mg of protein) (82). Guanosine-3',5'-tetraphosphate (ppGpp) and σ^s (RpoS) are two major factors controlling the transcription of genes in the stationary phase of growth, as well as genes involved in the antioxidant response (15, 35). Both ppGpp and RpoS dramatically affect the expression of Grx2. ppGpp and RpoS are thus necessary for the high up-regulation of Grx2 at stationary phase, whereas cyclic AMP inhibits Grx2 at exponential phase. Grx2 levels are also positively affected by osmotic upshock and acidic stress (2, 83).

Grx2 contributes to the defense against hydrogen peroxide, with the *grxB*⁻ cells being more sensitive to hydrogen peroxide as shown by increased carbonylation of intracellular proteins of the relevant mutant, particularly in the stationary phase (112). Despite this, the transcription factor OxyR did not affect the levels of Grx2 (83), and these were instead shown to be elevated in an *oxyR* null mutant. Additionally, the levels of Grx2 decrease after treatment with hydrogen peroxide (82). Recombinant *E. coli* Grx2 is also a potent antioxidant *in vitro* against dopamine-induced oxidative stress and cell death in rat cerebral granule neurons, preventing their apoptosis by activating the binding activity of NF- κ B (20). *E. coli* Grx2 was able to penetrate into the granule neurons and exert its activity by activating NF- κ B. Addition of Grx2 resulted in promotion of the phosphorylation and degradation of I- κ B α , thus causing translocation of NF- κ B from the cytoplasm to the nucleus. In addition, the DNA binding activity of preexisting nucleus NF- κ B was enhanced. The effect was mediated by up-regulation of Ref-1, which in turn activated NF- κ B. Moreover, Grx2 could activate both the Ras/phosphoinositide 3-kinase/Akt/NF- κ B and the JNK1/2/AP-1 cascades (21).

Grx3

Grx3 was identified and purified at the same time as Grx2 in the null mutant lacking Trx1 and Grx1 (3). It was given its name from being eluted after Grx2 on size-separating gel chromatography. Grx3 has 5% of the catalytic activity of Grx1 for ribonucleotide reductase, but lacks activity for PAPS reductase (3, 59). Even though Grx3 can act as an electron donor for ribonucleotide reductase 1a *in vitro*, it most probably cannot reduce ribonucleotide reductase 1a *in vivo*. Triple mutants lacking Trx1, Trx2, and Grx1 are nonviable and can grow when only cotransfected with a plasmid overexpressing any one of these three proteins (105). Grx3 consists of 82 amino acid residues (10-kDa protein), with 33% sequence identity to *E. coli* Grx1 (4). The active site of Grx3 is CPYC as in the other glutaredoxins (Fig. 2), and the three-dimensional structure

is similar to that of Grx1 (Fig. 3). The activity of Grx3 is reduced in a Grx3-H15V mutant, indicating electrostatic contributions for the stabilization of C11 (73). Denaturation of Grx3 with guanidine hydrochloride showed no difference in stability between the reduced and oxidized forms (5). The levels of Grx3 are relatively high (~3.5 µg/mg) and remain the same during all stages of growth. The null mutant for *grxC* shows increased sensitivity to menadione and cumene hydroperoxide (112). The mechanism(s) that regulates *grxC* expression remains unknown, but it is considered not to be affected by global regulators like RpoS, ppGpp, cyclic AMP, and OxyR.

GENETIC STUDIES ON THE THIOREDOXIN AND GLUTAREDOXIN SYSTEMS

In *E. coli*, neither glutaredoxin nor thioredoxin single mutation results in a lethal phenotype (105, 112). This is likely due to redundancy, because double mutants lacking both thioredoxin reductase (*trxB*) and GR (*gor*) are nonviable unless supplemented with a reductant like dithiothreitol, which chemically will reduce the redoxins (36, 39). Recently, Beckwith and co-workers isolated a viable mutant from the *trxB-gor* *E. coli* strain, which had a trinucleotide insertion in the gene for the oxidative stress defense enzyme alkylhydroperoxide reductase (AhpC) (91). The mutation results in conversion of AhpC from a peroxidase to an intradisulfide reductase, which in turn enables it to reduce Grx1 (91).

