



The Biological Impact of Oxidative Metabolism in Trypanosomatid Parasites: What Is the Perfect Balance Between Reactive Species Production and Antioxidant Defenses?

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Abstract

Diseases caused by trypanosomatids include leishmaniasis (*Leishmania* spp.), Chagas disease (*Trypanosoma cruzi*), and sleeping sickness (*Trypanosoma brucei*) that affect millions of people, especially low-income populations, being classified as neglected tropical diseases. Limitations in the clinical treatment, associated with the huge number of cases, make these infections a health and socioeconomic problem worldwide. To complete their life cycle, trypanosomatids survive to environmental changes in different hosts, including oxidative stress. A paradoxical role of reactive oxygen species (ROS) has been proposed, such as signaling as a proliferation regulator or even presenting cytotoxic activity, depending on the concentration. Mitochondrial electron transport chain, especially complex III, is figured as one of the most important ROS resources in trypanosomatids. In relation to antioxidant defenses, trypanothione pathway plays a crucial role, being a peculiar thiol-redox system responsible for the maintenance of protozoa functions mediated by thiol-dependent processes. In this chapter, we discuss the biological aspects of oxidative stress in trypanosomatids and its implications for the success of the infection. The possible ROS resources in these protozoa and their consequent antioxidant machinery involved in detoxification were also focused in this review, including alternative strategies for the development of new drugs for these diseases based on oxidative stress modulation.

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8.1 Introduction

The World Health Organization (WHO) defined neglected tropical diseases (NTDs) as a group of illnesses that affects low-income populations in tropical and subtropical areas, without the adequate sanitary conditions, reaching over than a billion people worldwide. These conditions which are far from the ideal, together with severe limitations in the current chemotherapy, led to high mortality and morbidity rates of these diseases in developing countries [1]. Trypanosomatid parasites are responsible for some of the most important NTDs. *Leishmania* species, *Trypanosoma cruzi*, and *Trypanosoma brucei* cause leishmaniasis, Chagas disease, and sleeping sickness, respectively [2], and the implication of oxidative metabolism in the success of these infections is the focus of this review.

8.1.1 *Leishmania* spp. and Leishmaniasis

Leishmaniasis is a complex of diseases caused by over 20 species of parasites of the genus *Leishmania* [3]. This disease is endemic in 98 countries, with more than 12 million people infected and 350 million in risk areas [4]. The parasite life cycle is digenetic, with two hosts: an invertebrate host (sandfly), being also the transmitter of the disease, and the vertebrate host (mammalian), including humans and animals such as rodents, canines, marsupials, primates, and others [5–8]. *Leishmania* is responsible for two major clinical manifestations, tegumentary and visceral leishmaniasis. The tegumentary form can be divided into cutaneous, diffuse, and mucocutaneous; however, it is the visceral form which can lead to death by affecting internal organs, such as the liver and spleen [9]. Leishmaniasis chemotherapy has been based over seven decades on pentavalent antimonials; however, even being the first choice of treatment in several countries, its side effects and longstanding therapy added to all the resistance reports led to alternative drug choices, such as amphotericin B, pentamidine, paramomycin, and miltefosine [10, 11]. Amphotericin B and its lipid formulation, which reduces side effects but has a higher cost, is the first-line therapy in some countries and an alternative in cases of antimonial failure. Nevertheless, along with pentamidine and paramomycin, there is a vast report of failure cases, with side effects, longstanding treatment, and resistance reports [9]. Miltefosine, the first oral drug for leishmaniasis, has been emerging in leishmaniasis therapeutic scenario, but the resistance case reports and teratogenic effects limit its use [12].

Leishmania biological cycle presents two major hosts and two forms. When the hematophagous sandfly host bites the infected mammal, it ingests a mixture of blood and phagocytic cells infected with amastigote forms, which are released upon

cellular rupture. Inside the insect gut (midgut or hindgut, depending on the *Leishmania* subgenus), amastigotes differentiate as procyclic promastigotes and develop in the sandfly. Promastigotes migrate to the proboscis and differentiate into metacyclic promastigotes, the mammalian infective form. When the infected sandfly bites a mammalian host, it regurgitates promastigotes, which are phagocytized by mononuclear phagocytic cells. Once, inside these cells, promastigotes transform into amastigotes, that proliferates up to host cell rupture, being phagocytized by other phagocytic cells, disseminating the infection [13].

8.1.2 *Trypanosoma cruzi* and Chagas Disease

Chagas disease, which is caused by the hemoflagellate protozoa *T. cruzi*, is typically a Latin American endemic illness. With the reduction in the transmission by triatominae vector, other transmission routes emerge, such as contaminated food or liquid ingestion in Brazil and transfusional transmission in Europe and North America, due to an increase in the migratory flux of infected people [14, 15]. In relation to clinical manifestations, Chagas disease presents an acute phase defined by high parasitemia in the patient bloodstream and a chronic phase where severe cardiac and/or digestive alterations are observed in 30–40% of the infected individuals decades after the acute infection [16, 17]. Up to now, benznidazole and nifurtimox are the clinical options for Chagas disease chemotherapy, being strongly effective on acute cases. On the other hand, both nitroderivatives show severe side effects as well as important activity limitations in the symptomatic chronic patients, particularly. Differences in the susceptibility of the parasite stocks isolated from distinct areas to these drugs also emphasize the necessity of the development of alternative compounds [18, 19].

The complexity of *T. cruzi* biological cycle, with different parasite evolutive stages and two hosts, also contributes for the delay in the development of novel active trypanocidal compounds. During the bloodmeal, triatomines ingest trypomastigotes with blood of the infected host. Reaching the midgut, bloodstream forms differentiate into proliferative epimastigotes that colonizes the insect digestive tract. The migration of epimastigotes to the low nutrient and acid environment of the triatomine posterior rectum triggers a new differentiation process in the parasite, and nonreplicative metacyclic trypomastigotes present in the insect feces will infect the vertebrate, invading host cells. In the intracellular environment, metacyclic forms differentiate into amastigotes that proliferates quickly. A new intracellular differentiation occurs to trypomastigotes that disrupt host cell and disseminate the infection by bloodstream [20, 21].

