

# Chapter 13

## Oxidative Stress in Infectious Diseases

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**Abstract** The “big three” infectious diseases HIV/AIDS, tuberculosis, and malaria were collectively responsible for nearly 260 million infected people in 2010. HIV, *Mycobacterium tuberculosis*, and *Plasmodium falciparum*, the causative agents of AIDS, tuberculosis, and malaria, are continuously exposed to reactive oxygen and nitrogen species endogenously produced or derived from the host immune system in response to infection. Oxidative stress has a key function in the pathogenesis of many infectious diseases, and represents moreover a promising strategy for chemotherapeutic development. Understanding the redox interactions and redox signaling mechanisms of pathogens and their hosts is crucial for developing (1) drugs that support the host antioxidant defense in order to protect cells from oxidative damage, (2) drugs that enhance specific reactive oxygen or nitrogen species to improve the host defense against pathogens, and (3) drugs that interfere with the redox system of the pathogen in order to block its growth and survival.

**Keywords** Antioxidants • HIV/AIDS • Malaria • Tuberculosis • Redox system

### Abbreviations

AhpC	alkyl hydroperoxide reductase
AIDS	acquired immunodeficiency syndrome
AOP	antioxidant protein
ASK	apoptosis signal-regulating kinase
G6PD	glucose 6-phosphate dehydrogenase
GR	glutathione reductase

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GST	glutathione <i>S</i> -transferase
gp120	glycoprotein 120
Grx	glutaredoxin
GSH	reduced glutathione
GSSG	oxidized glutathione
HAART	highly active anti-retroviral therapy
HIV	human immunodeficiency virus
KatG	catalase-peroxidase
iNOS	nitric oxide synthase
LTR	long terminal repeat
Mca	mycothiol <i>S</i> -conjugate amidase
MscR	mycothiol- <i>S</i> -nitroso reductase/-formaldehyde reductase
MSH	mycothiol
MSNO	<i>S</i> -nitroso mycothiol
MSSM	mycothiol disulfide
Msr	methionine sulfoxide reductases
Mtr	mycothiol reductase
NAC	<i>N</i> -acetylcysteine
NF $\kappa$ B	nuclear factor $\kappa$ B
NO	nitric oxide
NOX	NADPH oxidase
nPrx	nuclear peroxiredoxin
Plrx	plasmoredoxin
Prx	peroxiredoxin
RNS	reactive nitrogen species
ROS	reactive oxygen species
SOD	superoxide dismutase
Tat	transactivator protein
TNF	tumor necrosis factor
TPx	thioredoxin peroxidase
Trx	thioredoxin
TrxR	thioredoxin reductase

### 13.1 Introduction

Oxidative stress is not a disease, but an unspecific pathological state that can be worsened by depletion of antioxidants, immunosuppressants, zinc and selenium deficiency, xenobiotics, and infections, thus being involved in the pathogenesis of a variety of diseases (Stehbens 2004). Mammalian cells of the immune system use the production of reactive oxygen and nitrogen species (ROS, RNS) to control and defend themselves against infections with bacterial pathogens, parasites, or viruses. Infectious agents counteract oxidative stress derived from the host immune system by highly efficient antioxidant defense systems. Inhibiting the antioxidant

defense of parasites, bacteria, and viruses is an intensely studied strategy in order to develop effective anti-infectious drugs. AIDS (HIV), tuberculosis (*Mycobacterium tuberculosis*), and malaria (*Plasmodium falciparum*) are the three leading infectious diseases worldwide. In their pathogenesis, oxidative stress plays a major role, which will be comprehensively discussed in this review.

## 13.2 Oxidative Stress in HIV/AIDS

According to the WHO, 2.7 million people were newly infected and 34 million people were living with the human immunodeficiency virus (HIV) in 2010 (WHO 2011a). HIV infection leads to a complex disease with broad clinical symptoms and complex pathogenic mechanisms. Dysregulation of the immune system is caused by a constant decline of CD4<sup>+</sup> T cells (Pantaleo et al. 1993), which has been intensely studied. ROS and oxidative stress are critically involved in the pathogenesis of HIV infection, with the most important aspects being discussed in the following paragraphs.

### 13.2.1 Mechanisms of Oxidative Stress in the Pathogenesis of HIV Infection

A role of ROS in viral infections had already been described in 1970 (Belding et al. 1970) and has been intensely investigated since that time. Oxidative stress, ROS, and antioxidant defense systems appear to be implicated in many aspects of HIV infection and AIDS such as immune function, inflammatory response, virus replication, and apoptosis. Humans infected with HIV show chronically increased levels of oxidative stress, decreased concentrations of antioxidants, and perturbations in the antioxidant systems (Gil et al. 2010). Furthermore, high plasma concentrations of hydroperoxides and malondialdehyde were found in HIV patients, indicating increased lipid peroxidation (Suresh et al. 2009). The activation of CD4<sup>+</sup> T cells and monocytes/macrophages upon HIV infection is triggered by hydrogen peroxide, superoxide anion, and peroxynitrite. Moreover, HIV infection of macrophages results in enhanced production of peroxynitrite and superoxide (Elbim et al. 1999). Oxidative stress upon HIV infection can be induced by the HIV transactivator protein (Tat) and the envelope glycoprotein gp120 (Price et al. 2005). However, the mechanisms of oxidative stress induction have not been completely unraveled.

#### 13.2.1.1 Viral Replication

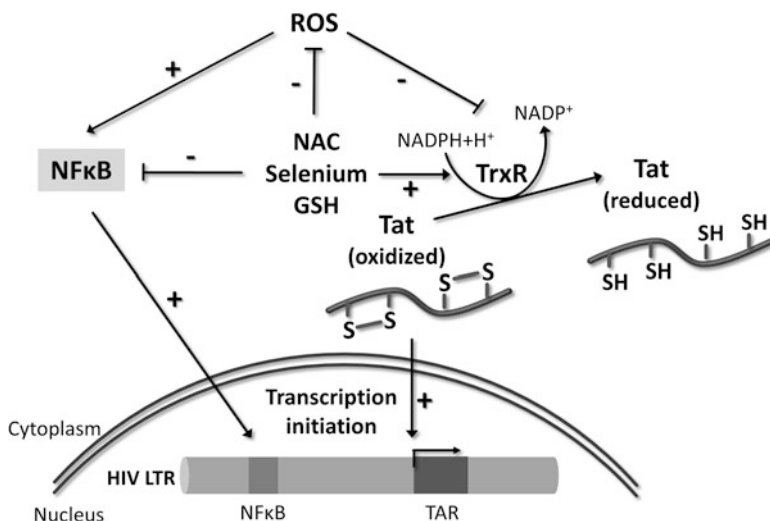
Redox signaling has an important function in the regulation of viral gene transcription and replication. Oxidative stress has been found to increase HIV replication

