

Thiol-Based Posttranslational Modifications in Parasites

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Abstract

Significance: Cysteine residues of proteins participate in the catalysis of biochemical reactions, are crucial for redox reactions, and influence protein structure by the formation of disulfide bonds. Covalent posttranslational modifications (PTMs) of cysteine residues are important mediators of redox regulation and signaling by coupling protein activity to the cellular redox state, and moreover influence stability, function, and localization of proteins. A diverse group of protozoan and metazoan parasites are a major cause of diseases in humans, such as malaria, African trypanosomiasis, leishmaniasis, toxoplasmosis, filariasis, and schistosomiasis. **Recent Advances:** Human parasites undergo dramatic morphological and metabolic changes while they pass complex life cycles and adapt to changing environments in host and vector. These processes are in part regulated by PTMs of parasitic proteins. In human parasites, posttranslational cysteine modifications are involved in crucial cellular events such as signal transduction (*S*-glutathionylation and *S*-nitrosylation), redox regulation of proteins (*S*-glutathionylation and *S*-nitrosylation), protein trafficking and subcellular localization (palmitoylation and prenylation), as well as invasion into and egress from host cells (palmitoylation). This review focuses on the occurrence and mechanisms of these cysteine modifications in parasites. **Critical Issues:** Studies on cysteine modifications in human parasites are so far largely based on *in vitro* experiments. **Future Directions:** The *in vivo* regulation of cysteine modifications and their role in parasite development will be of great interest in order to understand redox signaling in parasites. *Antioxid. Redox Signal.* 17, 657–673.

Introduction

TROPICAL DISEASES caused by *Plasmodium* (malaria), *Trypanosoma* (trypanosomiasis), *Leishmania* (leishmaniasis), *Schistosoma* (schistosomiasis), and others affect not only the health of millions of people mainly in southern countries, but also their social and economic development (25, 93, 177, 192). Parasitic diseases are characterized by a high morbidity and most of them by a high lethality, which is worsened by a lack of effective treatments (93, 97, 156, 177).

Cysteine accounts for 2% of the amino acids in proteins from eukaryotes (168). Due to their chemical characteristics, cysteines contribute to biochemical reactions based on thiol- or thiyl-dependent catalysis, form structurally important disulfide bonds, bind metal ions, and catalyze redox reactions (86, 87, 117). Differential modifications of the oxidation state of sulfur in cysteines mediate redox regulation and signaling in response toward the cellular redox potential (47, 85, 244). Cysteine modifications include reversible oxidation to thiyl radicals and sulfenic acids (Cys-SOH), which are unstable, but highly reactive (174, 178, 195). Further oxidation leads to sulfinic acid (Cys-SO₂H) and irreversibly overoxidized sulfonic acid (Cys-SO₃H) (23, 174, 178) (Fig. 1). Moreover, cysteines form intra- and intermolecular disulfide (Cys-SS-Cys),

and mixed disulfides with cysteine (*S*-cysteinylation, Cys-SS-Cys), glutathione (*S*-glutathionylation, Cys-SSG), and nitric oxide (*S*-nitrosylation, Cys-S-NO) (Fig. 2). Besides oxidative modifications, cysteine residues are susceptible to lipidation such as *S*-prenylation, *S*-palmitoylation, and *S*-dolichylation, which subsequently influence subcellular compartmentation, structure, and function of modified proteins (138, 213). This review provides a summary of the current research on oxidative and lipid modifications of cysteines with an emphasis on *S*-nitrosylation, *S*-glutathionylation, palmitoylation, and prenylation in human pathogenic parasites.

Nitric Oxide and S-nitrosylation

Nitric oxide (NO) is a ubiquitous signaling molecule that possesses miscellaneous bioactivities (154). Accumulating evidence indicates that many physiological and pathophysiological effects of NO are mediated by protein *S*-nitrosylation, a posttranslational modification (PTM) (104, 216). Protein *S*-nitrosylation occurs via the addition of a nitrosyl group to a reactive cysteine thiol of a protein forming a protein *S*-nitrosothiol, which can affect conformation, stability, localization, activity, protein-protein interaction, and function of the respective protein (98, 104, 125). The homeostasis of

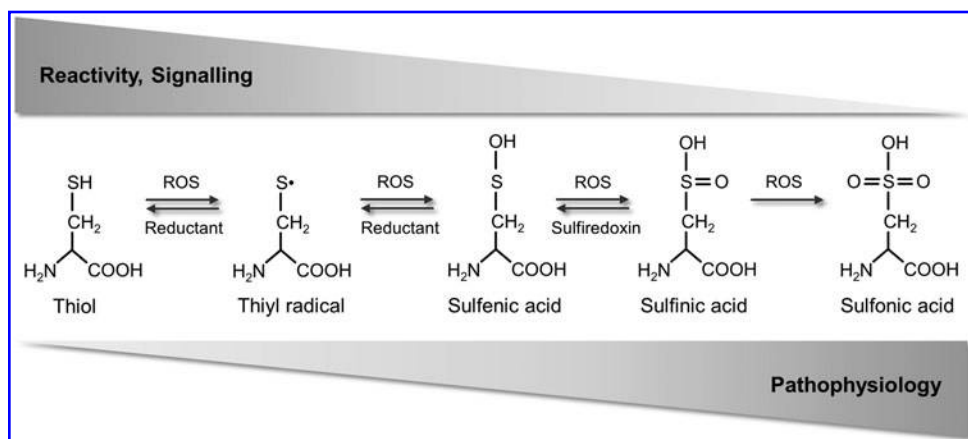


FIG. 1. Different oxidation states of cysteine residues. Cysteines can be oxidized by different reactive oxygen species to sulfenic acids, which can be reduced by several reductants such as glutathione and thioredoxin. Further oxidation leads to sulfinic acid that can be specifically reduced by the sulfinic acid reductase sulfiredoxin, and to irreversibly oxidized sulfonic acid that cannot be reduced.

S-nitrosylation is closely regulated by denitrosylation (the removal of the NO moiety) mediated by enzymes and nonenzymatic factors *in vivo* (Fig. 3) (21), such as S-nitrosogluthathione (GSNO) reductase (140), thioredoxin (20), superoxide dismutase (120), protein disulfide isomerase (211), carbonyl reductase (16), and glutathione (Fig. 3). Proteins regulated by S-nitrosylation can be found in almost all classes of proteins [reviewed in (104, 146, 201, 216)], and play important regulatory roles in cell signaling, apoptosis, and gene transcription (61, 201), thus attracting interest in discovering the mechanisms of NO redox signaling. The importance of S-nitrosylation is underlined by the fact that dysregulation of S-nitrosylation is correlated with the pathophysiology of many human diseases, such as sickle cell anemia, diabetes, cancer, and neurodegenerative disorders (75, 158).