8.1.3 *Trypanosoma brucei* and Sleeping Sickness

Sleeping sickness, which is caused by the trypanosomatid *T. brucei rhodesiense* or *T. brucei gambiense*, is a disease restricted to sub-Saharan Africa, where the vector

tsetse flies (*Glossina* spp.) is present. The transmission occurs by the insect bite, being *T. b. gambiense* the most abundant infection (98% of all cases), which is especially distributed in the Democratic Republic of Congo [22]. An estimation of WHO pointed to 70 million people under risk of infection and about 20,000 new cases per year [23–25]. Clinical manifestations of sleeping sickness mainly involve cognitive impairment, including mental confusion, personality alterations, and seizures, among others, deriving from the direct injury caused by the parasite presence in central nervous system of the host, being present for many years or months in *T. b. gambiense* or *T. b. rhodesiense* infections, respectively [26]. Unfortunately, this disease progression can lead to the patient death, if untreated. Due to the variety of illness stages and parasite subspecies, adaptations in chemotherapy approach are critical. Suramin and pentamine are the first-line drugs for early phase of *T. b. rhodesiense* and *T. b. gambiense* infections, respectively. On the other hand, the treatment of later stages is more complicated, once the compounds need to cross the blood-brain barrier. Melarsoprol and eflornithine (only for *T. b. gambiense*) are the current drugs for this stage, sometimes in combination with nifurtimox; however, their high toxicity associated with difficulties in the administration encourages the search for alternative therapies [27–29].

The evasion of the host immune system by the parasite represents a crucial challenge for the efficacy of novel drugs. Variant surface glycoproteins (VSGs) of *T. brucei* mammalian stages are produced constantly, varying the composition of the protozoa surface coat and hampering their recognition by host phagocytic cells [30]. The biological cycle of *T. brucei* starts during the tsetse fly foraging, when metacyclic trypomastigotes are inoculated after the insect bite, reaching the mammalian bloodstream. The first differentiation step takes place, and long slender forms proliferate, maintaining the infection. Central nervous system, as well as different other tissues, are infected when this stage crosses the endothelia. In order to guarantee the parasite survival in the tsetse environment, long slender forms differentiate into short stumpy forms that will be ingested by the insect. In the midgut, a new differentiation process occurs, and procyclic trypomastigotes will colonize the digestive tract of the flies. The migration of procyclic forms to the salivary glands takes place, tissue where the last parasite differentiation step will occur. Infective metacyclic trypomastigotes presented in the insect saliva will reach vertebrate host during tsetse bloodmeal [31].

8.2 Oxidative Stress

The harmful consequences of free radicals production for biological systems and its implications in aging and diseases were proposed only half century after the first description of these species by Moses Gomberg [32]. Curiously, many years later, it was demonstrated that free radicals can also present a beneficial role for the cells and tissues, and it was postulated their involvement in the killing of pathogens, and help in the immune system [33, 34]. So, the participation of these molecules has been demonstrated in a great variety of biochemical pathways, acting as regulators [35].

Even today, the terms “reactive species” and “free radicals” are employed as synonyms, generating a little confusion. Free radicals are instable and represent reactive molecules with an unpaired electron in their orbital [36, 37]. Some reactive species does not present an unpaired electron, being not considered a free radical [38]. Reactive nitrogen species (RNS) comprehend nitric oxide (NO), nitrogen dioxide (NO₂), peroxyxynitrite (ONOO⁻), and nitroxyl (HNO) that participate in many crucial cellular processes [39], while also reactive oxygen species (ROS) include superoxide anion (O₂⁻), hydrogen peroxide (H₂O₂), and hydroxyl radical (HO⁻). Here, we only focused on the mechanisms of oxidative stress and their detoxification in pathogenic trypanosomatids and also its implications for the infection success.

In oxidative conditions, antioxidant machinery is highly expressed in order to downregulate the reactive species to physiological levels. Indeed, when such balance is broken, the concentration of ROS and/or RNS becomes higher, defining the oxidative stress condition that presents different biological implications, depending on molecular targets oxidized and the efficacy of antioxidant defenses, among other factors [40, 41]. The increase in ROS generation usually promotes this disbalance; however, the decrease in levels of antioxidant enzymes, due to reduction in expression or inactivation, also contributed for the oxidative regulation [42]. Regardless of the causes, the availability of reactive species scavengers strongly modulates almost all of biochemical pathways [43].

In the oxidative context, among all organelles and cellular structures, the mitochondrion stands out. Nobel Prize winner, Peter Mitchel, in 1961, described the co-dependency of cellular respiration and oxidative phosphorylation, being the oxygen metabolism and the ATP production causes of each other [44–46]. In the mitochondrial cristae, oxidative phosphorylation takes place, being the proton electrochemical gradient generated by electron transport through the complexes, leading to ATP synthesis [47, 48]. In aerobic conditions, the great majority of the oxygen directly reduced to water by complex IV (cytochrome c oxidase) in an electron transport chain (ETC) [49]. The partial reduction of oxygen by ETC electrons leakage represents one of the main ROS sources in eukaryotic cells, usually occurring in complexes I and III, as well as in coenzyme Q [50]. Alternatively to ETC, other enzymatic reactions, such as those catalyzed by oxidases, also can represent important ROS resource. In ETC, coenzyme Q shows an oxidized (UQ) or a reduced state (partially reduced UQ⁻ or fully reduced UQH₂), becoming one of the largest ROS generators in the mitochondrion. It is directly associated with its role in oxidative phosphorylation, where coenzyme Q reduction by complexes I and II allows the electrons targeting to complex III, in a step dependent of the full reduction of ubiquinone. This process includes oxidized ubiquinone that is partially reduced to semiquinone (transference of only one electron). During the return to stable state, coenzyme Q needs to be reduced again, and such reduction occurs with the semiquinone formation. This reaction is not so quick; many molecules including oxygen could be also reduced by semiquinone, producing mitochondrial ROS [51–53]. Chronologically, O₂⁻ is the first ROS generated during ETC electron leakage, derived from oxygen reduction by only one electron. Due to its instability,

superoxide anion is detected in low concentrations in cells under physiological conditions, situation where superoxide dismutase (SOD) and other specific antioxidant enzymes are expressed in order to detoxify these free radicals [41, 52].

