

## Forum Review

# Thioredoxin-1 and Posttranslational Modifications

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### ABSTRACT

**Thioredoxin-1 is a 12 kDa protein that consists of a redox regulatory domain containing the active cysteine residues 32 and 35. These cysteines are conserved from bacteria to human. Unlike thioredoxins from lower species, mammalian thioredoxin-1 contains three additional nonactive cysteine residues at positions 62, 69, and 73 (for human thioredoxin-1). Key biological functions of thioredoxin-1 are antioxidative, anti-apoptotic, and pro-proliferative properties. Thioredoxin-1 is regulated by the ability of the thioredoxin reductase to reduce oxidized thioredoxin-1 at cysteines 32 and 35. However, posttranslational modifications of thioredoxin-1, including glutathionylation, thiol-oxidation, and S-nitros(yl)ation, at the nonactive cysteines importantly contribute to the regulation and functions of thioredoxin-1. This review focuses on the posttranslational modifications of the active and nonactive cysteines and their contribution for functional regulation of thioredoxin-1.**

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### INTRODUCTION

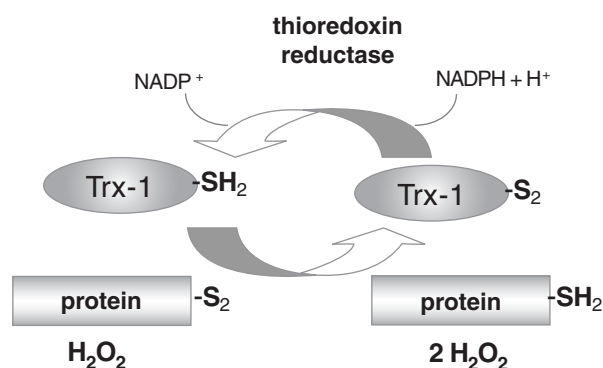
**O**XYGEN AND NITRIC OXIDE are physiologically relevant molecules. Both molecules act as double-edged swords. In high concentrations, oxygen and the resulting reactive oxygen species, as well as nitric oxide, are toxic, whereas in low concentrations these molecules play important roles in the regulation of a variety of cellular functions. Oxidant stress of the vascular wall is a hallmark of atherosclerosis (for review, see Ref. 21). To defend themselves from oxidative damage, including oxidative and nitrosative stress, cells possess antioxidative enzymes such as superoxide dismutase, catalase, and the thioredoxin system, to maintain intracellular levels of reactive oxygen species and reactive nitrogen species (41, 42).

The thioredoxin family includes three proteins, thioredoxin-1, thioredoxin-2, and Sp-thioredoxin (37, 47, 49). They contain a conserved -Cys-Gly-Pro-Cys- active site (cysteine 32 and cysteine 35 within thioredoxin-1), which is essential for the redox regulatory function of thioredoxins (26, 34). Thioredoxin-1 is a 12 kDa protein, which is ubiquitously expressed in mammalian cells (26). Thioredoxin-1 exerts its enzymatic activity as an oxidoreductase via the cysteines 32 and

35 in the active site of thioredoxin-1 (26, 34). This site is conserved among species from bacteria to humans (10, 26). The active site cysteines are accessible on the surface of the protein and are oxidized to a disulfide upon reduction of a target protein (27, 34, 44). Thioredoxin-1 itself is reduced by the thioredoxin reductase. These two oxidoreductases form the thioredoxin system in mammalian cells (Fig. 1). The fundamental importance of thioredoxin-1 has been demonstrated by the lethal phenotype of thioredoxin-1 deficiency in mice (35).

Posttranslational modifications of proteins are conserved during evolution and relate to all aspects of cell biology. These modifications include phosphorylation of serine, threonine, and tyrosine residues, modifications of cysteine thiols and transition metal centers by nitric oxide, and modifications of cysteine thiols by glutathione or oxygen. The latter three are so-called redox based protein modifications. All of these protein modifications are reversible and play an important role in cellular signaling and in human diseases.

With respect to the thioredoxin system, all redox-based modifications have been demonstrated to regulate thioredoxin-1. In contrast, phosphorylation of thioredoxin-1 has not been demonstrated. Oxidation has also been demon-



**FIG. 1. The thioredoxin system.** Cartoon represents the two oxidoreductases thioredoxin-1 and thioredoxin reductase, which form the thioredoxin system.

strated for thioredoxin-2 by different metals such as arsenic, cadmium, and mercury, resulting in a dissociation of thioredoxin-2 from apoptosis-signaling kinase 1 in cell culture (19). However, the impact of posttranslational modifications of thioredoxin-2 on cellular function remains to be elucidated. Therefore, this review will focus on the redox-based modifications of thioredoxin-1 and their influence for cellular signaling and human diseases.