Under physiological conditions, the direct formation of S-nitrosothiols is achieved by the reaction of a protein cysteine thiolate with NO radicals (e.g., NO⁺) (5). Additionally, S-nitrosylation occurs via transnitrosylation by transferring

an NO equivalent from a nitrosylated thiol to another protein thiol (245). Moreover, auto-S-nitrosylation can be catalyzed by protein-bound transition metals or by flavins.

The major part of nonprotein S-nitrosothiols *in vivo* is attributed to GSNO, a low-molecular-weight S-nitrosothiol derived from the interaction of glutathione with NO derivatives or protein S-nitrosothiols (210). GSNO significantly induces the formation of protein S-nitrosothiols by transferring the nitrosyl group to protein thiols (transnitrosylation), indicating an important role in the transduction of NO bioactivities (75, 119). In fact, GSNO can be generated from the degradation of protein S-nitrosothiols by glutathione, revealing that the metabolism of protein S-nitrosothiols via glutathione/GSNO pathway dynamically modulates NO signaling and maintains the homeostasis of protein S-nitrosylation (21).

Intracellular levels of GSNO are regulated by the GSNO-reducing activity of glutathione-dependent formaldehyde dehydrogenase, which is conserved throughout evolution

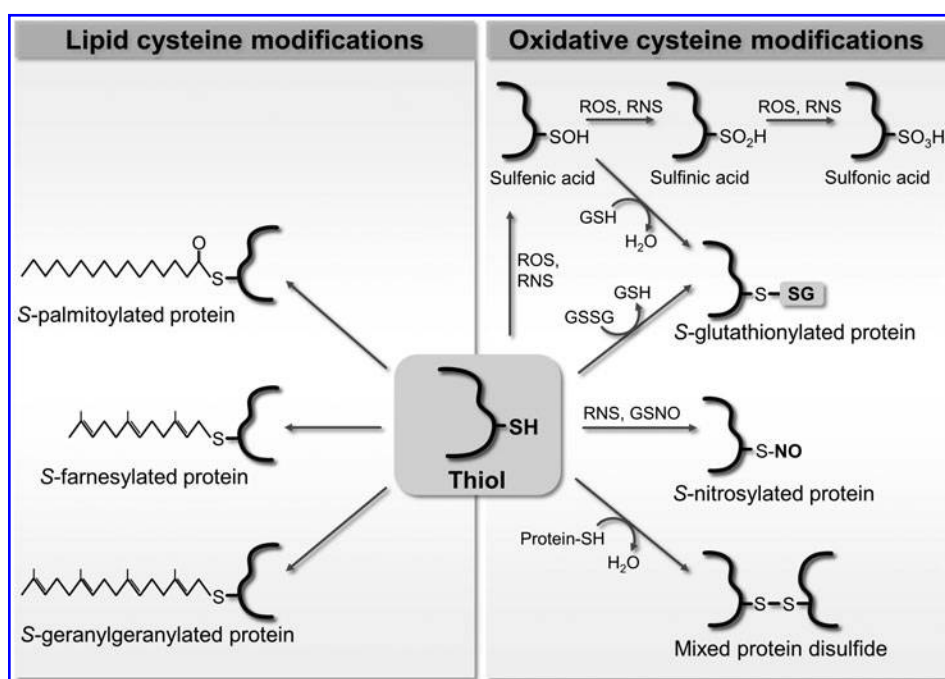


FIG. 2. Summary of the most prevalent posttranslational modifications of cysteine residues. Cysteine can either be oxidatively modified by hydroxylation, S-glutathionylation, S-nitrosylation, and mixed disulfide formation, or be modified by the attachment of lipid moieties.

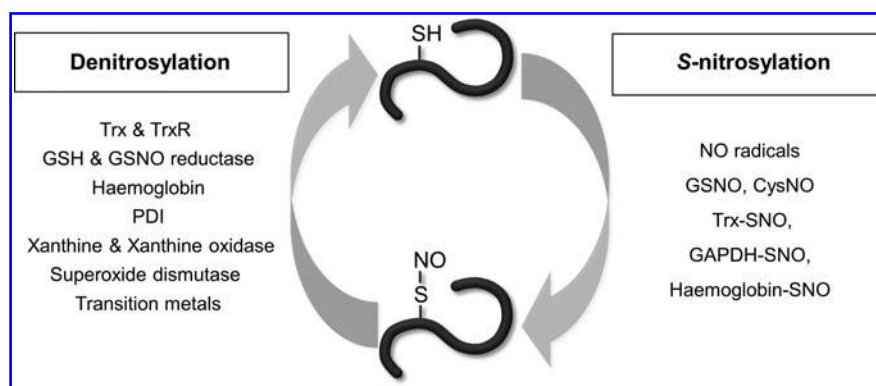


FIG. 3. Catalysis of protein S-nitrosylation and denitrosylation. S-nitrosylation can be mediated directly by NO radicals, or via transnitrosylation by low-molecular-weight S-nitrothiols (GSNO and CysNO) and several transnitrosylases, for example, Trx-SNO, GAPDH-SNO, and haemoglobin-SNO. Trx and glutathione (GSH) denitrosylate protein by transnitrosylation forming Trx-SNO and GSNO, which are then reduced by TrxR and GSNO reductase, respectively. Besides, hemoglobin, protein disulfide isomerase, xanthine/xanthine oxidase, and transition metals (e.g., copper and iron) also catalyze protein denitrosylation. GAPDH-SNO, glyceraldehyde-3-phosphate dehydrogenase-SNO; GSH, reduced glutathione; GSNO, S-nitrosoglutathione; TrxR, Trx reductase; Trx-SNO, thioredoxin-SNO.

from bacteria to mammals (140), but has not been identified in parasites so far.

Despite the ubiquitous distribution of cysteines, protein S-nitrosylation is considered as a highly specific modification since it selectively targets regulatory or catalytic cysteine residues. The specificity of protein S-nitrosylation is determined by the thiol pK_a , local hydrophobicity, and allosteric regulation by ions (104).

In human parasitic diseases, NO functions as an important effector molecule in host-parasite interactions and pharmacological treatments (7, 30). Recent studies have detected NO and reactive nitrogen species (RNS) within several human pathogenic parasites (126, 164, 197). Here, we review NO sources and protein S-nitrosylation in human parasites and discuss the role of S-nitrosylation in antiparasitic strategies.