*in vitro*, while antioxidants show the opposite effect and reduce virus replication (Schreck et al. 1991; Roederer et al. 1990). The promoter of HIV-1 is located in the long terminal repeat (LTR) at the 5'-end and contains binding sites for different transcription factors, including NF $\kappa$ B that mediate the activation of viral transcription in complex interplay with both viral and host factors (for review please see Hiscott et al. 2001). Reactive oxygen intermediates such as H<sub>2</sub>O<sub>2</sub> and oxygen radicals disturb the redox balance towards oxidizing conditions and thereby activate the translocation of NF $\kappa$ B into the nucleus, where it binds to the HIV LTR in order to increase the expression of viral genes and replication (Schreck et al. 1991). Moreover, peroxynitrite was shown to play a major role in virus replication, since a synthetic peroxynitrite decomposition catalyst (MnTBAP) had a strong inhibitory effect on virus replication. Peroxynitrite is suggested to also mediate its effects via the NF $\kappa$ B pathway (Aquaro et al. 2007). Overexpression of peroxiredoxin IV in T cells deactivated HIV LTR and thus inhibited HIV transcription by regulating hydrogen peroxide-mediated activation of NF $\kappa$ B (Jin et al. 1997). Both degradation of I $\kappa$ B and binding of NF $\kappa$ B to the LTR are suggested to be redox-controlled. Furthermore, the HIV LTR contains binding sites for the transcription factors p53 and AP-1, which are also sensitive to redox regulation (Pereira et al. 2000).

An HIV-encoded protein required for efficient viral transcription is Tat, a transactivator protein activated upon oxidizing conditions and inhibited upon reduction, thus functioning as a redox sensor (Koken et al. 1994; Washington et al. 2010). Dysfunction of Tat leads to disturbed transcription with the formation of prematurely terminated short transcripts (Kao et al. 1987). HIV Tat protein contains a cysteine-rich domain with several CxxC motifs that form intramolecular disulfide bonds required for the transactivation activity (Koken et al. 1994). *In vitro* inhibition of HIV expression by N-acetylcysteine (NAC) might at least in part be mediated by reduction and deactivation of Tat (Washington et al. 2010). Similarly, thioredoxin reductase has been shown to act as a negative regulator of Tat transactivation activity by reducing critical disulfide bonds (Fig. 13.1) (Kalantari et al. 2008). Moreover, Tat itself enhances oxidative stress by increasing the expression of tumor necrosis factor (TNF  $\alpha/\beta$ ) and by repressing the expression of antioxidant defense enzymes such as manganese superoxide dismutase, glutathione peroxidase, and  $\gamma$ -glutamylcysteine synthetase (Romani et al. 2010; Buonaguro et al. 1994; Flores et al. 1993; Richard et al. 2001; Choi et al. 2000). Therefore, Tat contributes to the oxidizing environment during HIV infection by decreasing the levels of several antioxidant enzymes.

### 13.2.1.2 Apoptosis

HIV manipulates apoptotic pathways of host cells by multiple factors in order to kill non-infected inflammatory or immune cells and infected CD4<sup>+</sup> T cells by apoptosis (reviewed in (Gougeon 2005)). Balancing of ROS and redox signaling are suggested to be critically involved in HIV-induced apoptosis (Agrawal et al. 2007; Romero-Alvira and Roche 1998; Buccigrossi et al. 2011; Banki et al. 1998). HIV infection



**Fig. 13.1** Scheme of the influence of reactive oxygen species on HIV transcription and replication. Increased cellular concentrations of reduced glutathione (GSH) and supplementation with selenium or N-acetylcysteine (NAC) decrease the concentrations of reactive oxygen species (ROS) and activate antioxidant enzymes such as thioredoxin reductase (TrxR). ROS activate NFκB-dependent gene expression, which is decreased under reducing conditions. HIV transactivator protein (Tat) is inhibited by reduction of critical disulfide bonds. TrxR has been shown to reduce Tat and thereby inhibits Tat-mediated HIV transcription (modified after Kalantari et al. 2008)

leads to an increase in mitochondrial ROS that subsequently trigger apoptosis together with other agents such as viral proteins (Tat, gp120) and cytokines (TNF $\alpha$ ). Moreover, caspases are cysteine-dependent enzymes and are thus sensitive towards the redox status of the cell (Hampton and Orrenius 1998).

Members of the thioredoxin (Trx) family including Trx itself, glutaredoxin (Grx), and peroxiredoxins have been discussed in the context of apoptotic signaling during HIV infection (Masutani et al. 2005). Trx is upregulated in the plasma of HIV-infected patients (Nakamura et al. 1996), and is known to inhibit the activity of apoptosis signal-regulating kinase 1 (ASK1) under reducing conditions, and thereby blocks induction of apoptosis, an effect that is reversed under oxidative stress and subsequent oxidation of Trx (Saitoh et al. 1998). In contrast, thioredoxin-dependent peroxidases, peroxiredoxins, are able to inhibit apoptosis by scavenging hydrogen peroxide (Kim et al. 2000).

Recently, it has been reported that HIV Tat protein can directly mediate apoptosis in enterocytes via a redox-dependent mechanism, leading to damage of the intestinal mucosa (Buccigrossi et al. 2011). Similarly, ROS have been shown to be crucial for HIV Tat-induced apoptosis in neurons (Agrawal et al. 2007). Tat-induced apoptotic signaling is suggested to be based on an increase in intracellular ROS concentrations and an imbalance in the GSH/GSSG ratio (Buccigrossi et al. 2011; Agrawal et al. 2007; Choi et al. 2000). Moreover, NAC not only prevents oxidative stress by

balancing ROS and GSSG concentrations, but also appears to inhibit Tat-induced apoptosis (Buccigrossi et al. 2011).

### 13.2.2 Antioxidant Systems During HIV Infection

Several clinical studies showed that the redox balance in HIV-infected patients without highly active anti-retroviral therapy (HAART) is severely disturbed, with perturbations affecting almost all components of the antioxidant defense system including glutathione, tocopherol, ascorbate, selenium, the thioredoxin system, superoxide dismutase, and glutathione peroxidase (Gil et al. 2010), as summarized in the following paragraphs.

#### 13.2.2.1 Thioredoxin Family

In order to enter host cells, HIV requires the viral glycoprotein gp120, which undergoes conformational changes depending on the reduction of disulfides. Reduction of gp120 can be catalyzed by Trx1, Grx1, and protein disulfide isomerase, thus demonstrating that the host redox system is required for virus entry into host cells (Reiser et al. 2012; Azimi et al. 2010; Auwerx et al. 2009).

Dysregulation of the Trx system appears to be involved in apoptosis in HIV-infected cells as outlined above. *In vitro*, HIV infection of T cell lines decreased the expression of Trx3 shortly after infection (Masutani et al. 2005). Similarly, Trx levels were decreased in monocytes from asymptomatic untreated patients, while Trx expression in cells from AIDS patients was shown to be at a higher level when compared to uninfected cells, which has been suggested to limit ROS levels and apoptosis at later disease stages (Elbim et al. 1999). Thioredoxin reductase 1 (TrxR1) negatively regulates the activity of Tat and thereby Tat-dependent transcription in human macrophages by reducing two disulfide bonds within the cysteine-rich motif of Tat (Kalantari et al. 2008). Inhibition of Grx1 activity by anti-Grx antibodies blocks HIV replication *in vitro*, most likely by inhibiting HIV entry into CD4<sup>+</sup> T cells (Auwerx et al. 2009).