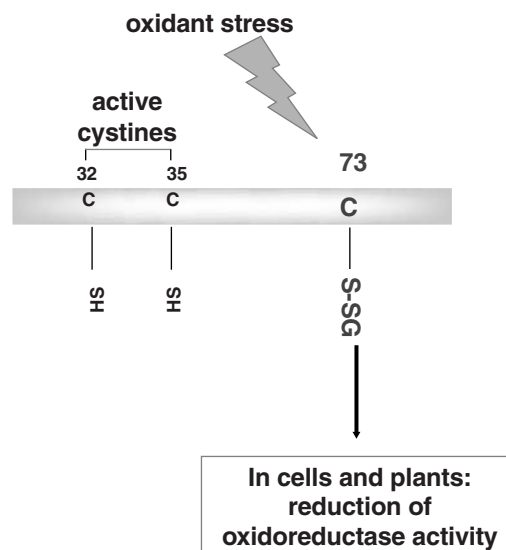
### CYSTEINES IN THIOREDOXIN-1

Thioredoxin-1 contains five cysteines. Cysteines 32 and 35 are in the redox-regulatory domain of thioredoxin-1, which is conserved throughout species (10, 26). Thioredoxin-1 exerts several functions via its redox-regulatory domain (43). Besides its enzymatic activity as an oxidoreductase in scavenging H<sub>2</sub>O<sub>2</sub> and thereby reducing H<sub>2</sub>O<sub>2</sub> to H<sub>2</sub>O (28), thioredoxin-1 directly interacts with other proteins by forming disulfide bridges such as ribonucleotide reductase, protein disulfide isomerase, apoptosis signaling kinase I, and vitamin D<sub>3</sub>-upregulated protein 1 (Txnip, also named VDUP-1) and interfering with the function of the proteins (9, 32, 33, 46, 55). Furthermore, thioredoxin-1 translocates into the nucleus under specific stimuli and directly binds different transcription factors and, thereby, modulates their DNA-binding activity, for example, p53, NFκB, and AP-1 via Ref-1 (8, 20, 23, 24, 29, 52). Besides the two cysteines at positions 32 and 35 in the redox-regulatory domain, thioredoxin-1 contains three cysteines at positions 62, 69, and 73, which are believed to be structurally important (1, 53) and are also conserved in mammals. These three cysteines have been implicated in redox-based protein modifications and will be described in more detail in the following sections of the review.

### GLUTATHIONYLATION OF THIOREDOXIN-1

Glutathionylation describes the formation of mixed disulfides between proteins and glutathione. Glutathionylation of proteins has been shown to occur under physiological condi-

tions, providing evidence that this protein modification does not only occur after oxidative stress (3, 4). Of note, the amount of glutathionylated proteins increased with oxidative stress up to 20–50% of the total glutathione content (15), given a rationale for the importance of this protein modification under physiological and pathophysiological conditions. However, the mechanism by which glutathione reacts with proteins is not understood. Several mechanisms have been proposed, ranging from an oxidation including an oxidant such as diazenecarbonyl derivative diamide (30) to a thiol/disulfide exchange (16). However, it is not clear which of these mechanisms occurs *in vivo*. Up to now it is only evident that glutathionylation is important as a reversible protein modification that can be detected *in vivo* under physiological and pathophysiological conditions. Several proteins have been described to undergo glutathionylation, including thioredoxin-1. However, glutathionylation of thioredoxin-1 could only be demonstrated under conditions of oxidative stress in eukaryotic cells and in plants (7, 36) (Fig. 2). In both cases glutathionylation of thioredoxin occurred not at cysteines spanning the redox regulatory domain, but at cysteine 73 in eukaryotes and at cysteine 60 in plants. Like cysteine 73, glutathionylated cysteines in plant thioredoxin are located in the flexible α3–β4 loop (11, 36). Glutathionylation of thioredoxin led to a reduction in the enzymatic activity of thioredoxin under conditions of oxidative stress (Fig. 2). Further studies are needed to address whether glutathionylation has an impact on the other known thioredoxin functions, such as altering its affinity for interacting proteins or its subcellular localization. Nevertheless, a possible crosstalk between the glutathione and thioredoxin systems under conditions of oxidative stress may act as an indicator of the redox status of the cell.



**FIG. 2. Regulation of thioredoxin by glutathionylation.** Glutathionylation of cysteine 73 occurs under conditions of oxidative stress in mammals and plants, which leads to inactivation of thioredoxin-1 activity.