NO sources in human parasites

Host-parasite interaction. A burst of NO generation in host cells is a classic paradigm of host immune defense against a wide range of intracellular and extracellular parasites (7, 30). In mammals, endogenous NO is predominantly biosynthesized by the conversion of L-arginine to L-citrulline catalyzed by constitutive and inducible NO synthase (NOS) (218), with the latter producing NO for immunological defense against cancer and microbial infections (30, 228). Similar antiparasitic effects of NO are also essentially involved in defending invertebrates against parasites (e.g., in the mosquito *Anopheles stephensi* against malaria parasites) (171,182), indicating a ubiquitous antiparasitic mechanism of NO in nature. Compelling evidence shows that NO produced by inducible NOS (iNOS) is involved in host immune response against parasites (27, 118, 144, 238, 254). The model of parasite killing by host NO generation is well established in human macrophages (215, 230). Parasite-induced pro-inflammatory cytokines stimulate iNOS expression and NO burst in macrophages during parasite infections (30, 157). Moreover, specific parasite antigens like *Plasmodium* glycosylphosphatidylinositol induce iNOS expression in macrophages (219). Considering that NO easily diffuses through membranes, parasitic pro-

teins are most likely exposed to RNS (44), thus potentially leading to S-nitrosylation of cysteine residues.

Besides that the induction of iNOS can kill parasites by direct action of parasitocidal NO, N^G -hydroxy-L-arginine (NOHA), an intermediate in the production of NO by iNOS, can also be an antiparasitic agent by inhibiting parasite arginase and subsequently inducing polyamine starvation in parasites (112). This provides another mechanism of iNOS in parasite elimination, which functions independently from NO.

Although the generation of NO from host immune defense combats parasitic infection, the parasite facilitates its survival in the host by developing strategies to alleviate the insult of nitrosative stress. For example, there is compelling evidence that parasite-encoded arginase attenuates the production of parasitocidal NO from host iNOS via arginine depletion (52, 236). Besides, parasites also manage to possess nonprotein thiols and enzymes for the detoxification of elevated oxidative/nitrosative stress, such as glutathione, 1-N-methyl-4-mercaptocysteine (ovothiol A), thioredoxin/thioredoxin reductase, trypanothione/trypanothione reductase, trypanothione S-transferase, and peroxidases (18, 185, 230, 237).

Pharmacologically derived NO. In addition to NO derived from the host immune system, pharmacologically used antiparasitic agents can induce the formation of NO. Enhanced intracellular nitrosative stress by NO donors leads to parasite death (7). Several NO donors, including S-nitroso-acetylpenicillamine, S-nitroso-N-acetyl-L-cysteine, GSNO, and S-nitrosocysteine, have a strong antiparasitic effect on a wide spectrum of parasites (13, 55, 183, 207, 219). Notably, GSNO is an NO carrier present readily and highly abundant *in vivo* (210), and its cytotoxicity is most likely mediated by transnitrosylation (24). The antiparasitic effects of pharmacological NO donors are attributed to inhibition of key parasitic enzymes by S-nitrosylation (see below). Compelling evidence that the antiparasitic action of NO-donors is at least in part mediated by S-nitrosylation could be shown by the development of oxadiazole compounds as antischistosomal agents (176, 198). Novel NO-releasing agents selectively targeting parasites with

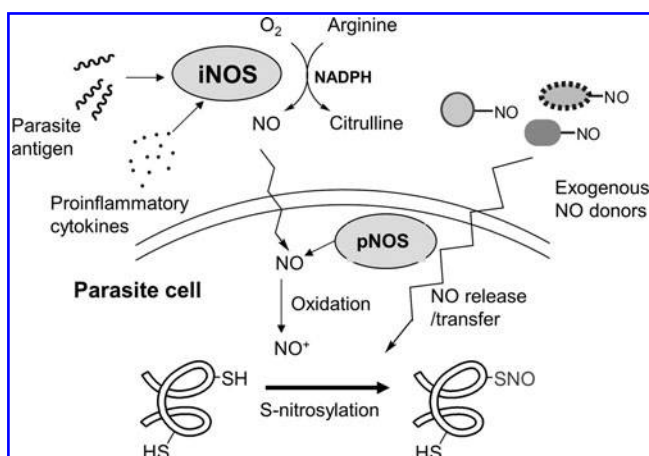


FIG. 4. NO sources and S-nitrosylation in human parasites. In response to parasite infection, the release of proinflammatory cytokines (e.g., IFN- γ , TNF- α , and IL- β) and parasite antigen stimulate the host iNOS to release parasitocidal NO via the conversion of arginine to citrulline. The antiparasitic NO readily diffuse into parasite cells and undergo oxidation to form NO radicals (NO⁺). Besides, the putative parasite NOS (pNOS) in some parasites may generate inherent NO in parasites. Furthermore, exogenous NO can be derived from pharmacological treatment with NO donors. The presence of NO and NO-derived molecules in parasites may lead to S-nitrosylation of redox-sensitive cysteine residues in proteins. NO, nitric oxide; NOS, nitric oxide synthase.

low toxicity to host cells have been developed, such as *trans*-[RuCl([15]aneN₄)NO]²⁺ (95, 229).

NO generation in parasites. Apart from exogenous NO, parasites potentially generate endogenous NO. So far, efforts in hunting for parasite NOS led to the discovery of a putative NOS in *Leishmania* spp., *Toxoplasma gondii*, *Trypanosoma cruzi*, *Entamoeba histolytica*, *Schistosoma japonicum*, and *Schistosoma mansoni* (15, 96, 103, 143, 167). Parasite NOS-like proteins share common features with mammalian NOS, such as NADPH-dependent L-arginine consumption, immunoreactivity against mammalian NOS antibodies, and inhibition by L-NAME, an arginine analog inhibiting NOS (15, 83, 96, 143). Conversely, NOS or NOS-like proteins could not be shown in *Plasmodium falciparum* (68, 164). However, NO production in *P. falciparum* might be attributed to a protein structurally similar to plant nitrate reductases, since it co-localizes with high NO production around the food vacuole (164). Taken together, the formation of NO in the above-mentioned pathways may contribute to the occurrence of S-nitrosylation in parasites (Fig. 4).