Peroxiredoxins reduce hydrogen peroxide by using Trx as an electron donor. In HIV-infected T cell lines, peroxiredoxin IV is downregulated, while T cells overexpressing peroxiredoxin IV show a decreased HIV transcription (Jin et al. 1997). Altogether, these results show that the Trx system is intriguingly involved in HIV infection.

#### 13.2.2.2 Glutathione

In HIV-infected patients, reduced levels of glutathione were found in the plasma, lymphocytes, monocytes, as well as in CD4<sup>+</sup> and CD8<sup>+</sup> T cells (Eck et al. 1989;

de Quay et al. 1992; Roederer et al. 1991; Buhl et al. 1989). Low levels of reduced glutathione (GSH) are associated with a poor survival of HIV-infected patients (Herzenberg et al. 1997). The mechanisms responsible for impaired GSH production and GSSG reduction upon HIV infection are unclear. Depletion in GSH is accompanied by increased concentrations of oxidized glutathione, indicating a shift in the GSH:GSSG ratio (Aukrust et al. 1995), which has been confirmed in infected macrophages (Morris et al. 2012). Progressively depleted intracellular GSH levels are at least partially mediated by reduced GSH synthesis, since HIV Tat protein decreases transcription and protein levels of  $\gamma$ -glutamylcysteinyl synthetase (Choi et al. 2000). This was supported by a recent study showing that expression of GSH biosynthesis enzymes is decreased in HIV patients, which was attributed to chronically enhanced production of inflammatory cytokines (IL-1, IL-17, and TNF- $\alpha$ ) that might interfere with GSH biosynthesis (Morris et al. 2012).

### 13.2.2.3 Superoxide Dismutase and Catalase

The first enzyme in the defense against superoxide anions is superoxide dismutase (SOD), which converts superoxide anions into hydrogen peroxide, which is subsequently reduced by catalase. The expression of mitochondrial manganese superoxide dismutase (MnSOD) is decreased in HIV-infected patients, with the effect being mediated by HIV Tat protein followed by increased oxidative stress with enhanced protein carbonylation and lipid peroxidation (Flores et al. 1993). In contrast, the expression of cytosolic CuZnSOD in macrophages is increased during HIV infection *in vitro*, most likely to counteract elevated superoxide anion concentrations (Delmas-Beauvieux et al. 1996). Hydrogen peroxide produced by SOD is scavenged by catalase, which shows an increasing activity with progressing HIV infection, and most likely compensates GSH deficiency in HIV-infected cells (Leff et al. 1992).

### 13.2.3 Antioxidants in the Treatment of AIDS

Decreased concentrations of antioxidants observed in HIV-positive patients are associated with deficiencies of micronutrients with antioxidant properties such as vitamins C and E, thiamine, selenium, and zinc. There are many indications that supplementation with antioxidants can have a beneficial therapeutic effect for HIV-infected patients (reviewed e.g. in Lanzillotti and Tang 2005; Singhal and Austin 2002).

### 13.2.3.1 N-Acetylcysteine

Enhancing cysteine bioavailability in order to increase GSH concentrations is most likely the major effect of the antioxidant NAC. Oral supplementation with NAC was reported to increase the glutathione pool in plasma and muscle (Atkuri et al. 2007).

NAC has been found to efficiently inhibit HIV replication. NAC is a potent inhibitor of NF $\kappa$ B by counteracting the effect of ROS (Staal et al. 1990), but has also been shown to block the TNF $\alpha$ -stimulated replication of HIV-1 (Roederer et al. 1990). Moreover, treatment with NAC can prevent Tat-induced apoptosis by restoring the GSH:GSSG ratio *in vitro* and *ex vivo*, and thereby protects the intestinal mucosa (Buccigrossi et al. 2011). An increase in GSH can be achieved by both NAC and glutamine supplementation, with NAC supplying cysteine and glutamine by delivering glycine (Borges-Santos et al. 2012). Similar to NAC, glutamine supplementation enhances plasma GSH levels and significantly increases lean body mass in patients with HIV infection (Borges-Santos et al. 2012).

### 13.2.3.2 Selenium

Selenium deficiency is strongly associated with disease progression and mortality in HIV-infected patients. Selenium supplementation of HIV-infected individuals improves the CD4 count, suppresses the virus load, decreases anxiety, and reduces the need for hospitalization (Hurwitz et al. 2007; Shor-Posner et al. 2003; McDermid et al. 2002). However, information on how selenium influences HIV infection is limited. The effect is most likely mediated via selenoproteins such as TrxR and glutathione peroxidase that shift the redox balance towards a reducing environment and thereby inhibit Tat and thus HIV transcription as explained above (Kalantari et al. 2008).

## 13.3 Oxidative Stress in Tuberculosis

Tuberculosis infected 8.8 million and killed 1.4 million people in 2010 and is after HIV the second leading cause of death from an infectious disease worldwide (WHO 2011b). *Mycobacterium tuberculosis*, its causative agent in humans, infects and multiplies in lung macrophages of the host. In immunodeficient individuals (e.g., HIV-positive individuals), *M. tuberculosis* can multiply to high numbers and induce an active disease. In contrast, the immune system of immunocompetent individuals is in most cases able to control the infection, and more than 90% of the infected remain asymptomatic (Lawn and Zumla 2011). Despite the bactericidal environment, *M. tuberculosis* is able to survive in macrophages, a fact that demonstrates the adaptation of the pathogen to the oxidant burden in the host.



### **13.3.1 Mechanisms of Oxidative Stress in the Pathogenesis of Tuberculosis**

The host immune system is able to influence the virulence of *M. tuberculosis* by producing ROS and RNS. As a reaction towards phagocytosis of *M. tuberculosis*, macrophages can induce the expression of NADPH oxidase (NOX) and nitric oxide synthase 2 (iNOS, NOS2) and thereby increase the oxidative burden. NOX generates superoxide by catalyzing the one-electron reduction of O<sub>2</sub> (Leto and Geiszt 2006). iNOS produces NO<sup>\*</sup>, which can react with superoxide to form highly reactive peroxynitrite and can kill mycobacteria (Shiloh and Nathan 2000). iNOS expression and release of RNS are suggested to be important for controlling the virulence of *M. tuberculosis* in humans. A range of studies based on murine models of tuberculosis using iNOS inhibitors and iNOS-deficient mice show that iNOS and RNS are required in order to control tuberculosis infection (MacMicking et al. 1997; Chan et al. 1995; Scanga et al. 2001). Moreover, NO appears to be important for latent tuberculosis infection in mice and prevents reactivation together with RNS-independent mechanisms (Flynn et al. 1998). Contrarily, another study reported no influence of a lack of iNOS on tuberculosis infection (Jung et al. 2002). Similarly, the function of ROS produced by NADPH oxidase in controlling *M. tuberculosis* is controversially discussed. Experiments using NOX-deficient mice models showed that the absence of NOX-produced superoxide increased bacterial growth during an early infection stage (Cooper et al. 2000; Adams et al. 1997). In contrast, another study did not show any differences between a murine knockout model lacking NOX and wildtype mice in ability to control *M. tuberculosis* infection (Jung et al. 2002). However, clear experimental evidence on the ROS/RNS-based mechanisms of infection control in humans is rare. Alveolar macrophages from *M. tuberculosis*-infected patients show increased concentrations of iNOS compared to non-infected individuals (Nicholson et al. 1996). Several single nucleotide polymorphisms of the *nos2a* gene in African Americans show associations with susceptibility to tuberculosis, thus supporting the role of iNOS for pathogenesis of tuberculosis in humans (Velez et al. 2009; Gomez et al. 2007).

