

Review Article

Antioxidant Function of Thioredoxin and Glutaredoxin Systems

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ABSTRACT

Selenium is an essential trace element with known antioxidant properties. Cytosolic thioredoxin reductase from mammalian cells is a dimeric flavin enzyme comprising a glutathione reductase-like equivalent elongated with 16 residues including the conserved carboxy-terminal sequence, Gly-Cys-SeCys-Gly, where SeCys is selenocysteine. Replacement of the SeCys residue by Cys in rat cytosolic thioredoxin reductase using site-directed mutagenesis and expression in *Escherichia coli* resulted in a functional mutant enzyme having about one percent activity with thioredoxin as a substrate through a major loss of K_{cat} and a shift in the pH optimum from 7 to 9. The truncated enzyme expected in selenium deficiency by the UGA mRNA codon for SeCys acting as a stop codon was also expressed. This enzyme lacking the carboxy-terminal SeCys-Gly dipeptide contained FAD but was inactive because the SeCys selenol is in the active site. These results show that selenium is essential for the activity of thioredoxin reductase, explaining why this trace element is required for cell proliferation by effects on thioredoxin-dependent control of the intracellular redox state, ribonucleotide reductase production of deoxyribonucleotides, or activation of transcription factors. The selenazol drug ebselen (2-phenyl-1,2 benzoselenazol-3 (2H)-one) is a known glutathione (GSH) peroxidase mimic with antioxidant properties. The hydrogen peroxide reductase activity of human thioredoxin reductase was stimulated 15-fold by 2 μ M ebselen. Glutaredoxins protect against oxidative stress by catalyzing reduction of protein mixed disulfides with GSH. The mechanism of glutaredoxins as efficient general GSH-mixed disulfide oxidoreductases may protect proteins from inactivation as well as play a major role in general redox signaling. *Antiox. Redox Signal.* 2, 811–820.

INTRODUCTION

THIOREDOXIN AND GLUTAREDOXIN are small proteins containing a redox-active disulfide (CXXC) and were both discovered from *Escherichia coli* as independent cofactors for the dithiol-dependent reduction of ribonucleotides to deoxyribonucleotides by the essential enzyme ribonucleotide reductase (Holmgren, 1985, 1989). Thioredoxin and glutaredoxin were subsequently shown to be general thiol-disulfide oxidoreductases and

members of the thioredoxin superfamily of structures (see review by Martin, 1995). Thioredoxins are reduced by NADPH-dependent thioredoxin reductases, which are dimeric flavoproteins present in all living cells. In contrast, glutaredoxins are reduced by glutathione (GSH), the oxidized form of which is GSSG and is reduced by GSH reductase (Holmgren, 1989) or formed directly from the rapid synthesis by the enzymes gamma-glutamyl-cysteine synthetase and GSH synthetase.

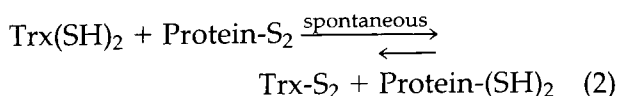
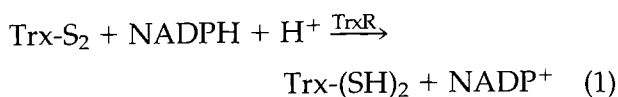
Antioxidant functions of thioredoxin and glutaredoxin are, e.g., as electron donors for ubiquitous methionine sulfoxide reductases participating in protein repair by reduction of methionine sulfoxide residues (Moskovitz *et al.*, 1999). Oxidation of methionine residues to the sulfoxide by reactive oxygen species (ROS) may impair protein function, and the methionine sulfoxide reductase restores the methionine side chain. Lately, a lot of focus has been on the antioxidant properties of thioredoxin-dependent peroxidases (peroxiredoxins), which reduce hydrogen peroxide with a low K_m value via cysteine residues and are ubiquitous with quite a large number of isoenzymes (Chae *et al.*, 1999).