S-nitrosylation inhibits key enzymes of parasites

The antiparasitic properties of NO are supposed to be mediated by S-nitrosylation of parasitic proteins, since the effects of NO and NO donors were correlated to inhibition of key parasitic enzymes through S-nitrosylation (8, 45). Well-studied S-nitrosylation targets in parasites are cysteine proteases (CPs), which utilize a catalytic cysteine residue to hydrolyze peptide bonds (45, 186). CPs are important antiparasitic drug targets, since they play pivotal roles in hemoglobin hydrolysis, host cell

invasion, and erythrocyte rupture (186, 193). It has been shown that NO donors potently inhibit the major cysteine protease of *P. falciparum* trophozoites (falcipain), *T. cruzi* epimastigotes (cruzipain), and *Leishmania infantum* promastigotes (6, 8, 24, 233, 234). Inhibition of *P. falciparum* falcipain and *T. cruzi* cruzipain by S-nitrosylation results in death of the parasite (233, 234). Transnitrosylation of catalytic cysteine residues of CPs (e.g., Cys25-NO for *T. cruzi* cruzipain) mediated by NO donors has been considered as the underlying inhibitory mechanism (24, 45, 234). Besides, the aspartic protease plasmepsin from *Plasmodium vivax*, which participates in hemoglobin degradation, is inhibited by several NO donors *in vitro* most likely due to S-nitrosylation of catalytic cysteine residues, which interrupts the parasite growth (203, 208). Furthermore, alcohol dehydrogenase 2 from *E. histolytica* is inhibited by S-nitrosylation (208).

Since the proteomic identification of S-nitrosylated proteins is technically possible (74), further studies on the S-nitrosoproteome of parasites may shed light on the largely unknown NO targets and the functions of S-nitrosylation in parasites.

Protein S-glutathionylation

The capacity of glutathione as a signaling molecule is based on its ability to form mixed disulfides with redox-sensitive protein thiols referred to as protein S-glutathionylation. This protein modification accounts for 85%–90% of S-thiolation and therefore represents the most frequent cysteine modification (37, 199). The susceptibility of cysteine thiols toward S-glutathionylation depends on the accessibility and the reactivity of the cysteine (84). Redox-sensitive cysteine residues typically have a low pK_a value as a consequence of neighboring positively charged amino acids (51).

Several reaction mechanisms lead to protein S-glutathionylation, including thiol–disulfide exchange between protein thiols and oxidized glutathione (GSSG), direct reaction between reduced glutathione (GSH) and oxidized intermediates such as sulfenic acid, S-nitrosyl, or thiyl radicals, and the reaction between protein thiols and S-nitrosothiols (51, 80, 84). Thiol–disulfide exchange can occur under high GSSG concentrations *in vitro* [e.g. (19, 181, 253)], but is unlikely to mediate S-glutathionylation at physiological GSSG concentrations (50, 51, 80). Additionally, glutaredoxin and glutathione S-transferase promote S-glutathionylation (217, 224).

S-glutathionylation is readily reversible by glutaredoxin, thioredoxin, sulfiredoxin, and glutathione S-transferase, or nonenzymatically by GSH (43, 53, 71, 81, 82, 94, 165, 191). Analogous to phosphorylation, S-glutathionylation is a regulatory PTM that induces functional changes in target proteins, either activation or in most cases inhibition, and subsequently leads to alteration of cellular pathways in response to oxidative stress [reviewed in (50, 51, 84, 108, 202, 246)]. S-glutathionylation protects cysteines from irreversible overoxidation and a persistent loss of protein function during increased oxidative stress and is thus an antioxidant defense mechanism. Changes in S-glutathionylation patterns are associated with several pathophysiological processes and human diseases, such as neurodegenerative and cardiovascular diseases (246). Moreover, several anticancer drugs mediate their effect at least in part by increasing protein S-glutathionylation (246).

Global S-glutathionylation was studied in mammals (76, 77, 137, 180, 199), plants (59, 115), and yeast (205), revealing numerous S-glutathionylated proteins involved in versatile cellular pathways.

Glutathione in parasites

In *P. falciparum*, the glutathione system was investigated in detail [reviewed in (17)]. Glutathione is synthesized by γ -glutamyl-cysteine synthetase and glutathione synthetase (148), and kept in a reduced form by glutathione reductase (17, 133). *Plasmodium* depends on reduced glutathione, which has to be either synthesized *de novo* or kept in a reduced state by glutathione reductase (31, 166, 232). In malaria parasites, glutathione is involved in the detoxification of electrophilic compounds by glutathione S-transferase (100) and in the degradation of methylglyoxal by glyoxalase (113), but also reduces glutaredoxin (175). Moreover, reduced glutathione might also be involved in the degradation of heme depending on concentrations of oxygen, heme, and glutathione (11).

Trypanosomatids such as *Trypanosoma brucei* and *Leishmania major* conjugate more than 70% of intracellular glutathione with spermidine forming the intermediate glutathionylspermidine and trypanothione, which replaces glutathione in most redox reactions (66, 67). Trypanothione and glutathionylspermidine are reduced by trypanothione reductase (132), a reaction that is essential for *T. brucei* and *L. donovani* (134, 221, 222). Trypanothione reduces tryparedoxin, dehydroascorbate, and glutathione, which in turn deliver reducing equivalents to the respective peroxidases [reviewed in (35, 114, 130, 131)].

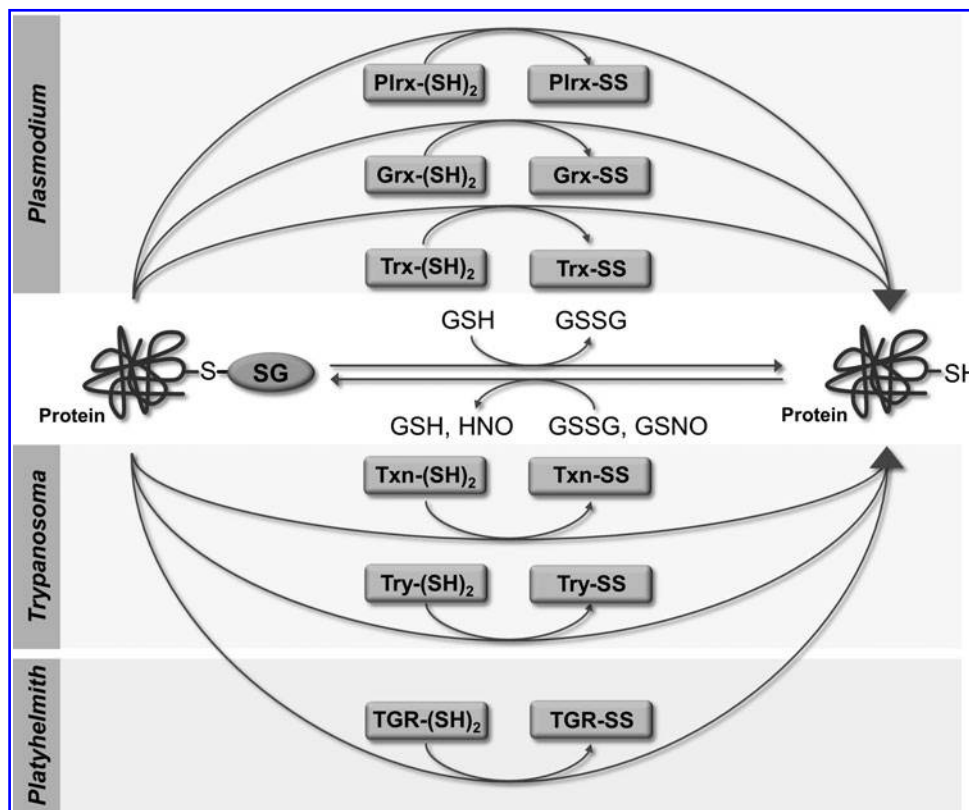
An antioxidant system based on glutathione was also demonstrated for *T. gondii* (58). Conversely, *S. mansoni* and *Ecchinococcus granulosus* employ the multifunctional selenoprotein thioredoxin glutathione reductase (TGR) for the reduction of both glutathione and thioredoxin (3, 136).