### **13.3.2 Antioxidant Defense Systems of Mycobacterium tuberculosis**

Several studies reported a remarkable resistance of *M. tuberculosis* towards oxidative stress both *in vitro* and *in vivo*; the bacterium can tolerate H<sub>2</sub>O<sub>2</sub> concentrations up to 10 mM (Voskuil et al. 2011). In contrast to enteric bacteria, *M. tuberculosis* shows very low but differential transcriptional responses after exposure to a range of H<sub>2</sub>O<sub>2</sub> and NO concentrations, and is resistant to DNA damage-mediated killing by H<sub>2</sub>O<sub>2</sub> (Voskuil et al. 2011; Garbe et al. 1996). Low H<sub>2</sub>O<sub>2</sub> or NO concentrations lead to an induction of few H<sub>2</sub>O<sub>2</sub>-/NO-responsive genes such as those encoding proteins

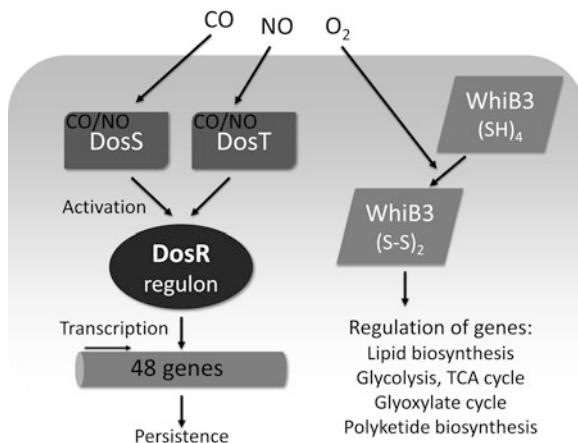
involved in H<sub>2</sub>O<sub>2</sub> scavenging, repair mechanisms, and iron acquisition (Voskuil et al. 2011). Similarly, treatment with cumene hydroperoxide also did not have a major impact on gene transcription (Garbe et al. 1996). Interestingly, the expression of many genes involved in antioxidant defense did not show major changes after H<sub>2</sub>O<sub>2</sub> or NO exposition indicating that they are constitutively expressed at a high level (Voskuil et al. 2011). Several antimycobacterial drugs, such as ethionamide, isoniazid, and the nitroimidazopyran PA-824, have to be reduced for activation and thus depend on the intracellular redox state. Moreover, an increased NADH/NAD<sup>+</sup> ratio, mutations in NADH dehydrogenase, and mutations in mycothiol biosynthesis have been related to resistance against isoniazid (Vilcheze et al. 2005; Xu et al. 2011; Miesel et al. 1998). Therefore, understanding the redox homeostasis of *M. tuberculosis* is important for drug identification strategies. As an intracellular pathogen, *M. tuberculosis* employs different antioxidant systems to counteract oxidative stress of the host defense system, as discussed in the following paragraphs.

### 13.3.2.1 Response Towards Oxidative Stress

*M. tuberculosis* shows an unusually low transcriptional response towards oxidative and nitrosative stress when compared to other enteric bacteria (Garbe et al. 1996). In different bacteria, transcriptional response towards oxidative stress is regulated by the transcription factors OxyR and SoxR, which modulate transcription in response to peroxide and superoxide, respectively. Both regulate the expression of a variety of genes, including a range of redox-active proteins (summarized in (Zahrt and Deretic 2002)). OxyR from *M. tuberculosis* is nonfunctional and is not able to sense peroxide stress. Several mutations (deletions and frameshifts) in the *oxyR* gene render the transcription factor inactive, which impairs the oxidative and nitrosative stress response in *M. tuberculosis* (Deretic et al. 1995; Sherman et al. 1995). Moreover, the *soxRS* regulon is missing in the genome of mycobacteria (Cole et al. 1998).

In *M. tuberculosis*, oxidative stress response can be mediated by the regulator *furA* and catalase-peroxidase KatG, which are mutated and dysfunctional in human pathogenic *M. leprae*. *furA* is located upstream of the catalase-peroxidase *katG*, and is supposed to act as a negative regulator of *katG* expression (Zahrt et al. 2001; Pym et al. 2001). This regulation was suggested to be important for virulence of *M. tuberculosis*, since *M. tuberculosis* mutants lacking *katG* showed a severely impaired persistence in mice and guinea pigs (Li et al. 1998). Moreover, KatG is required for the conversion of the prodrug isoniazid into its active form (Zhang et al. 1992).

The expression of *katG* can also be negatively regulated in a FurA-independent manner by the transcriptional regulator OxyS. Via a cysteine residue in its DNA-binding domain, OxyS binds directly to the *katG* promoter region, with the DNA-binding capacity being diminished upon oxidation of OxyS. Mycobacteria overexpressing OxyS show an increased susceptibility towards oxidative stress, thereby indicating that OxyS functions as a redox sensor (Li and He 2012).



**Fig. 13.2** Regulation of oxidative stress response in *Mycobacterium tuberculosis*. The DosR regulon is modulated by the histidine kinases DosS and DosT that sense NO, CO, and O<sub>2</sub>. The DosR regulon comprises 48 genes with functions for persistence and stress adaptation. On the basis of a redox switch mechanism, WhiB3 regulates lipid biosynthesis and other central metabolic pathways involved in virulence, persistence, and redox homeostasis in response to oxidative stress (modified after Kumar et al. 2011 and Singh et al. 2009)

The DosR/S/T system (also called DevR system) is a redox-sensing system involved in virulence and persistence of *M. tuberculosis* (Leistikow et al. 2010; Shiloh et al. 2008; Park et al. 2003). The DosR regulon is controlled by DosR (DevR), a response regulator, and DosS and DosT, two sensor histidine kinases. The DosR regulon is induced by conditions that inhibit aerobic respiration, since the heme proteins DosS and DosT can sense NO, O<sub>2</sub>, and CO by binding them to iron in their heme group (Shiloh et al. 2008). Subsequently, the DosR dormancy regulon is induced, which includes at least 48 genes suggested to play a role in persistence, latent infection, and stress adaptation (Fig. 13.2) (Park et al. 2003). The DosR regulon enables *M. tuberculosis* to follow and respond to conditions that do not allow aerobic respiration and is required for maintaining the redox balance and energy levels under anaerobic conditions (Leistikow et al. 2010).