The early work on thioredoxin in *E. coli* and yeast showed that the thioredoxins are stable disulfide-containing proteins with the conserved active site (Cys-Gly-ProCys) being reduced by a 70-kDa dimeric thioredoxin reductase, which generally is species specific for its own thioredoxin (Holmgren, 1985). However, when research started around 1970 to isolate thioredoxin systems from bovine and rat, as well as human tissues (Engstrom *et al.*, 1974; Holmgren, 1977), some important differences were noted that are important for understanding the role of these proteins in antioxidant defense. Thus, thioredoxin was a protein that only could be purified to homogeneity in the reduced form, because it contains two (calf thymus) or three (rat and human) additional structural sulfhydryl groups that easily oxidize to generate inactive aggregated molecules, dimers, or even multimers (Holmgren, 1977; Luthman and Holmgren, 1982; Ren *et al.*, 1993; Weichsel *et al.*, 1996). This may be of significance for redox regulation and particularly in conditions of severe oxidative stress (Ren *et al.*, 1993). However, the major difference was seen in the molecular properties and activity of thioredoxin reductase (Holmgren, 1977; Luthman and Holmgren, 1982).

This review will focus on some recent developments in the structure and function of human and other mammalian thioredoxin reductases, in particular in relation to the requirement of selenium, a well-known antioxidant element.

MAMMALIAN THIOREDOXIN SYSTEMS

Mammalian thioredoxin systems comprise the same reactions as in all other living cells:



Reduction of Trx-S₂ by thioredoxin reductase (TrxR) follows Michaelis-Menten kinetics with a K_m value of Trx-S₂ of about 2.5 μM and K_{cat} of about 3,000 per min (Reaction 1) (Luthman and Holmgren, 1982). Trx-(SH)₂ is a powerful protein disulfide reductase with a K_2 of $5 \times 10^4 \text{ M}^{-1} \text{ s}^{-1}$ for insulin, a substrate used in assays (Reaction 2) (Holmgren, 1979a). However, Reaction 2 is reversible and dependent on the redox potential of the protein disulfide/dithiol pair. Via Reaction 2, thioredoxin may therefore catalyze general reactions between pairs of thiols and disulfides acting as a shuttle (Holmgren, 1979b).

Among the properties noted early for mammalian thioredoxin reductase was its ability to directly reduce 5,5'-dithiobis (2-nitrobenzoic acid) (DTNB) (Holmgren, 1977), which is used today as a convenient substrate in assays of the purified enzyme (Holmgren and Bjornstedt, 1995). Furthermore, quite a remarkable number of molecules have been shown to be reduced by mammalian thioredoxin reductase (Table 1). These include alloxan (Holmgren and Lyckeberg, 1980), which is known to be particularly toxic for pancreatic Langerhans islet insulin-producing B cells, where thioredoxin reductase may be participating in generation of toxic ROS leading to cell death and diabetes (Halliwell and Gutteridge, 1999). Thioredoxin reductase will also reduce the disulfide bond of thioredoxins from different species. In the case of *E. coli* thioredoxin, there is a 14-fold higher K_m value but almost identical K_{cat} . The growing large number of proteins with thioredoxin domains (Ferrari and Söling, 1999) including protein disulfide isomerases (PDI) and

TABLE 1. SUBSTRATES FOR DIRECT REDUCTION BY NADPH AND MAMMALIAN THIOREDOXIN REDUCTASE

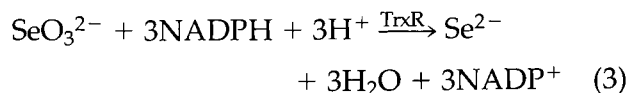
Substrate	Reference
Thioredoxin-S ₂	Holmgren (1985)
SeO ₃ ²⁻ and selenocystine	Kumar <i>et al.</i> (1992)
S-Nitrosoglutathione (GSNO)	Nikitovic and Holmgren (1996)
Plasma glutathione peroxidase	Bjornstedt <i>et al.</i> (1994)
Lipid hydroperoxides	Bjornstedt <i>et al.</i> (1995)
Alloxan	Holmgren and Lyckeberg (1980)

analogues are substrates for thioredoxin reductase (Lundstrom and Holmgren, 1990; Lundstrom *et al.*, 1995). How this has physiological relevance remains to be established, but it could well be involved in oxidative stress related functions of calcium movements (Morad and Suzuki, 2000) and requires further studies.