Interestingly, several parasitic protozoa such as *E. histolytica* (65), *Giardia duodenalis* (28, 29), and *Trichomonas foetus* (28) completely lack glutathione and enzymes of the glutathione metabolism, but rely on cysteine as the major low-molecular-weight thiol to protect from oxidative stress.

S-glutathionylation in parasites

Protein S-glutathionylation was studied in Platyhelminths, Apicomplexa, and Trypanosomatids. In parasitic Platyhelminths such as *S. mansoni* and *E. granulosus*, protein deglutathionylation and thus homeostasis of S-glutathionylation is mediated by TGR (Fig. 5) (26, 107). *E. granulosus* TGR catalyzes protein deglutathionylation via its glutaredoxin domain (26). The disulfide intermediate consisting of TGR and bound glutathione is resolved by selenocysteine in the thioredoxin reductase domain of TGR (26). In TGR from *S. mansoni*, Cys28 of the glutaredoxin domain attacks the S-glutathionylated target protein, which is consistent with the mechanism shown for *Ecchinococcus* TGR, but the mixed disulfide intermediate can be solved either by GSH representing a monothiol deglutathionylation mechanism yielding GSSG, or alternatively by neighboring Cys31 via a dithiol mechanism releasing GSH. In the latter case, the disulfide in the glutaredoxin domain is finally reduced by the selenocysteine of the TrxR domain (107). The difference between *Ecchinococcus* and *Schistosoma* TGR was

FIG. 5. Enzymes involved in protein deglutathionylation in human parasites. In *Plasmodium falciparum*, thioredoxin, glutaredoxin, and plasmoredoxin are able to deglutathionylate proteins. Trypanothione (Try) and tryparedoxin, but not glutaredoxin from *Trypanosoma*, were shown to deglutathionylate proteins. TGR from *Schistosoma* and *Ecchinococcus* catalyzes protein deglutathionylation via its glutaredoxin domain. Additionally, deglutathionylation can occur nonenzymatically by reduced glutathione (GSH). TGR, thioredoxin glutathione reductase.



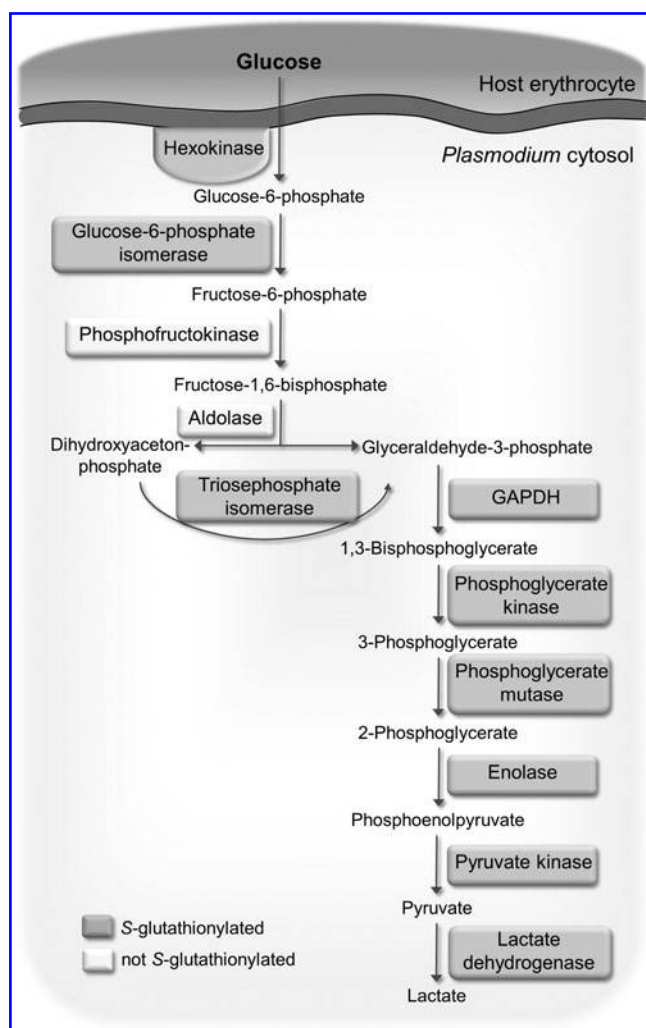


FIG. 6. Most enzymes involved in glycolysis in *Plasmodium falciparum* are S-glutathionylated. Except for phosphofructokinase and aldolase, all enzymes of the glycolytic pathway are S-glutathionylated. *In vitro*, the glycolytic activities of glyceraldehyde-3-phosphate dehydrogenase and pyruvate kinase are inhibited upon S-glutathionylation, while the activity of lactate dehydrogenase is not influenced by S-glutathionylation.

attributed to a greater distance between the two active site cysteines in the glutaredoxin domain of *Echinococcus* TGR (107), but might also be a result of different experimental design.

Recently, we identified 493 S-glutathionylated proteins from *P. falciparum* (124). Three hundred twenty-one of the S-glutathionylated proteins have a predicted function and many of them are involved in nitrogen compound metabolism, protein metabolism, and biosynthetic processes (124). Except for aldolase and phosphofructokinase, all enzymes of the glycolytic pathway are S-glutathionylated under physiological conditions (Fig. 6), and both *P. falciparum* glyceraldehyde-3-phosphate dehydrogenase and pyruvate kinase are inhibited efficiently and reversibly by S-glutathionylation *in vitro*. Furthermore, ornithine δ -aminotransferase is regulated by S-glutathionylation *in vitro* (124). As shown for other organisms (94, 204), *P. falciparum* glutaredoxin 1 and thioredoxin 1, but interestingly also the *Plasmodium*-specific

oxidoreductase plasmoredoxin, exhibit deglutathionylase activity (Fig. 5) (124). Approximately 10% of the proteome from *P. falciparum* is glutathionylated under physiological conditions, thus underlining the importance of S-glutathionylation as a central redox-regulatory mechanism. Changes in the S-glutathionylation patterns and subsequently in the metabolome during increased oxidative stress, for example, as a consequence of pharmacological treatment, are of great interest in order to understand the function of S-glutathionylation as a regulatory process in *Plasmodium*.