Another redox signaling pathway in *M. tuberculosis* is controlled by WhiB3, a redox regulator that senses NO and O<sub>2</sub> from the host and is involved in virulence and pathogenesis of mycobacteria (Fig. 13.2) (Steyn et al. 2002). WhiB3 from *M. tuberculosis* contains four cysteine residues coordinating an iron-sulfur cluster that can specifically bind NO and O<sub>2</sub> (Singh et al. 2007). DNA binding of WhiB3 occurs independently of its iron-sulfur cluster but depends on the oxidation state of its four cysteines: oxidation stimulates DNA binding, while reduction diminishes it (Singh et al. 2009). Oxidation of WhiB3 stimulates DNA binding to several lipid biosynthetic genes and directly regulates production of lipids including poly- and diacyltrehaloses, sulfolipids, and triacylglycerol. WhiB3 is regarded as a redox sensor that connects host redox signals with its intermediary metabolism,

since it induces a metabolic shift to fatty acids by regulating lipid anabolism in response to oxidative stress during tuberculosis infection (Singh et al. 2009). Thus, WhiB3 maintains the intracellular redox homeostasis in part by channeling reducing equivalents into *M. tuberculosis* lipid synthesis, which modulate inflammatory cytokine production (Singh et al. 2009).

### 13.3.2.2 Thioredoxin System

Intracellular redox homeostasis can be maintained by the Trx family, which can catalyze thiol/disulfide exchange reactions and comprises TrxR, Trx, and thioredoxin peroxidases (TPx). *M. tuberculosis* encodes one TrxR and three Trx (A, B, and C) (Akif et al. 2008). However, no mRNA transcripts of *trxA* have been observed. This is supported by the finding that recombinant TrxA cannot be reduced by TrxR. Thus, *trxA* was suggested to be a cryptic gene in *M. tuberculosis* and is most likely not involved in antioxidant defense (Akif et al. 2008). The TrxR/Trx couple from *M. tuberculosis* is able to reduce peroxides and dinitrobenzenes, while cumene hydroperoxide can only be reduced by TrxR and not by Trx *in vitro* (Zhang et al. 1999). Moreover, TrxC is able to reduce mycothiol, GSSG, and *S*-nitrosoglutathione *in vitro*, which was suggested to be important for defense against host-derived oxidative stress (Attarian et al. 2009). The crystal structure of *M. tuberculosis* TrxC, both oxidized and in complex with an inhibitor, has been solved and can be exploited for structure-based inhibitor development (Hall et al. 2006, 2011)

Thioredoxin peroxidase (TPx) from *M. tuberculosis* shows homology to atypical 2-cys peroxiredoxins but has been characterized as a 1-cys peroxiredoxin with Cys60 being the peroxidatic cysteine (Trujillo et al. 2006). TPx can use TrxB and C as electron donors to efficiently reduce hydrogen peroxide, *t*-butyl hydroperoxide, cumene hydroperoxide, and peroxyxynitrite (Trujillo et al. 2006; Jaeger et al. 2004). The crystal structure of dimeric TPx revealed a Trx fold similar to that of other peroxiredoxin family members (Rho et al. 2006). *M. tuberculosis* mutants lacking TPx show an increased sensitivity towards hydrogen peroxide and nitric oxide. Moreover, they are unable to survive and grow in macrophages, cannot establish acute infections or maintain persistent infections in murine tuberculosis models, and show an attenuated virulence. This indicates that TPx is an essential component of the antioxidant defense of *M. tuberculosis* (Hu and Coates 2009).

### 13.3.2.3 Mycothiol

Like other actinomycetes, *M. tuberculosis* lacks detectable levels of glutathione and glutathione peroxidases and employs mycothiol (MSH, AcCys-GlcN-Ins) as its major low molecular weight thiol. MSH is a cysteinyl pseudo-disaccharide consisting of N-acetylcysteine, glucosamine, and *myo*-inositol, and was discovered in 1993 (Newton et al. 1993). In *M. smegmatis* and *M. tuberculosis*, MSH concentrations are in a low millimolar range, comparable to the concentrations of glutathione in

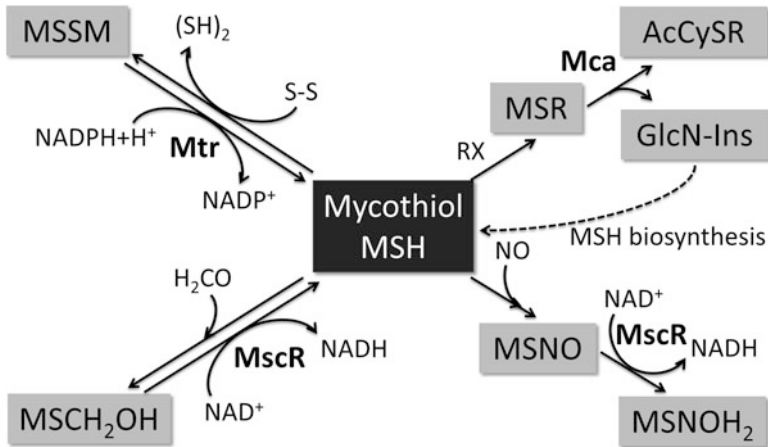
eukaryotes (Newton et al. 1996). MSH is required for the survival of *M. tuberculosis* (Sareen et al. 2003), but not for *M. smegmatis* (Rawat et al. 2002).

The biosynthetic pathway of MSH consists of five steps catalyzed by four enzymes, which cannot be found in eukaryotes or eubacteria and are thus discussed as highly feasible targets for chemotherapeutic interventions against mycobacteria. MshA is an N-acetylglucosamine transferase that forms 3-phospho-GlcNAc-Ins, which is converted into GlcNAc-Ins by dephosphorylation catalyzed by a phosphatase termed MshA2. The deacetylase MshB deacetylates GlcNAc-Ins to form Gln-Ins, which is then ligated to cysteine by MshC, a mycothiol ligase. Cys-Gln-Ins is subsequently acetylated by mycothiol synthase MshD generating MSH (for detailed reviews of MSH biosynthesis please see (Jothivasan and Hamilton 2008; Fan et al. 2009)).