Of specific interest was the discovery that lipid hydroperoxides (HPETE) are direct substrates for NADPH and thioredoxin reductase using either the human or the bovine enzymes and that free selenocyst(e)ine was shown to enhance this reaction (Bjornstedt *et al.*, 1995).

REACTIVITY OF SELENIUM COMPOUNDS WITH THIOREDOXIN REDUCTASE

The first studies on the reactivity of thioredoxin reductases with selenium compounds (Holmgren and Kumar, 1989) were aimed at understanding the reported inhibitory effects of inorganic selenium compounds like selenite on the growth of mouse tumor cells (reviewed by Ip, 1998). When we tested selenite (1–10 μ M), it was surprisingly found to be a direct substrate for the mammalian thioredoxin reductase (Kumar *et al.*, 1992) (Reaction 3):



The product selenide (Se²⁻) generated anaerobically is required for selenocysteine synthesis. Under normal aerobic conditions, the reaction between selenite and mammalian thioredoxin reductase is redox cycling by oxygen resulting in nonstoichiometric oxidation of large amounts of NADPH (Kumar *et al.*, 1992). This

is true also for selenodiglutathione (GS-Se-SG) (Bjornstedt *et al.*, 1992). Selenocystine is also a substrate for thioredoxin reductase with a K_m value of 6 μ M and a K_{cat} of $3,000 \times \text{min}^{-1}$ (Bjornstedt *et al.*, 1997). In the presence of 10 μ M selenite, a strong inhibition of the ribonucleotide reductase reaction (85%) as well as general protein disulfide reduction was observed (Bjornstedt *et al.*, 1992). These results showed that selenite is toxic to particularly tumor cells because of the redox cycling and potential generation of free radicals via thioredoxin reductase. Selenide (Se⁻ and HSe⁻) is readily autooxidized and generates DNA-damaging free radicals as observed in model studies (Whiting *et al.*, 1980; Seko and Imura, 1997). Many tumor cells express 10-fold higher levels of thioredoxin reductase, with up to 0.5% of total protein (Gladyshev *et al.*, 1996; Gallegos *et al.*, 1997; Berggren *et al.*, 1997). Cells do not contain a free pool of selenocysteine, as this would prohibit using oxygenated lipid intermediates like prostaglandins or leukotrienes (Bjornstedt *et al.*, 1995), and it would furthermore redox cycle by oxygen by thioredoxin reductase and thioredoxin (Kumar *et al.*, 1992). As will be discussed below, selenocysteine synthesis utilizes a cotranslational machinery for the proteins having this rare 21st amino acid encoded by TGA in DNA and UGA in mRNA (Böck *et al.*, 1991; Low and Berry, 1996).

STRUCTURE OF MAMMALIAN THIOREDOXIN REDUCTASE

Thioredoxin reductase from rat liver cytosol was purified to homogeneity in 1982 and shown to have subunits of M_r 58,000 (Luthman and Holmgren, 1982). The enzyme contained