In *T. brucei*, monothiol glutaredoxin 1, trypanedoxin peroxidase III, and thioredoxin were shown to be specifically and reversibly S-glutathionylated and S-glutathionylspermidinylated *in vitro* (149). Trypanedoxin, trypanothione, as well as dithiol glutaredoxin 1 and 2 are able to catalyze deglutathionylation by reducing mixed protein-SSG disulfides *in vitro*, thus demonstrating a functional system in *T. brucei* required for S-glutathionylation *in vivo* (Fig. 5) (36, 149). The effect of S-glutathionylation on enzyme activity and subsequently cellular function for *T. brucei* *in vivo* remains to be elucidated. Other Trypanosomatids such as *L. major* and the insect parasite *Crithidia fasciculata* also utilize the GSH conjugate trypanothione as their major redox buffer (46, 48, 67, 102), but S-glutathionylation has not yet been studied in these organisms.

In *E. histolytica*, *G. duodenalis*, and *T. foetus*, cysteine replaces glutathione as the major low-molecular-weight reducing agent (28, 29, 65). In *E. histolytica*, cysteine depletion induces metabolic changes, which are not reflected by changes in expression of the respective genes, thus indicating a role of posttranscriptional modifications or PTMs (109, 110). It remains to be studied whether these parasites employ cysteinylolation instead of glutathionylation as a PTM for protein regulation in response to oxidative stress.

Studies on the regulation and effect of protein S-glutathionylation *in vivo* are missing in the majority of studies, but are essential to enhance the understanding of redox signaling in parasites.

Lipid Modifications of Cysteine Residues

Proteins can be posttranslationally modified by the attachment of lipid moieties to cysteines, such as palmitoylation, prenylation, and dolichylation. In general, lipid modifications increase the hydrophobicity of proteins in order to stabilize membrane localization, but are also crucial for protein trafficking to subcellular compartments and protein-protein interactions. Protein palmitoylation and prenylation were studied in various human parasites with respect to function and mechanism.

Protein palmitoylation

The addition of palmitate, a C_{16:0} fatty acid, to the thiol group of a cysteine via a reversible thioester linkage is termed protein S-palmitoylation, sometimes also more general S-acylation or thioacylation (138, 212). If the palmitoylated cysteine is located at the protein's N-term, the thioester is rearranged into an irreversible amide bond (N-palmitoylation) (170). Proteins can be palmitoylated spontaneously in the presence of palmitoyl-CoA (14), or enzymatically by protein acyltransferases (151, 172). Depalmitoylation reactions are catalyzed by acylprotein thioesterases (106, 248).

The family of palmitoylated proteins is large and diverse with membrane affinity as a common feature. Palmitoylation regulates the localization, stability, and activity of diverse proteins by promoting their membrane association, targeting them to specific membrane domains, mediating protein interactions and degradation (101, 116, 138, 194, 206, 212).

The palmitoyl-proteome was studied by proteomic approaches, identifying 124 (trypanosomes), 300 (rat), and 391 (human) palmitoylated proteins (62, 123, 247), which emphasize the cellular importance of this PTM.

Palmitoylation in parasites

Protein palmitoylation is crucial for the survival of *T. brucei*, since treatment with 2-bromopalmitate, a palmitate analog, results in complete growth inhibition of procyclic and bloodstream forms (62). *T. brucei* possesses 12 putative palmitoyl acyltransferases with redundant functions (62, 63). Recently, 124 palmitoylated proteins were identified in *T. brucei* (62). The palmitoylation of some *Trypanosoma* proteins was studied in more detail: palmitoylation of calcium-binding calflagins specifically induces trafficking of calflagins to the membrane of the flagellum (63). In contrast to a high redundancy of many palmitoyl transferases (62, 188), calflagins can only be palmitoylated by palmitoyl acyltransferase 7 (63). A role of myristate and palmitate for specifically targeting proteins to the flagellar membrane was also shown for *T. brucei* calpain-like proteins (141), *L. major* SMP-1 (226), and *T. cruzi* flagellar calcium binding protein (90). Phosphoinositide-specific phospholipase C from *T. cruzi*, which is involved in parasite differentiation, is targeted to the plasma membrane by the concerted action of *N*-myristoylation and palmitoylation (79, 162). Acylated surface proteins from *L. major* are translocated to and anchored in the membrane by *N*-myristoylation and palmitoylation (56). Furthermore, PPEF-like phosphatases from *L. major* and CAP5.5 from *T. brucei* are targets of palmitoylation *in vivo* (150).

In *Toxoplasma* and *Plasmodium*, cysteine palmitoylation occurs on proteins associated with gliding motility and invasion into host cells. A *T. gondii* myosin light chain, which is associated with myosin D, is attached to the parasite plasma membrane via palmitoylation (173). Moreover, hypoxanthine-xanthine-guanine phosphoribosyltransferase (HXGPRT) II from *T. gondii* is associated with the inner membrane complex (IMC) solely via palmitoylation of a Cys-Cys-Cys motif (Fig. 7) (40), and might supply purine nucleotides for the glideosome complex (40), which is responsible for gliding motility (49).

Dual acylation of *P. falciparum* calcium-dependent protein kinase 1 (PfCDPK1) with myristate and palmitate in combination with a basic cluster is required for targeting PfCDPK1 to the plasma membrane (153), where it phosphorylates components of the acto-myosin motor, such as the 45 kDa gliding-associated protein (GAP45; Fig. 7) (92). *P. falciparum* GAP45 is attached to the IMC by *N*-myristoylation and palmitoylation (Fig. 7), and thereby links the acto-myosin motor to the IMC (179), which might also be the case for *T. gondii* GAP45 (88). Thus, the addition of palmitate mediates the binding of several glideosome-associated proteins to the IMC in *Plasmodium* and *Toxoplasma* and is thus most likely crucial for host cell invasion. A link between palmitoylation and invasion is further supported by the finding that palmitoylation targets proteins to lipid rafts (1, 91, 240), and lipid rafts of the