## THIOL-OXIDATION OF THIOREDOXIN-1

Thioredoxin-1 reduces disulfide bridges in oxidized target proteins via cysteines 32 and 35. The active site cysteines become oxidized. This disulfide is cycled back under NADPH consumption to the dithiol by thioredoxin-1 reductase (see Fig. 1). In the reduced form, thioredoxin-1 can bind to different proteins and thereby regulate their protein functions. The regulatory function of thioredoxin-1 on different proteins via the active cysteines is described by Yoshioka *et al.* in Part II of this Forum in more detail (56). Interestingly, a second dithiol/disulfide motif was found within thioredoxin-1 form by the cysteines 62 and 69 (51). Watson *et al.* discovered that upon oxidative stress induced by diamide first the oxidation of the active cysteines and the cysteine 62 and cysteine 69 occurred. Of note, the disulfide between cysteines 62 and 69 inhibited the reduction of the active site cysteines of thioredoxin-1 by thioredoxin reductase (51). Structural modeling of the disulfide cysteine 62 and cysteine 69 predicted a profound effect on the tertiary structure of thioredoxin-1 by disrupting the helical structure of the  $\alpha 3$  helix. These data suggested that the interaction between thioredoxin-1 and thioredoxin reductase is sensitive to the presence of a nonactive site disulfide in the  $\alpha 3$ -helix. Thus, it is tempting to speculate that thioredoxin reductase binds to thioredoxin-1 at the  $\alpha 3$ -helix region. This interpretation is further supported by the finding that homodimerization of thioredoxin-1 via cysteine 73, which is in close proximity to the  $\alpha 3$ -helix, made the active site cysteines inaccessible for thioredoxin reductase (14). Taken together, these data support the concept that reversible oxidation of the conserved nonactive site cysteines of mammalian thioredoxin-1 play an important regulatory role for the function of thioredoxin-1. One may speculate that the nonactive site cysteines, thereby, also influence the binding proteins of thioredoxin-1 and thereby their functions. However, further studies are needed to fully elucidate the in-

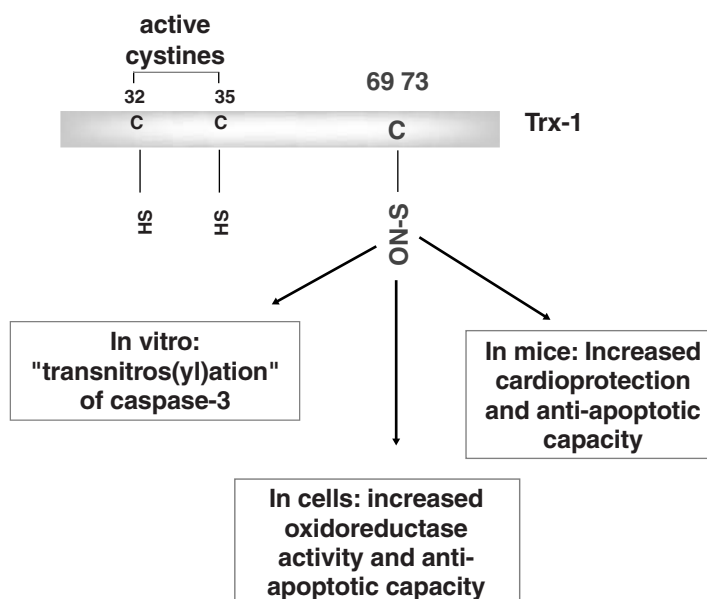
fluence of the oxidation of the nonactive site cysteines on the regulation of thioredoxin-1 binding proteins.

## S-NITROS(YL)ATION OF THIOREDOXIN-1

Nitric oxide (NO) is a crucial factor for the integrity and function of the endothelium (2, 40). Besides its role in blood pressure regulation, NO exerts anti-inflammatory, antithrombotic, and anti-apoptotic effects in the cardiovascular system (2, 5, 13, 22, 54). The initial discovery of endothelium-derived NO-mediated cell signaling was the reaction with the heme-iron center of the guanylate cyclase, leading to increased cyclic guanosine monophosphate (cGMP) accumulation and thus, to vasorelaxant activity (12, 13, 39). Over the past 10 years, it became clear that NO can also function in a cGMP-independent manner by reacting with cysteine residues in target proteins, a reaction named *S*-nitros(yl)ation (48). *S*-nitros(yl)ation has since then been implicated in the control of a wide array of protein functions. Indeed, a head-to-head comparison with phosphorylation revealed that both posttranslational modifications play a role in regulation of almost all cellular functions (for review, see Ref. 31).