After superoxide anion production, the next ROS generated is H_2O_2 by the $O_2^{\cdot-}$ reduction with two protons accepted, concomitantly. H_2O_2 does not present an unpaired electron, being more stable and less reactive than $O_2^{\cdot-}$. Once such molecule is still more reactive than molecular oxygen, it is called ROS but it is not considered a free radical. Peroxidases and catalases are specific antioxidant enzymes involved in H_2O_2 removal [41]. In a new reduction step, HO^{\cdot} is produced from H_2O_2 , a highly reactive free radical that interacts with more protons and electrons, generating water as a product from Fenton reaction [54]. For sure, HO^{\cdot} is the most damaging ROS, impairing a great variety of biological processes; however, due to its high instability, this molecule presents low half-life in cells compared to other ROS [41, 55, 56]. In summary, cellular physiology is directly affected by the consequences of these species production, damaging macromolecules, organelles, and structures, which can lead to phospholipids peroxidation, including in the plasma membrane, and causing subsequent cell rupture [57] (Fig. 8.1).

8.2.1 Oxidative Metabolism in Pathogenic Trypanosomatids

The mitochondrial metabolic processes that occur in the majority of the organisms are also present in trypanosomatids, despite some specific peculiarities of this organelle [58] (Fig. 8.1). ETC exhibits unique features when comparing their enzymatic complexes to the canonical system. In higher eukaryotes, the complex I (NADH: ubiquinone oxidoreductase) contains up to 30 accessory subunits whose function remains largely unknown [59–61]. It catalyzes the transfer of electrons from NADH to ubiquinone, restoring the NAD^+ , with the concomitant translocation of four protons across the mitochondrial inner membrane [62]. In trypanosomatids, this complex consists in 19 subunits which were determined by proteomic analysis or deduced from genome sequence searches [63]. However, the functionality of complex I in these protozoa has been debated. Among the described subunits, all molecules known to participate in electron transfer are present, but four membrane subunits supposedly involved in proton translocation are missing. Indeed, NADH-dependent substrates are not able to stimulate ATP production in isolated mitochondrion [64]. Natural *T. cruzi* mutants which showed deletions in ND4, ND5, and ND7 genes coding for complex I subunits presented no significant differences in oxygen consumption, respiratory control ratio, and mitochondrial membrane potential in the presence of NADH-dependent substrates or $FADH_2$ -generating succinate. In mammals, the complex I is also a site of ROS production; however, H_2O_2 formation induced by different substrates was not associated to complex I subunit deletions, demonstrating that these mutations are not important for the control of oxidative burst in trypanosomatids [65]. In *T. brucei*, NADH-induced respiration is sensitive to the complex I inhibitor rotenone, at a higher concentration than that dose required for inhibiting this complex in other models [66, 67], which is suggestive of the