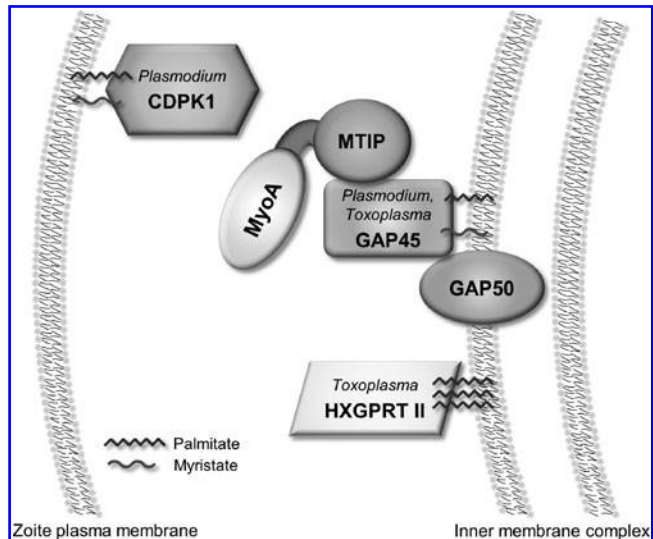


FIG. 7. Palmitoylation of proteins from *Plasmodium falciparum* and *Toxoplasma gondii* involved in gliding motility and invasion. Hypoxanthine-xanthine-guanine phosphoribosyltransferase II (HXGPRTII) from *T. gondii* is attached to the inner membrane complex via palmitoylation of a Cys-Cys-Cys motif, while calcium-dependent protein kinase 1 from *P. falciparum* is located at the parasite plasma membrane by both myristoylation and palmitoylation. The 45 kDa gliding-associated protein (GAP45) is a component of the glideosome complex and mediates the membrane attachment of myosin a tail domain interacting protein (MTIP, myosin light chain) and myosin A. The inner membrane localization of 45 kDa GAP45 from *P. falciparum* and *T. gondii* is mediated by myristoylation and palmitoylation.

erythrocyte membrane are important for erythrocyte invasion of *P. falciparum* (129, 155).

Genomic analysis identified 13 potential palmitoyl transferases in *P. falciparum* (4). However, only a study on one DHHC-domain-containing protein, PfAnkDHHC (200), was published so far. Calpain, a cysteine protease essential for cell cycle progression (190), is bound to the plasma membrane by palmitoylation of two cysteines in combination with *N*-myristoylation. Interestingly, upon removal of the palmitoyl moiety, calpain is located in the nucleus, thus suggesting a palmitoylation-dependent regulation of localization (189). Palmitoylation furthermore promotes membrane association of cGMP-dependent protein kinases from *T. gondii* and *Eimeria tenella* (60).

In *Giardia lamblia*, variant specific surface proteins are palmitoylated at cysteines at their C-terminal tail (105, 220). *G. lamblia* codes for three DHHC-containing proteins, but only one was confirmed as a functional palmitoyl transferase *in vivo* (220). Although this palmitoyl transferase is not essential for *G. lamblia*, general palmitoylation inhibitors stop cell growth, indicating that palmitoylation fulfills an essential role for *G. lamblia* (220).

Protein prenylation

Another lipid modification of cysteines is prenylation, in which an isoprenoid group is covalently attached to a cysteine. A typical protein sequence susceptible to prenylation

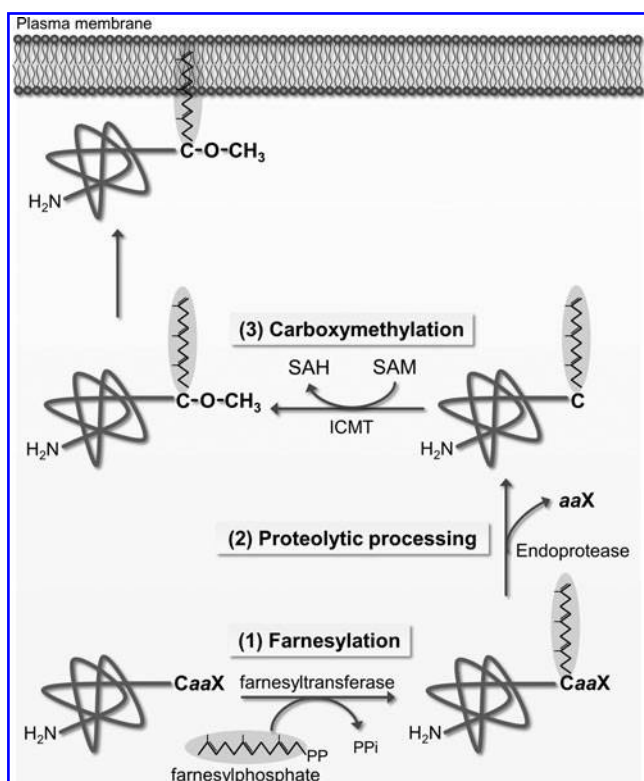


FIG. 8. CaaX processing of prenylated proteins. Proteins are prenylated at a CaaX motif with *a* representing aliphatic amino acids and X any amino acid. The prenylation (here shown for protein farnesylation) is followed by a proteolytic removal of the aaX tripeptide catalyzed by different Cxxx endoproteases such as Rce1. Subsequently, the prenylcysteine gets carboxymethylated by isoprenylcysteine carboxyl methyltransferase.

consists of a core prenylation motif including a cysteine (CaaX motif, with C denoting cysteine, *a* representing aliphatic residues, and X as any residue) at or close to the C-terminus (147). Proteins can be prenylated by a farnesyl (C₁₅) or a geranylgeranyl lipid (C₂₀) consisting of three and four isoprene moieties, respectively. In eukaryotes, around 0.5% of all proteins are prenylated, with geranylgeranlylcysteine being more frequent than farnesylcysteine (64). Whether a protein gets farnesylated or geranylgeranlylated is determined by the last amino acid of the CaaX motif and the specificity of prenyltransferases (34, 69, 152, 187). Prenylated protein are subjected to additional PTM steps referred to as CaaX processing: by proteolytic cleavage, the aaX tripeptide is removed leaving prenylcysteine as the ultimate residue, which subsequently can be carboxymethylated (Fig. 8) (9, 22). In accordance with palmitoylation, prenylation mediates membrane association, determines the subcellular localization, and is involved in protein–protein interactions (209).

Inhibitors of prenyltransferases and enzymes catalyzing the prenylation-dependent processing steps were intensely studied in order to develop anticancer agents (2, 128, 241, 243).

Protein prenylation in parasites

Protein prenylation has been studied intensely in numerous parasites (32, 39, 41, 70, 111, 135, 145, 250), with a

special emphasis on drug discovery strategies. Interestingly, various prenyltransferase inhibitors were found to inhibit the differentiation and growth of *Plasmodium* (121, 161, 242), *Trypanosoma* (251, 252), *Toxoplasma* (111), *Schistosoma* (163), and *Leishmania* (251), thus suggesting that prenyltransferases are promising targets for novel antiparasitic drugs development.