Recent studies demonstrated that thioredoxin-1 is also a target for *S*-nitros(yl)ation (Fig. 3). In endothelial cells, thioredoxin-1 has been shown to be *S*-nitros(yl)ated at cysteine 69. *S*-nitros(yl)ation of thioredoxin-1 at cysteine 69 increased the enzyme activity of thioredoxin-1. Interestingly, *S*-nitros(yl)ation of thioredoxin-1 at cysteine 69 in part accounts for the anti-apoptotic capacity of thioredoxin-1 in endothelial cells, whereas mutation of cysteine 69 had no protective effect in human embryonic kidney cells, which do not produce NO endogenously, underscoring the importance for *S*-nitrosylated thioredoxin-1 in NO-producing cells (17). Moreover, the most important physiological stimulus for the activation of the endothelial nitric oxide synthase and thus, for the synthesis of nitric oxide in endothelial cells, is laminar flow in the blood vessel (6). Recently, it has

**FIG. 3. Regulation of thioredoxin-1 by *S*-nitros(yl)ation.** *S*-nitros(yl)ation of thioredoxin-1 can occur at cysteine 69 and 73. *S*-nitros(yl)ation at cysteine 69 in nitric oxide producing cells leads to increased thioredoxin-1 activity and to enhanced anti-apoptotic properties. *S*-nitros(yl)ation of cysteine 73 can “transnitros(yl)ate” caspase-3 *in vitro*. In animals, *S*-nitros(yl)ated thioredoxin-1 demonstrated enhanced cardioprotective and anti-apoptotic functions.



been demonstrated that laminar flow regulated *S*-nitros(yl)ation of different target proteins (25). *S*-nitros(yl)ation of the caspase-3 subunit p17, the small GTPase p21<sup>ras</sup>, and thioredoxin-1 were significantly increased, which resulted in a deactivation of caspase-3 and an increase of the activity of the small GTPase p21<sup>ras</sup> and of thioredoxin-1 (25). These data suggest that *S*-nitros(yl)ation might be one signal transduction pathway for mediating the response to laminar flow. Recently, a novel antioxidative effect of HMG-CoA reductase inhibitors (statins), which are lipid-lowering drugs that also exert pleiotropic vasculoprotective effects via activation of the endothelial NO synthesis, has been demonstrated via increasing *S*-nitros(yl)ation of thioredoxin-1 in endothelial cells (18). Furthermore, Mitchell *et al.* has demonstrated that thioredoxin-1 can transfer NO to caspase-3 and thereby inactivating the enzyme, further suggesting an important anti-apoptotic function for *S*-nitros(yl)ation of thioredoxin-1 (38). Mitchell *et al.* found that purified thioredoxin-1 is *S*-nitrosylated at cysteine 73 and not at cysteine 69 (38). Thus, one may hypothesize that cysteine 69 and cysteine 73 are both required for *S*-nitros(yl)ation and transferring nitric oxide to several target proteins in cells. Based on the recent finding that thioredoxin-1 contains a second dithiol/disulfide motif spanning cysteine 62 and cysteine 69, which was predicted to have a profound effect by disrupting the helical structure of the  $\alpha 3$  helix of thioredoxin-1 (51) and that cysteine 73 is responsible for homodimerization of thioredoxin-1 (45), a second hypothesis arises that *S*-nitros(yl)ation of thioredoxin-1 at cysteine 69 and/or 73 depends on the redox-status of the cell and thus, on the availability of a reduced cysteine 69 and/or cysteine 73. Strikingly, in a mouse model for myocardial ischemia and reperfusion, the cardioprotective and anti-apoptotic effects of thioredoxin-1 were significantly potentiated by thioredoxin-1, which was *S*-nitrosylated prior to i.p. injection (50). Taken together, *S*-nitros(yl)ation of thioredoxin-1 importantly contributes to the cardioprotective and anti-apoptotic functions of thioredoxin-1 in cells and in mice. Thus, *S*-nitros(yl)ation of thioredoxin-1 could offer a potential approach to increase endogenous protective mechanisms and could be a potential therapeutic tool to improve cardiovascular diseases.

## CONCLUSION

The active cysteines 32 and 35 of the redox-regulatory domain within thioredoxin are required for reduction of oxidized proteins and H<sub>2</sub>O<sub>2</sub> as well as for the interaction and regulation of target proteins. However, the nonactive cysteines of thioredoxin-1 importantly contribute to the key biological activities. Posttranslational modifications of the nonactive cysteines not only interfere with the oxidoreductase activity of thioredoxin-1, but also with the regulation of its interacting proteins. Thus, further studies are needed to fully understand the impact of the nonactive cysteines within thioredoxin-1, which may uncover new signaling mechanisms of thioredoxin-1.

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## ABBREVIATIONS

cGMP, cyclic guanosine monophosphate; NO, nitric oxide; Txnip, vitamin D<sub>3</sub>-upregulated protein 1.

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