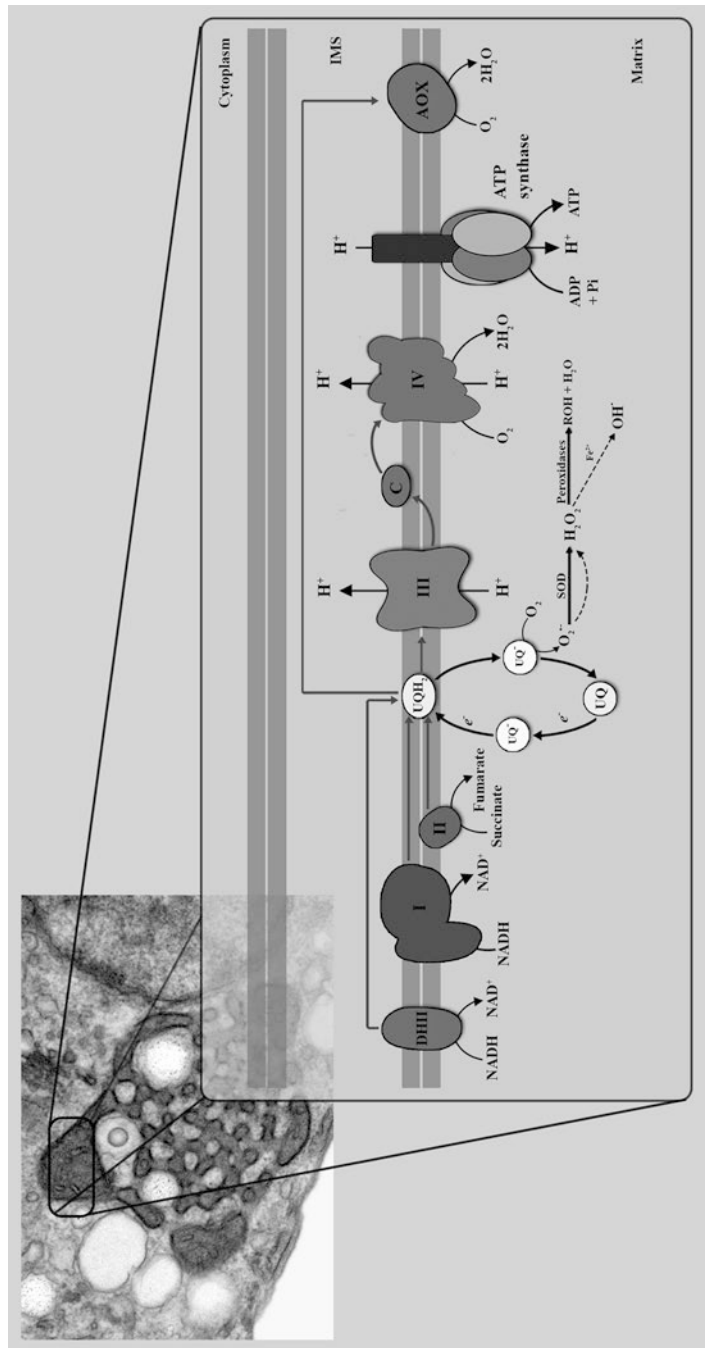


Fig. 8.1 During catabolic pathways, reduced equivalents are produced and enter in the respiratory chain at complexes I and II and at type-II NADH dehydrogenases (DHII), reducing coenzyme Q (UQH₂) pool in the inner membrane. Electrons from UQH₂ are successively transported to complex III, to cytochrome C (C), and to complex IV, where they reduce molecular O₂ to H₂O. Electron transference through complexes III and IV is coupled to H⁺ translocation from the mitochondrial matrix to intermembrane space (IMS). This process induces the formation of an electrochemical gradient between both sides of the inner mitochondrial membrane, which is used to produce ATP from ADP and inorganic phosphate (Pi) by the ATP synthase. In *T. brucei*, the respiratory chain possesses an alternative oxidase (AOX) that catalyzes the reduction of O₂ to H₂O by UQH₂. The electron transference between coenzyme Q and complex III or AOX is a process dependent to the full reduction of ubiquinone (UQH₂). The partial reduction of this molecule generates a semiquinone (UQ⁻), an unstable molecule that can reduce O₂, forming O₂⁻. Naturally (dashed arrows) or by the action of superoxide dismutase (SOD), O₂⁻ is transformed into H₂O₂, which can be reduced by the action of peroxidases or can react with metal ions, such as Fe²⁺ in a Fenton reaction, producing HO⁻

inhibition of other electron carriers [68] or even a characteristic of an atypical complex I. Besides that, previous findings pointed to an increased mRNA levels of several kDNA encoded complex I subunits in bloodstream compared to *T. brucei* procyclic forms [69, 70], suggesting a more important role for complex I in this parasite stage. Nevertheless, RNAi knockdown of three subunits indicates that complex I is not required for normal culture growth of *T. brucei* procyclic forms [71], the same phenotype was observed in *T. cruzi* natural knockouts [65].

Trypanosomatids, as many other organisms, have alternative pathways to transfer electrons without concomitant proton translocation, such as type-II NAD(P)H dehydrogenases and alternative oxidases [57]. The contribution of the alternative NADH oxidizing enzymes to the entry point of electrons into the respiratory chain is not completely established. Type-II NAD(P)H dehydrogenases are single polypeptides that catalyze the transfer of two electrons from NAD(P)H to ubiquinone without coupled proton pumping [72, 73]. These enzymes are able to oxidize both NADH and NADPH produced either in cytosol or in the mitochondrial matrix, depending on the orientation of NADH binding site. In trypanosomatids, the alternative NADH dehydrogenase was first described in *T. brucei*, where a rotenone-insensitive NADH oxidation activity and superoxide production in procyclic forms were reported [74, 75]. Contrasting to the lack of phenotype observed for complex I mutants, the knockdown of type-II NAD(P)H dehydrogenases affects parasite growth and decreases mitochondrial membrane potential [71, 76, 77].

In most trypanosomatids, succinate is the major end product of glucose metabolism. This substrate of complex II (succinate:ubiquinone oxidoreductase) is produced in the glycosome and/or in the mitochondrial matrix by NADH-dependent fumarate reductases. These enzymes oxidize NADH generating succinate from fumarate [78–81]. The excretion of succinate probably indicates that the respiratory chain is not able to deal with the input of reducing equivalents, supporting the exclusive occurrence of oxidative phosphorylation from complex II to complex IV in trypanosomatids. Some data suggest that malonate, an inhibitor of complex II, impaired oxygen consumption when complex I and II substrates were added [64, 65, 82]. Complex II of *T. cruzi* epimastigotes and *L. donovani* promastigotes produce ROS after the treatment with thenoyltrifluoroacetone (TTFA), another inhibitor of complex II [83, 84].

The ubiquinol:cytochrome c oxidoreductase, or complex III, works similarly in trypanosomatids and other eukaryotes. This complex carries the electrons flow to cytochrome c, which reduces the complex IV. As well as in other organisms, trypanosomatid complex III is usually the major source of mitochondrial ROS, being responsible for O_2^- formation in *L. donovani* promastigotes and *T. cruzi* epimastigotes induced by antimycin A, a classical inhibitor of this enzyme [83]. The only exception was *T. brucei*, in which this complex is not considered a potential ROS producer site [75]. Trypanosomatids possess two terminal oxidases: a classic complex IV KCN-sensitive and a KCN-insensitive alternative oxidase (AOX) [85–87]. The classic complex IV is similar to mammalian cytochrome c oxidase, transferring electrons from cytochrome c to the final acceptor, an oxygen molecule. This complex is important to mitochondrial functions, causing a decrease in this organelle

membrane potential, reduced ATP production via oxidative phosphorylation, and redirected oxygen consumption to AOX when their indispensable subunits were repressed in *T. brucei* procyclic stage [88]. The impairment of cytochrome c oxidase also resulted in other severe mitochondrial phenotypes. Without active complex IV, the electrons flow through complex III is not able to completely reduce the oxygen. Therefore, the electrons flow from cytochrome-mediated pathway can be deviated to AOX. Gnipová et al. [88] also showed that knockdown of *T. brucei* complex IV subunits affects the complex III activity, suggesting that these subunits are responsible for the signaling mechanism that allows communication between these two sequential respiratory complexes. It can contribute to ROS production detected when cytochrome c oxidase was repressed in these parasites.

AOX, the second terminal oxidase in trypanosomatids, is restricted to the inner mitochondrial membrane of both *T. brucei* bloodstream and procyclic forms, not exhibiting proton translocation capacity and subsequent contribution to proton gradient that drives ATP formation. In bloodstream forms, the complex IV can be completely replaced by AOX, while in the insect stage, the enzyme coexists with this complex. Interestingly, KCN, a complex IV inhibitor, does not completely abolish *T. cruzi* and *L. donovani* respiratory rates, suggesting the existence of an AOX as an alternative to cytochrome c oxidase. However, the activity of salicylhydroxamic acid, an AOX inhibitor, was observed only in *T. cruzi*, suggesting a role of this enzyme in this parasite energetic metabolism [89, 90]. In *L. donovani*, the respiration KCN-insensitive still remains unclear, needing further investigation [91]. Fang and Beattie [72] showed that the inhibition of AOX by salicylhydroxamic acid stimulates ROS formation in *T. brucei*, resulting in an increase in oxidation of cellular proteins. Besides that, AOX activity increased when parasites were incubated in the presence of H₂O₂ and antimycin A, which leads to high ROS levels. These data suggested that the excess of reducing equivalents was removed by AOX in *T. brucei* transferring these equivalents to oxygen, preventing ROS production.