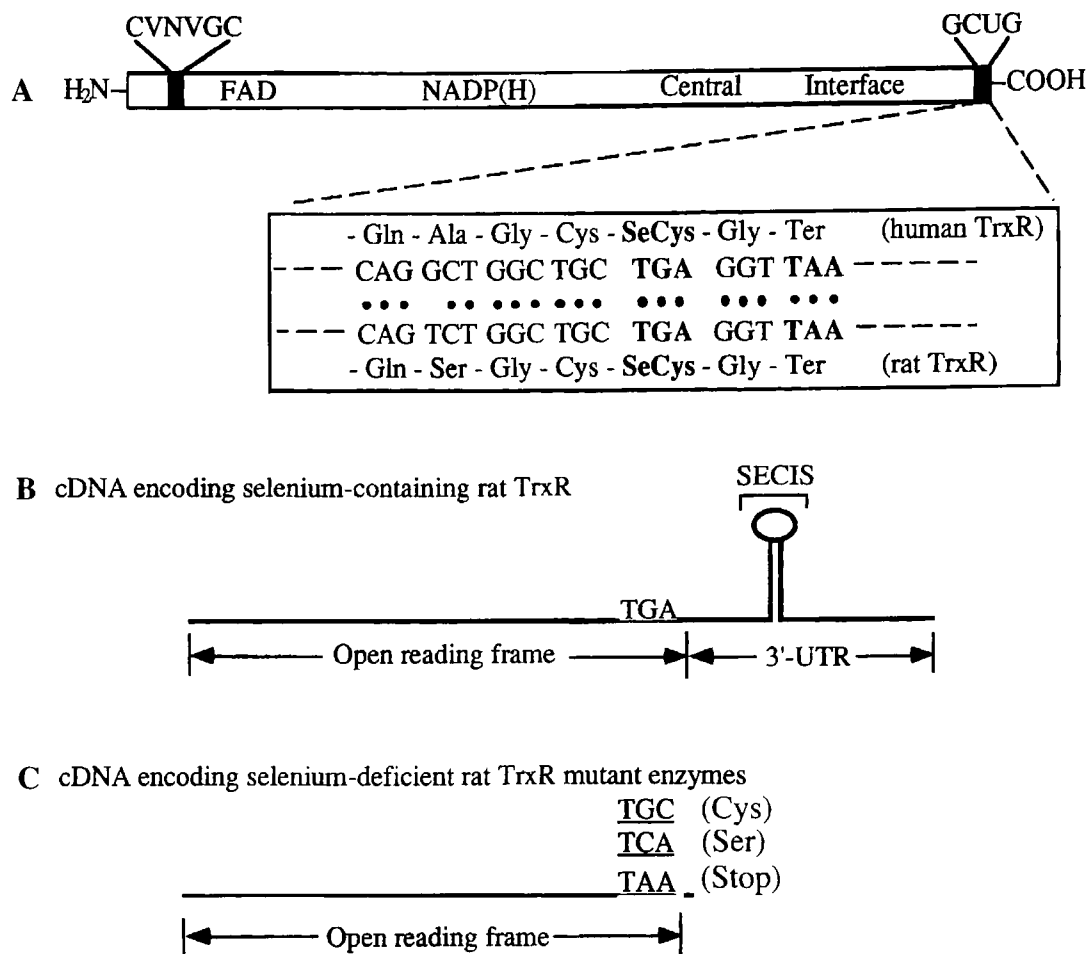


FIG. 1. (a) Schematic structure of rat and human cytosolic thioredoxin reductase based on the homology to GSH reductase, with the conserved active site redox active disulfide in one-letter abbreviations and the nucleotide and protein sequence of the carboxyl terminus of the proteins. (b) Native rat TrxR cDNA with the TGA codon for selenocysteine and the SECIS element in the 3'-untranslated region. (c) Engineered cDNA for expression of rat TrxR mutants replacing the SeCys residue by Cys, Ser or by a stop generating the Des-SeCys-Gly mutant protein (Zhong and Holmgren 2000). Structures are not drawn to scale.

two moles of FAD, and titration with NADPH resulted in a spectral change similar to that of glutathione reductase (Arscott *et al.*, 1997). The enzymes from calf thymus and liver as well as the human placenta enzyme purified by a different method had similar activity (Holmgren and Bjornstedt, 1995; Gromer *et al.*, 1998). These enzymes generally cross-react with the cytosolic thioredoxins from human, bovine, or rat with full activity (Ren *et al.*, 1993).