The functions of MshA-D have been intensely investigated by gene knockout studies in *M. smegmatis* and *M. tuberculosis*. MshA and C are indeed essential for growth and survival of *M. tuberculosis* (Buchmeier and Fahey 2006; Sareen et al. 2003), while mutants lacking MshB and D are still viable (Buchmeier et al. 2006). These studies show that only the absence of MshA or C leads to complete depletion of MSH, while still 10 and 2% of normal MSH levels could be detected in the mutants lacking MshC or MshD, respectively (Sareen et al. 2003; Buchmeier and Fahey 2006; Buchmeier et al. 2003, 2006). Moreover, disruption of the MshD gene in *M. tuberculosis* results in high levels of the MshD substrate Cys-GlcN-Ins and N-formyl-Cys-GlcN-Ins, with the latter being maintained in a reduced state. Thus, N-formyl-Cys-GlcN-Ins might function as a surrogate for MSH under normal conditions, but is not sufficient under increased oxidative stress (Buchmeier et al. 2006). These studies indicate that MshA and C might be more feasible as targets for anti-mycobacterial drug development (Fan et al. 2009).

MSH exerts a range of protective functions in mycobacteria by serving as an intracellular redox buffer as a functional analog of GSH and by maintaining the redox balance. Low MSH levels in *M. smegmatis* result in a remarkably increased sensitivity towards free radicals, oxidants, alkylating agents, and antibiotics including erythromycin, rifamycin, and penicillin G (Rawat et al. 2002; Buchmeier et al. 2006). Thus, MSH is involved in protection against oxidative stress and antibiotics. In contrast, MSH-depleted mutants show a 200-fold increased resistance towards isoniazid, demonstrating a function of MSH in the drug mechanism of isoniazid (Rawat et al. 2002). Furthermore, MSH protects against electrophilic xenobiotics by forming MSH-toxin conjugates (Rawat et al. 2004).

MSH-dependent enzymes are involved in several cellular processes, including defense against ROS and RNS and detoxification of electrophilic xenobiotics (Fig. 13.3). Mycothiol disulfide (MSSM) can be reduced by the NADPH-dependent flavoenzyme mycothiol disulfide reductase (Mtr, mycothione reductase), which maintains a high MSH:MSSM ratio by the same disulfide reducing mechanism found in glutathione reductase (Argyrou et al. 2004; Argyrou and Blanchard 2004). MSH-toxin conjugates can be hydrolyzed by mycothiol S-conjugate amidase (Mca) forming a mercapturic acid and GlcN-Ins. While the mercapturic acid derivative can be exported from the cell, GlcN-Ins is recycled for re-synthesis of MSH (Newton



**Fig. 13.3** Functions of mycothiol, the major low molecular weight thiol in *Mycobacterium tuberculosis*. Mycothiol (MSH) can reduce proteins and oxidants and is thereby oxidized to mycothiol disulfide (MSSM). MSSM is recycled by mycothiol reductase (Mtr) under consumption of  $\text{NADPH} + \text{H}^+$ . *S*-nitrosomycothiol (MSNO) can be reduced by mycothiol-*S*-nitroso reductase/-formaldehyde reductase (MscR) to MSH sulfonylmycothiol (MSNOH<sub>2</sub>). MSH can react with formaldehyde (HCOOH) to form the hemithioacetal formylmycothiol (MSCH<sub>2</sub>OH), which is reduced by MscR. Thiol-reactive reagents (RX) form MSH-toxin conjugates that are hydrolyzed by mycothiol *S*-conjugate amidase (Mca) yielding a mercapturic acid and GlcN-Ins. The latter can enter the MSH biosynthesis pathway to be recycled to MSH (modified after Newton et al. 2008)

et al. 2000). *M. tuberculosis* Mca has a crucial function in drug resistance, a fact that directed interest towards the development of inhibitors against Mca (Nicholas et al. 2003). MSH can rapidly react with formaldehyde forming a hemithioacetal, which is a substrate of mycothiol-*S*-nitroso reductase/-formaldehyde reductase (MscR) (Vogt et al. 2003). Moreover, MscR can reduce *S*-nitrosomycothiol (Vogt et al. 2003) and is required for growth of *M. tuberculosis* (Sasseti et al. 2003).

#### 13.3.2.4 Further Enzymes of Antioxidant Defense

*M. tuberculosis* encodes a catalase peroxidase (KatG) that exhibits catalase, peroxidase, and peroxyxynitritase activity and can therefore detoxify ROS and RNS (Rouse et al. 1996; Manca et al. 1999; Wengenack et al. 1999). Experiments using transgenic murine models indicated that the major role of KatG is the defense against the oxidative burden in the host by metabolizing peroxides generated by the host phagocyte NADPH oxidase (Ng et al. 2004). In order to exhibit its antimycobacterial activity, the most effective and specific antimycobacterial drug isoniazid has to be converted from a prodrug form into its active form by KatG (Zhang et al. 1992). Mutations in the mycobacterial *katG* gene are associated with resistance to isoniazid. At least 130 known mutations of *katG* are characterized by a

decreased or diminished activity of KatG and thus reduced formation of the adduct INH-NAD (reviewed in Vilcheze and Jacobs 2007).

The peroxiredoxin-type alkyl hydroperoxide reductase (AhpC) can directly detoxify hydroperoxides and peroxynitrite (Bryk et al. 2000; Master et al. 2002). Although AhpC is considered to be a 2-cys peroxiredoxin, it involves a third cysteine in catalysis (Koshkin et al. 2004). AhpC employs the Trx-like protein AhpD, a protein with a low alkylhydroperoxidase activity of its own, as an electron donor but cannot be reduced by Trx (Hillas et al. 2000; Bryk et al. 2002). Moreover, *M. tuberculosis* codes for a 1-cys peroxiredoxin named alkyl hydroperoxide reductase E (AhpE), which is involved in peroxide and peroxynitrite detoxification (Hugo et al. 2009). In order to detoxify superoxide radicals, *M. tuberculosis* encodes two SODs, an iron-dependent SOD, and a Cu and Zn-dependent one (Zhang et al. 1991; D’Orazio et al. 2009). Two methionine sulfoxide reductases (MsrA and B) are supposed to reduce methionine sulfoxide to methionine in *M. tuberculosis*. MsrA and B appear to have redundant functions, since only a mutant lacking both genes would be more sensitive to nitrite and hypochlorite compare to wildtype (Lee et al. 2009).

## 13.4 Oxidative Stress in Malaria

Besides HIV/AIDS and tuberculosis, malaria is one of the world’s most devastating diseases. Although the number of reported malaria cases was reduced by more than 50% between 2000 and 2010, the estimated number of malaria-related deaths is with 665,000–1,133,000 people in 2010 still high (WHO 2011c; Murray et al. 2012). Approximately 86% of malaria deaths globally were of children under 5 years of age, and 91% of the deaths were in Africa (WHO 2011c). Tropical malaria is caused by *Plasmodium falciparum*, a unicellular eukaryotic parasite that lives and multiplies both in *Anopheles* mosquitoes and humans. An infected *Anopheles* mosquito injects sporozoites into the subcutaneous tissue of the human host. The sporozoites migrate to the liver, where they develop into merozoites, which subsequently can invade red blood cells. There, the parasites undergo asexual replication until merozoites are formed and released by rupture of the red blood cell membrane. Most merozoites infect new red blood cells and thus restart the intraerythrocytic cycle leading to the typical symptoms of tropical malaria. Some parasites differentiate into the sexual forms required for transmission into the mosquito vector (for review please see Tuteja 2007; Kappe et al. 2010).