Kinetoplastid parasites have a complex life cycle in which they transit between invertebrate and vertebrate hosts. During the cycle, the protozoa change their morphology and metabolic profile, adapting to diverse environmental conditions [92, 93]. In *T. cruzi*, the comparison between the energetic and oxidative metabolisms of bloodstream trypomastigotes and epimastigotes showed more active complex II–III and a restriction in electron flux to complex IV, reducing oxygen consumption and resulting in increased H₂O₂ generation in bloodstream forms [94]. These findings can be explained by the access to glucose at constant concentration that trypomastigotes have in vertebrate bloodstream. Similar results were found in *T. brucei* bloodstream stage that is essentially glycolytic, also living in an environment that presents high glucose levels. Besides that, these protozoa also lack many tricarboxylic acid cycle enzymes and cytochromes, affecting energy production [95–97]. In this regard, the invertebrate environment is glucose poor but is rich in amino acids released from intense digestion of blood proteins [92, 98, 99], resulting in high hemolymphatic levels of histidine [100, 101]. Several groups have discussed the possibility of oxidative environment as a stimulus to trypanosomatid growth. In *T. cruzi* epimastigotes, an increase in parasite proliferation was observed in response

to H₂O₂ incubation, mediated by calmodulin kinase II activation. The exposure of epimastigotes to different redox-state molecules including heme, a pro-oxidant molecule derived from the insect blood digestion, increased mitochondrial ROS production and parasite replication, whereas mitochondrion-targeted antioxidant reduces ROS generation, impairing protozoa proliferation and increasing metacytogenesis [102–104].

8.2.2 Oxidative Metabolism in the Hosts

Both invertebrate and vertebrate hosts of trypanosomatids share a common machinery of oxidative metabolism, which occurs in the mitochondrion. After decades of research in this field, critical proteins and molecules involved in the oxidative metabolism were described. The sequenced mitochondrial genome and uncoupling proteins (UCP) assays were extremely important for the overall comprehension of this process [105–107]. As described above for trypanosomatids, ETC is presented in the mitochondrial inner membrane, being the complexes I, II, III, IV, and ATP synthase functional [46]. The electrons entry in ETC occurs in complexes I or II, passing to complex III through coenzyme Q. Having received the electrons from complexes I or II, complex III uses cytochrome c to pass the electrons to complex IV, responsible for the reduction reaction that generates H₂O from O₂ [108]. As in trypanosomatids, hosts mitochondria are the main source of cellular ROS. To date, 11 sites of superoxide and/or hydrogen peroxide in mammalian mitochondria have been described, depending on the substrate metabolism, electron transport, and oxidative phosphorylation. The majority of these site-specific mitochondrial ROS production has been studied, measuring the maximum capacities of these sites under optimal conditions [52, 109]. As described above, complexes II and IV are not important ROS sources in mammals. Here, these two complexes are the main ROS-generating enzymes.

Differently of trypanosomatids, in mammals, complex I is the only entry point of electrons from NADH into the respiratory chain. This enzyme presents two domains: a hydrophilic portion located into mitochondrial matrix and a hydrophobic one, embedded in the inner mitochondrial membrane. All the known redox centers of complex I, the flavin mononucleotide cofactor (FMN), and eight FeS clusters are located in the hydrophilic domain [110]. The complex I has been recognized for a long time as one of the main sources of ROS production by the mammalian mitochondrial respiratory chain. This process was previously demonstrated, where the reduction of coenzyme Q pool and the generation of a large $\Delta\Psi_m$ by succinate led to H₂O₂ production [111]. Subsequently, other authors showed that isolated complex I, in the presence of NADH, produces O₂^{•-} and that this production is enhanced by rotenone [112]. The mechanism of O₂^{•-} generation by isolated complex I is well understood, by the reaction of O₂ with the fully reduced FMN (set by NADH/NAD⁺ ratio), which explains the enzyme inhibition by rotenone [113, 114]. During stress conditions, as ETC inhibition by damage, loss of cytochrome c, or low ATP demand and consequent low cellular respiration, the ratio of NADH/NAD⁺ increases,

leading to $O_2^{\cdot-}$ production [52]. The overexpression of a yeast NADH dehydrogenase in mammalian mitochondria reduces $O_2^{\cdot-}$ generation through the NADH/NAD⁺ decrease [115]. As described previously to trypanosomatids, in mammals, the ROS production by complex III is dependent of coenzyme Q-cycle and semiquinone formation [116].

The oxidation of energetic substrates generates reducing cofactors, as NADH and FADH₂, which donate electrons to ETC. During the electron flow between the mitochondrial complexes, the dissipated energy is used by complexes I, III, and IV to translocate protons to intermembrane space, generating an $\Delta\Psi_m$ across the inner membrane. Protons return to the mitochondrial matrix through ATP synthase, decrease the electrochemical gradient, and promote ATP synthesis [44]. However, the oxidative phosphorylation is partially coupled since protons can return to the mitochondrial matrix independently of ATP synthase and thereby without ATP synthesis [44, 117]. The energy-dissipating process (proton translocation to intermembrane space followed by the proton re-entry in mitochondrial matrix) apparently is present in all eukaryotic cells in a high proportion of cellular metabolic rates (up to 25% of the basal metabolic rate in the rats) and could prevent the oversupply of electrons to ETC, minimizing the probability of electron leak and $O_2^{\cdot-}$ production [118, 119]. Some authors showed the close relationship between the proton leakage and ROS production: uncoupler molecules and ADP, which increase respiration rate, stimulate ATP synthesis, and decrease $\Delta\Psi_m$, are known for impaired ROS production in isolated mitochondria [120, 121].