The sequence of cloned human thioredoxin reductase was reported by Powis and co-workers (Gasdaska *et al.*, 1995), who found a protein homologous to glutathione reductase. However, the cloned protein was a putative thioredoxin reductase because expression in *E. coli*

resulted in a subunit of the expected size (57 kDa), but the protein did not bind FAD and consequently lacked activity. Selenium in human thioredoxin reductase was discovered by Stadtman and co-workers (Tamura and Stadtman, 1996) using ³⁵S-labeled selenite in tissue culture experiments of carcinoma cells aimed at isolating a cytochrome P450 potentially containing selenium. This instead resulted in the isolation of a novel yellow protein that turned out to have thioredoxin reductase activity similar to the known rat liver enzyme (Tamura and Stadtman, 1996). The protein contained selenocysteine, and it was later shown that the TGA interpreted as a stop codon (Gasdaska *et al.*, 1995) encoded selenocysteine (Fig. 1) and the

true stop codon was the TAA downstream (Gladyshev *et al.*, 1996). In our own work, we had sequenced large parts of calf thymus thioredoxin reductase in 1996 and identified an unusual amino acid in the carboxy-terminal peptide and also found an active site sequence identical to that of glutathione reductase (Zhong *et al.*, 1998). On the basis of this, we cloned and sequenced the rat enzyme and found a high homology to GSH reductase, including a 16-residue elongation with the carboxy-terminal conserved sequence-Gly-Cys-SeCys-Gly. We also identified a typical selenocysteine insertion sequence (SECIS) element in the 3'-untranslated region required for selenocysteine synthesis (Zhong *et al.*, 1998). Alkylation of selenocysteine residue inactivating the enzyme was only possible after reduction by NADPH. Furthermore, treatment of this reduced enzyme with carboxypeptidase Y removed selenocysteine and also resulted in loss of enzyme activity in reduction of DTNB and thioredoxin (Zhong *et al.*, 1998). These results demonstrated that all the mammalian cytosolic enzymes contained selenocysteine, which was required for enzyme activity.

ESSENTIAL ROLE OF SELENOCYSTEINE AND RECOMBINANT EXPRESSION OF RAT THIOREDOXIN REDUCTASE

Because the SECIS element of the mRNA forms a complicated hairpin secondary structure not recognized by the *E. coli* selenocysteine synthesis machinery (Low and Berry, 1996), we decided to remove this element from the gene (Fig. 1) and introduce mutations at the selenocysteine residue (Zhong and Holmgren, 2000). Thus, we have expressed and purified to homogeneity recombinant enzymes with the selenocysteine replaced by cysteine or by serine. We also engineered the truncated protein expected in selenium deficiency by the UGA in the mRNA acting as a stop codon (Fig. 1). All three proteins were purified to homogeneity in high yields (Zhong and Holmgren, 2000). The truncated enzyme (Des-SeCys-Gly) and the Ser mutant lacked activity as reductants of thioredoxin. In contrast, the selenocysteine to cysteine mutant enzyme had about 1.5% activity with a

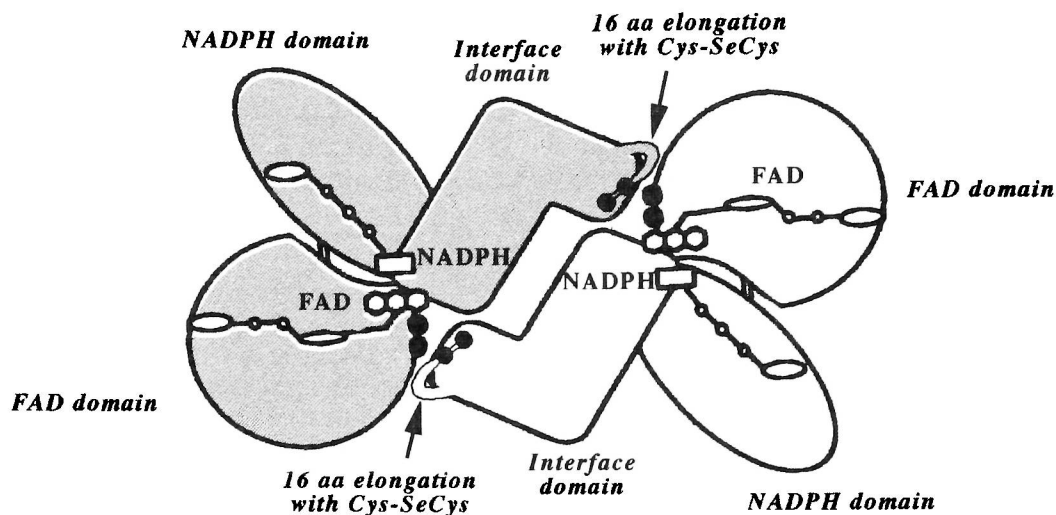
major loss in K_{cat} but also a lower K_m value for human thioredoxin compared to the wild-type rat liver enzyme (Zhong and Holmgren, 2000). Most important, the pH optimum for the cysteine mutant enzyme was 9 as supposed to 7 for the selenocysteine containing wild-type enzyme, strongly suggesting that a low pKa (5.2) selenol directly participates in the mechanism.