### 13.4.1 Sources of Oxidative Stress in Malaria Parasites

During their intraerythrocytic development, malaria parasites face high concentrations of oxygen and iron and are exposed to intense oxidative stress derived

from different sources. *Plasmodium* parasites degrade host hemoglobin as their major source of nutrients for protein synthesis, which is at the same time also a major source of oxidative stress. Hemoglobin is taken up from the erythrocyte cytoplasm into the acidic food vacuole and is systematically degraded by proteases into free heme and amino acids (Francis et al. 1997). Most of the highly toxic free heme (ferriprotoporphyrin IX) aggregates to crystalline hemozoin, the so-called malaria pigment (Stiebler et al. 2011). Alternative detoxification pathways of heme comprise heme degradation and binding to glutathione or heme-binding proteins (Loria et al. 1999; Ginsburg et al. 1998). However, small amounts of heme escape from the detoxification mechanisms and cause major oxidative damage including lipid peroxidation and DNA damage (reviewed in Kumar and Bandyopadhyay 2005). In the acidic food vacuole, free heme is oxidized from Fe(II) to Fe(III) with concomitant production of superoxide and H<sub>2</sub>O<sub>2</sub> (Atamna and Ginsburg 1993). Additionally, malaria parasites have to counteract ROS released by the host immune system in order to fight the infection (Becker et al. 2004).

### 13.4.2 Oxidative Stress in the Pathogenesis of Malaria

Oxidative stress has been implicated in different aspects of malaria pathogenesis (reviewed in Becker et al. 2004; Hunt and Stocker 1990). Human glucose-6-phosphate dehydrogenase (G6PD) deficiency is the most common enzymopathy and confers resistance to infection and/or the development of severe clinical symptoms of malaria (Ruwende and Hill 1998). Protection from malaria is thought to be based on a lack of reducing equivalents in the form of NADPH, leading to oxidation of hemoglobin to membrane-associated hemochromes, which finally lead to early IgG-based detection and degradation of G6PD-deficient parasitized erythrocytes (Cappadoro et al. 1998). Moreover, a reduced multiplication rate was attributed to an intracellular accumulation of toxic oxidized molecules such as oxidized glutathione and hemozoin. Similar protection mechanisms were proposed for glutathione reductase-deficient erythrocytes (Gallo et al. 2009).

During disease manifestation, the redox balance of the patient is disturbed. The levels of glutathione, tocopherol, catalase, and superoxide dismutase in the erythrocyte and the concentrations of ascorbate and albumin in the plasma are significantly decreased in patients with malaria when compared to uninfected erythrocytes (Das and Nanda 1999; Pabon et al. 2003; Narsaria et al. 2011). Reduced  $\alpha$ -tocopherol content in the erythrocyte membrane was associated with malaria and may contribute to erythrocyte loss and anemia in severe malaria (Griffiths et al. 2001). Moreover, increased lipid peroxidation has been reported in patients infected with *falciparum* or *vivax* malaria (Polat et al. 2002; Das et al. 1990; Pabon et al. 2003; Narsaria et al. 2011). Micronutrients including vitamins A, E, and zinc may have a beneficial effect on the severity of malaria by modulating immune response and decreasing oxidative stress (Nussenblatt and Semba 2002; Zeba et al. 2008).



The role of macrophage-derived ROS in controlling malaria infection has been controversially discussed. It has been hypothesized that phagocyte-derived ROS are involved in host immunity against malaria infections (Hunt and Stocker 1990). Superoxide produced by NADPH oxidase was reported to be involved in malaria transmission and gametocyte development but not in parasitemia patterns, as shown in murine malaria models lacking NADPH oxidase (Harada et al. 2001). Similarly, another study did not show any effect of the absence of functional NADPH oxidase and thus of phagocyte-derived ROS on parasitemia and parasite burden in murine malaria models. This indicates that ROS generated by phagocytes are not involved in controlling malaria infection (Potter et al. 2005). Furthermore, phagocyte-derived ROS are not associated with the pathogenesis of cerebral malaria in mice malaria models (Sanni et al. 1999) but have been implicated in neuronal damage in humans (Becker et al. 2004).

In uncomplicated and severe malaria, low levels of nitric oxide (NO) were detected and are associated with increased disease severity and mortality. Plasma levels of IL-10, a cytokine that suppresses NO synthesis, were increased with severity, while levels of NOS2 were decreased in cerebral malaria (Anstey et al. 1996). Moreover, severe malaria is associated with depletion of arginine, the precursor of NO, and elevated levels of plasma arginase, which catabolizes arginine (Weinberg et al. 2008). Therefore, suppression of NO was suggested to protect against severe disease rather than to contribute to malaria pathogenesis (Anstey et al. 1996).

A beneficial role of antioxidants as an adjunctive treatment of severe malaria has been discussed. Treatment of adults with NAC increased the rate of normalization of plasma lactate by a TNF-independent mechanism that was attributed to improved red cell deformability or increased GSH levels (Watt et al. 2002). However, NAC as an adjunctive treatment with artesunate did not influence the disease outcome in patients with severe *falciparum* malaria (Charunwatthana et al. 2009). The effect of NAC appears to be concentration-dependent: low doses of NAC decrease H<sub>2</sub>O<sub>2</sub> levels and lipid peroxidation by increasing GSH concentrations, while supplementation with high doses of NAC had the opposite effect *in vitro* (Fitri et al. 2011). Thus, putative beneficial effects of NAC treatment remain controversial.

As explained above, NO is supposed to have a significant function in controlling malaria infection (Weinberg et al. 2008). Supplementation with L-arginine, the substrate of NO synthase and precursor of NO, leads to recovery of arginine levels and improvement of endothelial function in patients with severe malaria as shown in a Phase I trial (Yeo et al. 2008).

### 13.4.3 Antioxidant Defense System

In order to avoid oxidative damage and maintain a redox balance, malaria parasites employ an efficient combination of antioxidant systems based on GSH and Trx as outlined in the following paragraphs. Moreover, *Plasmodium* codes for two SODs,

which convert superoxide radicals to hydrogen peroxide (Gratepanche et al. 2002; Sienkiewicz et al. 2004). However, enzymes with major antioxidant functions in other organisms such as catalase, glutathione peroxidase, and methionine sulfoxide reductase are missing in *Plasmodium* (Sztajer et al. 2001; Clarebout et al. 1998).