There are at least two types of proton leakage: a basal and an inducible. The basal proton leak is unregulated and depends only on the presence but not on the activity of carrier proteins. In this case, the proton return to mitochondrial matrix occurs through the lipid bilayer and has low impact. The inducible proton leakage is a protein-mediated process that is regulated and could be reversibly activated and/or inhibited. Among the inner mitochondrial membrane carriers, the UCPs, proteins belonging to mitochondrial anion carrier protein (MACP) family, are the mitochondrial carriers whose participation in ROS production is better understood [122, 123]. In the late 1970s, the first UCP was described in mammalian brown adipose tissue and was designated UCP1; afterwards, UCP1 homologues were found in mammalian tissues (UCP1-5) [124–127]. While proton leakage mediated by UCP1 is crucial for adaptative thermogenesis in the cold [124, 128], the function of these protein homologues is not yet fully elucidated. One of the differences between UCP1 and their homologues is the abundance in individual cells and nonthermogenic tissues, influencing the oxidative phosphorylation and ROS production [129]. The role of UCP in H₂O₂ generation was first demonstrated in 1997, showing that the inhibition of UCP2 by GDP results in higher $\Delta\Psi_m$ and ROS production [130]. Studies with UCP2 knockout mice demonstrated an oxidative burst in macrophages and liver and also improved resistance to *Toxoplasma gondii*. In contrast, UCP2 overexpression decreased ROS generation. In addition, $O_2^{\cdot-}$ and lipid peroxidation products (4-hydroxy-2-nonenal (HNE)) have been described to activate UCPs [131, 132]. Chemical uncouplers, such as 2,4-dinitrophenol (DNP) and FCCP (carbonyl cyanide p-tri-fluoromethoxyphenylhydrazone), also had a protector effect, where

they contributed to a decrease in oxidative stress in the skeletal muscle, heart, and brain [133–135].

8.3 Antioxidant Machinery

As discussed above, mitochondrion is one of the major ROS sources. It is well-known that the reactions involving ATP synthesis are able to release toxic products such as ROS and RNS. ROS accumulation led to severe biological consequences, and a machinery to regulate oxidative stress is essential to minimize its deleterious effects [136]; therefore, eukaryotic cells, among them, trypanosomatids and their hosts, possess enzymatic and nonenzymatic antioxidant defenses. Antioxidants are molecules responsible for the prevention of substrates oxidation (or delay), decreasing the intensity of the characteristic oxidative phenotype that includes genotoxicity and injury in crucial molecules such as proteins and lipids, among others [137]. Eukaryotic cells use two distinct strategies against the oxidative stress described up to now: the blockage of radical formation by antioxidant molecules (enzymes or not) or even the increase in the expression of specific enzymes that remove oxidized biomolecules [138, 139].

Considering the molecular mass, antioxidants are classified into (i) high molecular mass antioxidants (≥ 10 KDa), which include antioxidant enzymes, such as transferrin, albumin, and ferritin, which strongly bind to metal ions, among other pro-oxidant molecules with high oxidizing potential [43], and (ii) low molecular mass antioxidants (≤ 1 KDa), such as tocopherol (vitamin E), ascorbic acid (vitamin C), anthocyanins, carotenoids, uric acid, and polyphenols, which are obtained during the alimentation of almost all organisms [43, 138].

8.3.1 Antioxidant Defenses in Pathogenic Trypanosomatids

8.3.1.1 Trypanothione/Trypanothione Reductase

The antioxidant system of trypanosomatids is based on trypanothione/trypanothione reductase, an alternative system to glutathione/glutathione reductase, absent in these protozoa [140] (Fig. 8.2). The trypanothione [N1, N8-bis (glutathionyl) spermidine] is well-characterized, being formed by the binding of two glutathiones (GSH) and one spermidine (SPD) molecule in the cytosol [141–145]. Trypanothione biosynthesis is divided into three different steps, including GSH and SPD synthesis, similar to the pathway in other organisms.

GSH synthesis begins with the formation of γ -glutamylcysteine from the binding of L -glutamate and L -cysteine, catalyzed by γ -glutamylcysteine synthase (GCS). Such step is a limiter of the reaction in mammals and trypanosomatids. Previous studies showed that low GCS levels in *L. infantum* reduce the resistance to oxidative stress and consequently parasite survival in activated macrophages [146–149]. In *T. brucei*, the reduction in GCS levels resulted in a decrease in GSH and trypanothione concentrations; however, GCS knockdown led to an increase in GSH uptake,

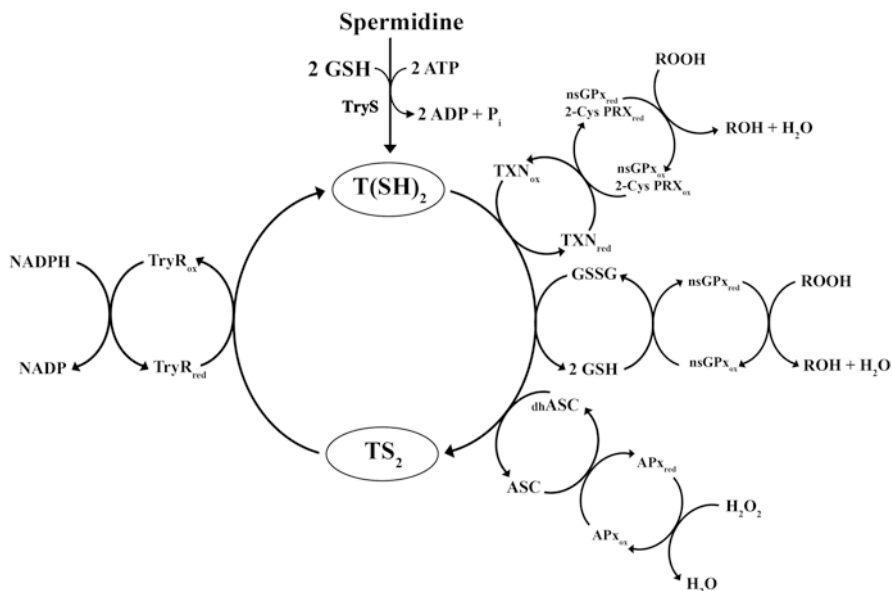


Fig. 8.2 The trypanothione is formed by the binding of two glutathione (GSH) molecules and one spermidine molecule in a reaction catalyzed by trypanothione synthetase (TryS). In this system, the maintenance of reduced trypanothione [dihydrotrypanothione – T(SH)₂] is dependent on trypanothione reductase (TryR) action by NADPH consumption. T(SH)₂ directly reduces trypanothione (TXN), dehydroascorbate (dhASC) to ascorbate (ASC), and glutathione disulfide (GSSG) to GSH. Trypanothione disulfide (TS₂); 2-Cys peroxidase (2-Cys PRX); non-selenium glutathione peroxidase-like enzymes (nsGPx); ascorbate peroxidase (APx); hydroperoxides (ROOH)