HYDROPEROXIDE REDUCTASE ACTIVITY OF MAMMALIAN THIOREDOXIN REDUCTASE

Hydroperoxides like hydrogen peroxide (H_2O_2) and different lipid hydroperoxides are generated in cells, e.g., from the electron transport chain, the metabolism involving cytochrome P450 or from arachidonic acid intermediates in the formation of prostaglandins and leukotrienes (Halliwell and Gutteridge, 1999). Previously, we discovered that mammalian thioredoxin reductases directly reduced HPETE by NADPH resulting in production of HETE (Bjornstedt *et al.*, 1995). This activity was strongly stimulated by the addition of free selenocysteine and was reported before the subsequent discovery that the enzyme itself contained selenocysteine. Human thioredoxin reductase directly reduced H_2O_2 with initial an apparent K_m value of 2.8 mM and K_{cat} of 100 per min (Zhong and Holmgren, 2000). Analyzing the cysteine mutant enzyme demonstrated no detectable H_2O_2 reductase activity consistent with the selenocysteine residue being essential for this activity (Zhong and Holmgren, 2000).

STRUCTURE MODEL AND MECHANISMS OF MAMMALIAN THIOREDOXIN REDUCTASE

Today at least three different isoenzymes of mammalian thioredoxin reductase have been described. Apart from the classical cytosolic enzyme with potential splice variants (Rundlof *et al.*, 2000), there is a mitochondrial thioredoxin system involving a selenocysteine-containing enzyme (Rigobello *et al.*, 1998; Lee *et al.*, 1999; Miranda-Vizuete *et al.*, 1999). In addition, there



Thioredoxin Reductase

FIG. 2. Schematic structure of mammalian thioredoxin reductase based on homology to GSH reductase. The enzyme contains two identical subunits that from a functional perspective are arranged in a head-to-tail fashion. The NADPH, FAD, and interface domains are shown. The redox active disulfides in the FAD domains are represented as black circles. The selenenylsulfides in the interface domains are also shown. Electrons are transferred from NADPH to FAD and to the redox active disulfide in one subunit and across to the other subunit where the resulting selenolthiol is the active site (Zhong *et al.*, 2000).

is a third form reported, which appears to be testis specific and is elongated at the amino terminus (Sun *et al.*, 1999). However, all of these enzymes have the classical glutathione reductase structure active site (CVNVGC, Fig. 1) and the carboxy-terminal sequence -Gly-Cys-Se-Cys-Gly absolutely conserved.

All three mutant rat enzymes described above (Fig. 1), including the truncated version lacking the SeCys-Gly dipeptide, contained one mole of FAD per monomeric subunit and were enzymatically active proteins (Zhong and Holmgren, 2000). This was shown by titrations under anaerobic conditions with NADPH. The long wave-length spectral changes characteristic of the thiolate-flavin charge transfer complex (Arscott *et al.*, 1997) were observed, demonstrating that the reductive half-reaction characteristic of glutathione reductase operated also in the truncated enzyme (Zhong and Holmgren, 2000). This involves transfer of electrons from NADPH to the FAD and then to the redox active disulfide located in the amino-terminal part of the enzyme (Fig. 1). From the native oxidized enzyme we isolated the carboxy-

terminal peptide, which contained a bridge joining the neighboring cysteine and selenocysteine residues (Zhong *et al.*, 2000). This unique selenenylsulfide is the state of the selenium in the oxidized form of the enzyme, which will be present as a selenolthiol in the NADPH-reduced enzyme (Zhong *et al.*, 2000). The active site of the enzyme (Fig. 2) is directly reducing thioredoxin or the other substrates, including hydroperoxides. The enzyme is thus a head-to-tail structure with transfer of electrons across the subunits (Zhong *et al.*, 2000).