So far, there are only a few reports on prenylated proteins in *Plasmodium* (39), and the extent and function of cysteine prenylation in malaria parasites remains unclear. A database search for CaaX motifs revealed 14 potentially farnesylated proteins in *P. falciparum* (169). One of these proteins is a PRL protein tyrosine phosphatase that is indeed farnesylated *in vitro* (169). The *P. falciparum* SNARE protein Ykt6 is prenylated at its C-terminal CaaX motif, but also geranylgeranlylated. Prenylation is required to target *P. falciparum* Ykt6 to the membrane (12). *P. falciparum* farnesyltransferase and type I geranylgeranyltransferase were characterized as antimalarial drug targets (38, 39). A range of highly selective *Plasmodium* farnesyltransferase inhibitors such as compounds based on a benzophenone scaffold, terpenes inhibiting isoprenoid synthesis, tetrahydroquinoline-based compounds, ethylenediamine-based inhibitors, and the nitrogen-containing bisphosphonate risedronate were intensely studied and inhibit the growth of *P. falciparum* *in vitro* and *Plasmodium berghei* or *Plasmodium vinckei* infection in mice (38, 72, 89, 121, 127, 161, 184, 231, 242). Together, these findings support the inhibition of *Plasmodium* farnesyltransferase as a valuable concept for the development of antimalarial drugs and emphasize crucial functions of protein prenylation in *Plasmodium*.

At least 14 prenylated proteins were detected in *T. brucei*, with geranylgeranlylated proteins being more abundant than farnesylated proteins (70), and distinct patterns of protein farnesylation and geranylgeranlylation (250). Farnesyltransferases from *T. brucei*, *T. cruzi*, and *Leishmania* spp. show a different substrate specificity toward the CaaX motif compared to mammalian farnesyltransferases due to distinct amino acids in the substrate binding pocket, and have several insertions with unknown function (32, 33, 250). Moreover, *T. cruzi* employs a type I geranylgeranyltransferase with a distinct CaaX specificity that is exploited for the development of selective inhibitors (249, 250). Imidazole-containing CaaX peptidomimetics inhibit the growth of *T. brucei*, with the effect being attributed to inhibition of *T. brucei* farnesyltransferase (160, 161).

Experiments based on metabolic labeling and polyclonal antibodies confirmed the presence of prenylated proteins and a farnesyltransferase in *T. gondii*, which can be inhibited by known peptidomimetic farnesyltransferase inhibitors (111). Interestingly, *T. gondii* synthesizes the substrates for prenylation, farnesylphosphate, and geranylgeranylphosphate, by a bifunctional farnesyl-diphosphate/geranylgeranyldiphosphate synthase (139).

A farnesyltransferase was also identified in *E. histolytica*, which has narrow substrate specificity and is not inhibited by known CaaX peptidomimetic inhibitors of mammalian farnesyltransferase (135).

By measuring the incorporation of labeled mevalonate into proteins as farnesyl or geranylgeranyl isoprenoids, several prenylated proteins were detected but not identified in *G. lamblia* (145). However, no prenyltransferase in *Giardia* has been described to our knowledge.

General protein prenylation was demonstrated in *S. mansoni* (41). A rab-related GTP-binding protein gets geranylgeranylated at its CCXXX motif (142), a Ras protein is farnesylated at a CCIQ motif (163), and Rho1 is geranylgeranylated, but not farnesylated (235). All three prenylated proteins are GTP-binding membrane-associated proteins involved in signaling pathways, thus suggesting a role for prenylation in signal transduction in *S. mansoni*.

Pathophysiological implications of posttranslational cysteine modifications

In eukaryotes, oxidative cysteine modifications such as S-glutathionylation and S-nitrosylation have been connected to pathophysiological processes and several diseases. Accumulation of S-glutathionylated proteins was observed in the context of type 2 diabetes (196), Friedreich's ataxia (214), cystic fibrosis (239), and Alzheimer's disease (57, 159). Moreover, S-glutathionylation was suggested to be involved in drug resistance in cancer (54). Similarly, altered protein S-nitrosylation was detected in neurodegenerative diseases such as Parkinson's and Alzheimer's disease (42, 225, 227), cardiovascular diseases (99, 122), and cancer (78). Remarkably, some anti-tumor agents such as adriamycin and NOV-002, a mix of GSSG and cisplatin, act at least in part by affecting S-glutathionylation (10, 223), while other anticancer drugs such as carmustine, bis-chloroethylnitroso-urea (BCNU) and auranofin affect protein S-nitrosylation (20, 73). Even though interpretation of cause and consequence of cysteine modifications in pathophysiological processes is difficult, potential pathophysiological roles of cysteine modifications in parasitic diseases and their implications in drug resistance is an important field of future studies. Furthermore, it might be interesting to investigate whether S-glutathionylation is involved in the action of antiparasitic drugs acting by increasing oxidative stress, as it has been suggested for anticancer agents (10, 223).

Conclusion

Cysteine modifications regulate the activity and function of diverse proteins in protozoan and metazoan parasites. S-glutathionylation is employed as a redox-regulatory modification of proteins from versatile cellular pathways. S-nitrosylation is especially interesting with respect to drug development, since parasites react vulnerably toward increased NO concentrations and increased S-nitrosylation. To which extent and on the basis of which mechanisms S-nitrosylation is employed as a way of redox regulation in parasites remains to be studied in detail. Cysteine palmitoylation and prenylation target proteins to subcellular membrane compartments and are thus crucial for the function of numerous membrane-bound proteins. However, many aspects of regulation and function of cysteine modifications remain unknown and the current knowledge is largely based on *in vitro* data. Further studies are needed to understand the complex interplay between the cellular redox state in health and disease, cysteine modifications, their influence on protein function, and subsequently their (patho-) physiological role in the cell in response to various stimuli. Studying the role of cysteine modifications in parasite metabolism and development will be of great interest in order to gain more insight into the redox biology of human parasites.

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Abbreviations Used

CDPK = calcium-dependent protein kinase
 CP = cysteine protease
 Cys-SS-Cys = intra- or intermolecular disulfide
 or cysteinylolation
 Cys-SSG = S-glutathionylation
 Cys-S-NO = S-nitrosylation
 GAP45 = 45kDa gliding-associated protein
 GSH = reduced glutathione
 GSNO = S-nitrosoglutathione
 GSSG = oxidized glutathione
 HXGPRT = hypoxanthine-xanthine-guanine
 phosphoribosyltransferase
 IMC = inner membrane complex
 NO = nitric oxide
 NOS = nitric oxide synthase
 PfCDPK1 = *Plasmodium falciparum* calcium-
 dependent protein kinase 1
 PTM = posttranslational modification
 RNS = reactive nitrogen species
 TGR = thioredoxin glutathione reductase