reversing trypanothione levels in this parasite [145, 150]. Once human blood has low GSH levels, the GSH uptake is not the primary source of these molecules in *T. brucei* bloodstream forms [151]. Curiously, GSH transporters were not described in *Leishmania* spp. and *T. cruzi* [145]. For GSH synthesis, it is necessary the presence of cysteine, an amino acid with a thiol group, that confers its redox capacity. In trypanosomatids, cysteine can be taken and/or biosynthesized, although, despite *Leishmania* spp. and *T. cruzi* express cysteine carriers, the uptake levels are much lower than in *T. brucei*, which expressed highly efficient transporters [152–155]. Alternatively, *Leishmania* spp. and *T. cruzi* have two biosynthetic pathways, also present in other eukaryotes, de novo or cysteine assimilatory pathway (CAP) and trans-sulfuration pathway (TSP). Increased levels of protein expression and activity of cysteine synthase and cystathionine β -synthase in *L. braziliensis*, key enzymes of these pathways, led to elevated thiol concentrations in response to oxidative and nitrosative stresses, confirming the association between cysteine biosynthesis and stress response. Promastigotes and amastigotes expressed differently these pathways, with TSP pathway increased in insect form and higher de novo synthesis in mammalian form [156]. *T. brucei* possesses gene sequences only of TSP pathway; nevertheless, this parasite does not synthesize cysteine [145, 152–155]. The stage/

species-specific regulation of cysteine biosynthetic pathways may be due to complex life cycle and exogenous nutrients, which differ considerably between invertebrate and mammalian hosts. The de novo pathway occurs predominantly in the mammalian intracellular form, while the TSP is present in insect form. These observations are consistent with the fact that *T. brucei* and *Trypanosoma rangeli*, parasites without an intracellular stage, possess only TSP pathway [155–159].

Polyamines are simple aliphatic compounds that are found in all mammalian tissues and also in microorganisms. These molecules are essential for cell growth and differentiation and have several biological roles. In trypanosomatids, SPD is one of the most important polyamines, being involved in crucial cellular processes including synthesis of trypanothione. Polyamines could be obtained by de novo synthesis from ornithine and in some cases from arginine, or by the uptake from the extracellular medium [160]. *T. brucei* synthesize SPD through the ornithine decarboxylation mediated by ornithine decarboxylase, which generates putrescine, a substrate for spermidine synthase, while *Leishmania* spp., beyond de novo synthesis, can also uptake this molecule [161, 162]. In *T. cruzi*, enzymes of putrescine biosynthetic pathway are absent, being this parasite auxotrophic for polyamines [163, 164]. An increase in *T. cruzi* polyamine transport improves the resistance to oxidative stress in this protozoa, which can be generated by incubation with H_2O_2 or trypanocidal drugs, such nifurtimox and benznidazole [165].

The last step in trypanothione biosynthesis is the binding of GSH and SPD. This process is exclusive of few organisms, including trypanosomatids [145]. Trypanothione biosynthesis consists in an ATP-dependent addition of two GSH molecules to SPD amino groups by different pathways, depending on the protozoa. In pathogenic trypanosomatids, trypanothione is synthesized by trypanothione synthetase (TryS) in two steps: first this enzyme catalyzes the binding of one GSH molecule and SPD, forming glutathionylspermidine (intermediate product). After this, the same enzyme added a second GSH, forming the trypanothione molecule. In addition, TryS presents amidase function, hydrolyzing trypanothione and glutathionylspermidine to form GSH and SPD, suggesting an involvement in polyamine levels [145, 166–169].

In trypanosomatids, trypanothione can be found in reduced form dihydrotrypanothione ($T(SH)_2$) and/or in the oxidized form trypanothione disulfide (TS_2). $T(SH)_2$ is more reactive than GSH, being a dithiol, which favors the reduction of disulfides (different pKa values: 7.4 and 8.4 to trypanothione and GSH, respectively) [170–172]. Depending on the reactive species, $T(SH)_2$ can suffer one- or two-electron oxidation, forming thiyl radicals (RS^\cdot) or sulfenic acid ($RSOH$), respectively. The thiyl radicals are formed in the reactions with peroxy and hydroxyl radicals, nitrogen dioxide, and others, whereas the sulfenic acid is formed during the reactions with H_2O_2 and peroxynitrite [145]. Moreover, $T(SH)_2$ participate in many antioxidant pathways, reducing intermediate molecules which transfer electrons to peroxidases [173].

The $T(SH)_2$ levels are maintained by NADPH-dependent flavoenzyme trypanothione reductase (TryR). TryR has 40% identity with mammalian glutathione reductase and shares several physical and chemical characteristics with host enzyme,

being their specificity of disulfides the main difference. The enzyme reduces positively charged oxidized forms of glutathionyl-polyamine conjugates, such as trypanothione, glutathionylspermidine, and others [174], whereas glutathione reductase only accepts negatively charged oxidized glutathione as a substrate. This characteristic is determined by the presence of five amino acid residues in the catalytic site, make this part wider, more hydrophobic and negatively charged when compared with glutathione reductase [175]. TryR distribution is still discussed, but some previous data suggested cytosolic and mitochondrial locations, while other reports proposed a glycosome localization [176–178]. *T. cruzi* and *T. brucei* have a carboxy-terminal extension with a tripeptide segment that would direct the enzyme to glycosome [179–181]. TryR is a potential drug target due to its importance for the survival of trypanosomatids. *L. donovani* mutants that presents only 15% of the wild-type TryR activity presented a normal growth in culture, but also showed an increased susceptibility to oxidative stress and a reduced viability inside macrophages. Similarly, the depletion of this enzyme in *T. brucei* led to an increase in sensitivity to H_2O_2 of the parasite, which then cannot successfully infect mice [182–184].