ROLE OF SELENIUM IN ANTIOXIDANT DEFENSE

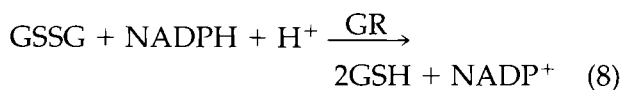
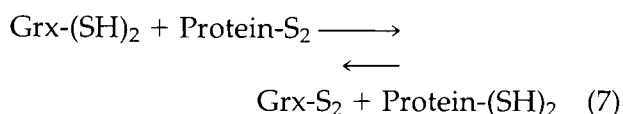
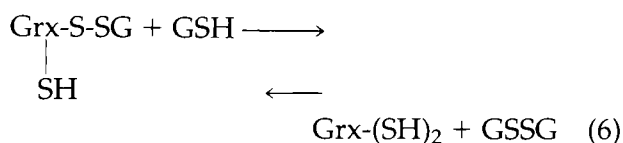
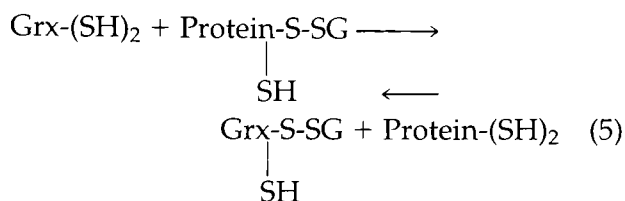
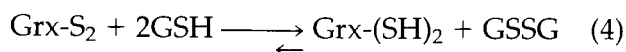
The essential role of selenium in thioredoxin reductase provides a new mechanism for coupling decreased antioxidant defense and loss of cell growth with selenium deficiency. As previously shown, the immunomodulating electrophile 1-chloro-2,4-dinitrobenzene (DNCB) is a strong irreversible inhibitor of thioredoxin reductase, inactivating the enzyme only in the

presence of NADPH (Arner *et al.*, 1995). We showed that the carboxy-terminal adjacent cysteine and selenocysteine residues were both alkylated by DNCB (Nordberg *et al.*, 1998). However, the modified enzyme is still active and has a more than 30-fold increase in activity as an NADPH oxidase activity producing superoxide from NADPH and oxygen (Arner *et al.*, 1995). This ROS may account for some of the immunomodulating properties of DNCB (Arner, 1999). It has been reported that the selenium content of thioredoxin reductase varies with the selenium status (Hill *et al.*, 1997) and that more active enzyme is particularly produced when selenium is supplemented (Berggren *et al.*, 1997; Gallegos *et al.*, 1997; Fujiwara *et al.*, 1999). Thus, if the truncated version of the enzyme is made, our results show that this may well produce more superoxide from FAD and account for an increased production of reactive species resulting in a higher mutation frequency in cells. This hypothesis would be consistent with known protective roles of selenium in carcinogenesis (Ganther, 1999) and should be tested experimentally.

In electron paramagnetic resonance (EPR) spin trap experiments, we have observed that the pure rat thioredoxin reductase incubated with NADPH in a closed system with initial containing atmospheric oxygen will consume NADPH corresponding to dissolved oxygen ($\sim 240 \mu\text{M}$) and then give rise to a burst of hydroxyl radicals (S. Kuprin, T. Kerimov, and A. Holmgren, unpublished). The selenium-containing enzyme showed a small burst, whereas *E. coli* thioredoxin reductase and the selenocysteine-to-cysteine mutant rat enzyme produced more of this free radical also inactivating the enzyme. This may be one reason why the mammalian enzyme contains selenium to remove H_2O_2 to avoid toxic production of free radicals.