#### 13.4.3.1 The Glutathione System

Glutathione is the major low molecular weight thiol in malaria parasites and functions as a thiol redox buffer by cycling between a reduced and an oxidized form (Becker et al. 2003b). GSH is a cofactor for detoxification of electrophilic compounds and methylglyoxal (Harwaldt et al. 2002; Iozef et al. 2003), reduces the dithiol glutaredoxin (Rahlfs et al. 2001), and directly reduces a range of ROS, RNS, protein disulfides, and sulfenates (Becker et al. 2003b). GSH is synthesized by the consecutive activity of  $\gamma$ -glutamyl-cysteine synthetase and glutathione synthetase. A lack of the glutathione biosynthesis pathway leads to decreased GSH levels and a significant growth delay during the intraerythrocytic stage but completely blocks oocyte development in the *Anopheles* vector (Vega-Rodriguez et al. 2009). During the intraerythrocytic stage, the parasites depend on either GSH *de novo* synthesis or efficient reduction of GSSG by glutathione reductase, since a knockout of both enzymes is lethal for the parasites (Pastrana-Mena et al. 2010).

High intracellular concentrations of GSH in malaria parasites are maintained by an NADPH-dependent reaction catalyzed by the flavoenzyme glutathione reductase (GR). A range of studies examined the kinetic mechanism of GR in detail and developed selective inhibitors of the parasite enzymes (e.g. Bohme et al. 2000; Krauth-Siegel et al. 1996; Sarma et al. 2003). As a consequence of its central position in antioxidant defense, *P. falciparum* GR was regarded as a highly attractive drug target (Becker et al. 2003b, 2004). However, recent studies demonstrated that *P. berghei* GR is not essential during the intraerythrocytic stage but is required for sporogony in the *Anopheles* vector (Buchholz et al. 2010; Pastrana-Mena et al. 2010). High functional redundancy in the antioxidant network of *P. falciparum* allows reduction of GSSG by several GR-independent pathways such as direct reduction by Trx, reduction by protein S-glutathionylation, and by dihydrolipoamide-dependent reactions catalyzed by Grx (Becker et al. 2003b, 2004; Kanzok et al. 2000). In order to maintain low intracellular GSSG concentrations, the parasite exports GSSG into the erythrocyte cytosol (Atamna and Ginsburg 1997).

A major function of glutathione is the non-enzymatic reduction of Grx, a dithiol protein that catalyzes the reduction of a variety of proteins on the basis of a dithiol exchange mechanism (Holmgren 1989). *Plasmodium* encodes one classic dithiol Grx (i.e., PfGrx) and three monothiol Grx (Rahlfs et al. 2001; Deponte et al. 2005). PfGrx can serve as a hydrogen donor for ribonucleotide reductase (Rahlfs et al. 2001), interacts with several proteins from different metabolic pathways in *Plasmodium* (Sturm et al. 2009), and catalyzes the deglutathionylation of proteins *in vitro* (Kehr et al. 2011).

GSH is a cofactor of glutathione *S*-transferase, an enzyme that catalyzes the conjugation of electrophiles with GSH for detoxification of xenobiotics (reviewed in Eaton and Bammler 1999). *P. falciparum* GST cannot be assigned to any of the described GST classes and has been investigated in detail (Harwaldt et al. 2002; Fritz-Wolf et al. 2003).

### 13.4.3.2 The Thioredoxin System

Thioredoxins are central proteins in redox homeostasis and reduce a large variety of protein and non-protein substrates. Trx are directly involved in antioxidant defense and furthermore contribute to redox signaling and regulation by modulating the structure and/or activity of many proteins in response to the intracellular redox state (Arner and Holmgren 2000; Holmgren 1989). *Plasmodium* employs three Trx and two Trx-like proteins with distinct subcellular localization (Nickel et al. 2006). Cytosolic Trx1, the most intensely studied *P. falciparum* Trx, detoxifies hydroperoxides and glutathione disulfide directly, functions as an electron donor for peroxiredoxins and plasmoredoxin (see below), and regulates a variety of proteins (Nickel et al. 2006; Sturm et al. 2009; Jortzik et al. 2010).

Thioredoxin reductase (TrxR) maintains Trx in a reduced state in an NADPH-dependent reaction. TrxR regulates antioxidant defense and cell growth either indirectly by reducing Trx or directly by reducing other substrates including hydrogen and lipid peroxides, dehydroascorbate, selenium compounds, Grx, protein disulfide isomerase, and ubiquinone (reviewed in Becker et al. 2000). *P. falciparum* TrxR contains two catalytic centers each consisting of two cysteine residues, while mammalian TrxR contains a selenocysteine-cysteine in its C-terminal active site (Gladyshev et al. 1996; Williams et al. 2000). By using alternative translation initiation, *P. falciparum* expresses two isoforms of TrxR, which are located in the cytosol and in the mitochondrion (Kehr et al. 2010). *P. falciparum* TrxR was discussed as an excellent drug target (Becker et al. 2000; Nickel et al. 2006). Knockout studies demonstrated that TrxR is indeed essential for *P. falciparum* (Krnajski et al. 2002) but not for the rodent malaria parasite *P. berghei* (Buchholz et al. 2010). Whether the discrepancy is due to *in vitro* culture conditions, technical aspects, or indeed major differences in the redox metabolism of *P. falciparum* and *P. berghei* remains to be studied. However, high redundancies in the Trx and GSH systems might allow compensation for the loss of single components. Simultaneous inhibition of the two *Plasmodium* disulfide reductases GR and TrxR provides a good strategy for the development of antimalarial chemotherapeutic interventions (Buchholz et al. 2010).

Trx protects from oxidative damage by serving as an electron donor for Trx-dependent peroxidases, which catalyze the reduction of different peroxides including hydrogen peroxide, peroxynitrite, cumene hydroperoxide, and *tert*-butylhydroperoxide. According to the number of catalytic cysteines, the enzymes are clustered into 1-cys and 2-cys peroxiredoxins (Wood et al. 2003). *Plasmodium* harbors six peroxidases (recently reviewed in Gretes et al. 2012): Prx1a (TPx1) and

Prx1m (TPx2) (Nickel et al. 2005; Komaki-Yasuda et al. 2003), Prx5 (antioxidant protein, AOP) (Sarma et al. 2005), and Prx6 (1-cys peroxiredoxin) (Nickel et al. 2006) are classic peroxiredoxins. Additionally, a glutathione peroxidase-like TPx and a nuclear peroxiredoxin (PrxQ, nPrx) associated with chromatin have been described (Sztajer et al. 2001; Richard et al. 2011). Except for nPrx (Richard et al. 2011), all *P. falciparum* peroxidases prefer Trx as a reducing substrate. Additionally, malaria parasites import human peroxiredoxin 2 as an enzymatic scavenger of hydroperoxides into their cytosol (Koncarevic et al. 2009).

A *Plasmodium*-specific oxidoreductase is plasmoredoxin (Plrx), a dithiol protein belonging to the thioredoxin superfamily. Plrx can be reduced by glutathione but more effectively by Trx and Grx *in vitro*; it transfers electrons to ribonucleotide reductase and glutathione disulfide and interacts with several enzymes involved in different cellular pathways (Becker et al. 2003a; Nickel et al. 2005; Sturm et al. 2009). In *P. berghei*, Plrx is dispensable under unstressed conditions, indicating a high functional redundancy with other redox-active proteins (Buchholz et al. 2008).

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