The role of the glutaredoxins and thioredoxins in *E. coli*, the best characterized bacterial cell, can be viewed in relation to studies of other minimal gene sets in bacteria to sustain a living cell. Such studies to specify a minimum bacterial cell have been done with *Bacillus subtilis* and *Mycoplasma genitalium* (46, 55). The latter contains only 480 genes (46) out of which maybe 260 genes are essential. Recently, essential *Bacillus subtilis* genes were studied by single inactivation of a gene (55). The genome size of *Bacillus subtilis*, a gram-positive organism without GSH (27), is similar to that of *E. coli*, with 4,100 genes. In *Bacillus subtilis*, there are ~10 known thioredoxin genes and four genes for thioredoxin reductase. The single gene inactivation study showed that a total of three genes (one for thioredoxin and two for thioredoxin reductase) were essential (58, 99). Obviously, the essential but redundant thioredoxin genes in *Bacillus subtilis* code for protein functions, which cannot be replaced by other gene products. This is in all likelihood due to the requirement of an electron donor for ribonucleotide reductase, which is needed for the synthesis of the deoxyribonucleotides for DNA (55). In view of the results for gram-positive organisms lacking GSH and some other organisms not having GSH (27), the role of the glutaredoxin system can be seen as a paralogue allowing the cell to respond to changing environmental conditions and provide means of regulation and defense. The role of the glutaredoxin and thioredoxin set of genes under conditions of oxidative stress (84) or on minimal medium would probably encompass more functions. For instance, sulfate assimilation with PAPS reductase requires either Trx1 or Grx1 when grown on minimal medium (97), whereas ribonu-

cleotide reductase requires Trx1, Trx2, or Grx1 (105). Growth in arsenite requires arsenite reductase, which in turn most likely requires GSH and Grx2 (100).

Concluding remarks

Today the glutaredoxin and thioredoxin systems are considered to be parallel redox systems. In fact, the absence of cross-reactivity between the redoxins and the respective NADPH-dependent reductases may have a special importance in regulation because the systems can operate independently. The more robust system, in terms of keeping a reduced environment in the cell by reducing protein disulfides even under severe oxidative stress, is obviously the thioredoxin system. This is probably also the more evolutionary old system (27). In comparison, the glutaredoxins may be viewed as the more sophisticated system, being able to reduce both protein disulfides and GSH-mixed disulfides. This enables the glutaredoxins to compensate for the thioredoxin system to a large extent, and at the same time have its own unique function. Oxidative stress conditions or energy lack may lead to oxidized glutaredoxin due to lack of GSH and accumulation of GSSG. In mammalian cells, there seems to be cross talk between the thioredoxin system and the glutaredoxins. Human thioredoxin can be glutathionylated on Cys73 with inactivation probably catalyzed by glutaredoxin (14).

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ABBREVIATIONS

AhpC, alkylhydroperoxide reductase; AP-1, activator protein 1; ArsC, arsenate reductase; As(III), arsenite; As(V), arsenate; GR, glutathione reductase; Grx1, Grx2, and Grx3, glutaredoxins 1, 2, and 3; GSH, glutathione; GSSG, glutathione disulfide; GST, glutathione S-transferase; HED, β-hydroxyethyl disulfide; JNK, c-Jun N-terminal kinase; NF-κB, nuclear factor-κB; PAPS, 3'-phosphoadenylylsulfate; PICOT, protein kinase C-interacting cousin of thioredoxin; ppGpp, guanosine-3',5'-tetrphosphate; RpoS, or σ^S, *rpoS*-encoded sigma factor S; Trx1 and Trx2, thioredoxins 1 and 2.

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