GLUTAREDOXINS AS ANTIOXIDANTS

Glutaredoxins catalyze the reduction of protein as well as of low-molecular-weight mixed disulfides with GSH and are themselves reduced by glutathione via a specific binding site (Reactions 4–8):



As a dithiol protein disulfide reductase (Reactions 4 and 7), glutaredoxin is known to work with ribonucleotide reductase and other proteins (Holmgren and Aslund, 1995). The reaction of glutaredoxin is coupled to GSH reductase and NADPH (Reaction 8) or *de novo* synthesis of GSH. Under oxidative stress, glutaredoxin may catalyze formation of mixed disulfides from GSSG (reversal of Reaction 5 and 6), which may be of a protective function to avoid oxidation of a thiol to higher oxidation states. Regulating the activity of phosphotyrosine phosphatases, which contain a low pKa catalytically active SH-group, is one such example (Lee *et al.*, 1998; Barrett *et al.*, 1999). Under conditions, when oxidative stress is relieved, glutaredoxins are the major catalysts to remove glutathione mixed disulfides, which generally lead to inactivation of protein function (Chai *et al.*, 1991).

In the context of GSH peroxidase, it was shown that the extracellular plasma enzyme could utilize glutaredoxin as well as thioredoxin or mammalian thioredoxin reductase as an electron donor. Because plasma lacks free GSH, this may explain how GSH peroxidase can operate in the extracellular space via glutaredoxins (Bjornstedt *et al.*, 1994). How this is related to intracellular functions is not known. However, it was observed that glutaredoxin also functions as an electron donor for

the cytosolic GSH peroxidase (Bjornstedt *et al.*, 1994).

Because glutaredoxin and GSH reductase have no requirement for selenium, this system will be operative under conditions of low selenium and may then partly compensate for the loss of thioredoxin reductase activity. However, all functions of thioredoxin cannot be performed by glutaredoxins.

REACTIONS OF EBSELEN WITH MAMMALIAN THIOREDOXIN REDUCTASE

Ebselen is a selenazol drug with GSH peroxidase-like properties and has extensive effects on cells (Sies, 1995). Because of its antioxidant properties, it has been used in clinical trials against stroke and other forms of ischemic disease (Ogawa *et al.*, 1999). We have found that ebselen promotes the activity of thioredoxin reductase as a hydroperoxide reductase. With H_2O_2 as a substrate, ebselen at 2 μM will stimulate reductase activity 15-fold (M.H. Amiri, H. Masayasu, and A. Holmgren, unpublished). These results suggest that major effects of ebselen are via thioredoxin reductase.

CONCLUSIONS

Because the number of thioredoxin reductases, thioredoxins, and glutaredoxins is still growing, the complexity of redox reactions involved in defense against oxidative stress requires analysis of the enzymatic mechanisms and expression of each enzyme. As with ribonucleotide reductase, the relative contribution and functions of thiols and selenol groups from the thioredoxin systems and thiols from the glutaredoxin systems in a cellular context of defense against oxidative stress and other stresses is yet unknown.

ACKNOWLEDGMENTS

The excellent secretarial assistance of Ms Lena Ringdén is gratefully acknowledged. Research was supported by grants from the Swedish Medical Research Council, The

Swedish Cancer Society, the K.A. Wallenberg Foundation, and the I.-B. and A. Lundberg Foundation.

ABBREVIATIONS

DTNB, 5,5'-Dithiobis(2-nitrobenzoic acid); DNCB, 1-chloro-2,4-dinitrobenzene; ebselen, 2-phenyl-1,2-benzisoselenazol-3(2H)-one; Grx, glutaredoxin; HPETE, hydroperoxyeicosatetraenoic acid; HETE, hydroxyeicosatetraenoic acid; SECIS, selenocysteine insertion sequence; SeCys, selenocysteine; Trx, thioredoxin; TrxR, thioredoxin reductase.

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Received for publication April 23, 2000; accepted June 29, 2000.

This article has been cited by:

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