8.3.1.2 Tryparedoxin, a Trypanothione-Dependent Peroxidase System

Catalase and glutathione peroxidase (GPx) are absent in pathogenic trypanosomatids, making these parasites more susceptible to high concentrations of hydroperoxides [185, 186]. For many years, the elimination of low H_2O_2 concentrations was attributed to trypanothione [187, 188]. Recent studies showed the presence of three different classes of peroxidases; however, trypanothione remains essential for hydroperoxide removal (Fig. 8.2). Among these peroxidases, tryparedoxin (TXN) is a member of thioredoxin superfamily (Trx) that transfers reducing equivalents to different thiol proteins, which are found exclusively on Kinetoplastida [189, 190]. In contrast to classical thioredoxins, TXN is not directly reduced by a NADPH-dependent flavoprotein; however, these molecules are reduced by $T(SH)_2$ /TryR system at the expenses of NADPH in the parasite [191–193]. Experimental analyses pointed cytosol as the localization of TXN in different trypanosomatids, but *in silico* approaches also suggested the mitochondrion and endoplasmic reticulum as possible target organelles to the enzyme in *Leishmania* spp. and *T. cruzi* [173, 177, 191–195]. TXN depletion in *L. infantum* and *T. brucei* promoted the impairment of the antioxidant metabolism, compromising the parasite survival [195, 196]. Studies with *L. infantum* and *L. donovani* showed that TXN is essential for promastigotes and amastigotes stages, particularly during the establishment of infection [195, 197, 198].

Tryparedoxin peroxidase (TXNPx) is a class of enzymes that use TXN as electron donor. This process occurs in two steps: (1) $T(SH)_2$ reduces TXN, being considered a regulatory reaction in the pathway; and (2) TXNPx is reduced by TXN [199]. The TXNPx includes two types of peroxidases, the peroxiredoxins (PRXs) and non-selenium glutathione-like enzymes (nsGPx). PRXs are a family of antioxidant enzymes that are present in several organisms, detoxifying hydroperoxides and

peroxynitrite through cysteine (Cys) residues. These enzymes are divided in two categories, depending on the quantity of Cys residues involved in the reaction. The enzyme of trypanosomatids is a typical 2-Cys peroxiredoxin (2-Cys PRX) distributed in cytosol and mitochondrion, although, in *Leishmania* spp., one of the genes that encode this protein has a glycosomal signal sequence [190, 200]. The 2-Cys PRX has two identical reactions centers, being the substrate reduced by one of the Cys residues present in these centers, forming a cysteine sulfenic acid (Cys-SOH). Then, this residue is attacked by a Cys residue, forming a stable disulfide bond that is removed by TXN oxidoreductase [201]. 2-Cys PRX overexpression in *Leishmania* spp. and *T. cruzi* increased the resistance to hydroperoxides and peroxynitrite; however, the excess of substrate can reduce the enzyme activity in *T. cruzi* [202–205].

The second class of TNXPx, the nsGPxs, is structurally similar to glutathione peroxidase, but the selenocysteine residue in the active site of this enzyme was replaced for Cys residue [206]. These enzymes are classified as nsGPx-AI-III and nsGPx-B with different localizations. In *T. cruzi*, nsGPx-A1 is found in glycosome and cytosol, while nsGPx-AII-III are restricted to the cytoplasm. Interestingly, nsGPx-B is exclusively located in the endoplasmic reticulum in this parasite [177, 207]. In *T. brucei* and *Leishmania* spp., nsGPx-AI-II exhibit cytosolic localization, but on the other hand, nsGPx-AIII shows glycosomal and mitochondrial signal peptides [181, 208]. The nsGPx mechanism of action is similar to 2-Cys PRX, with the two Cys residues in the active site being responsible for substrate oxidation. The affinity of nsGPxs to substrates is a peculiarity of these enzymes. The depletion and/or mutation of amino acid residues in the catalytic site is responsible for a decrease in glutathione-binding capacity [207]. In this way, nsGPx-A uses TXN during substrate reduction, while nsGPx-B shows low affinity to both molecules [177, 209, 210].

8.3.1.3 Ascorbate Peroxidase

Despite the first description by Clark et al. [211], the biological relevance of ascorbic acid (vitamin C) in trypanosomatids was demonstrated almost a decade later [212]. This molecule acts as a cofactor for a wide range of enzymes involved in distinct metabolic processes, among them the antioxidant system [213]. The ascorbate peroxidase (APx), an antioxidant enzyme that uses ascorbic acid as a reductor agent, is a heme-containing peroxidase that catalyzes H_2O_2 reduction [209]. This enzyme has an endoplasmic reticulum localization in *T. cruzi* and *Leishmania* spp., whereas in *T. brucei*, there are no reports about this existence [185, 214, 215]. APx acts by cleaving O-O bound in H_2O_2 through the reaction between heme and reactive species, producing water. This process generates an intermediate that is reduced by ascorbate in two sequential electron transfer, restoring APx. Dehydroascorbate, the oxidized molecule, returns to the reduced form in two nonenzymatic reactions that may include $T(SH)_2$ and TXN [212, 216, 217]. Taylor et al. [218] showed that APx overexpression in *T. cruzi* confers protection against H_2O_2 exposure, whereas its depletion results in enhanced sensitivity. The enzyme activity is not required to parasite fundamental processes, such as replication and virulence.

8.3.1.4 Fe-Superoxide Dismutase

The SOD is an antioxidant enzyme described in most eukaryotes, being responsible for $O_2^{\cdot-}$ dismutation in H_2O_2 and O_2 [219]. This enzyme action is dependent on a metallic cofactor, such as Cu/ZnSOD and MnSOD, which are found in mammalian cytosol and mitochondria, respectively. In trypanosomatids, *in silico* analyses showed four SOD genes that use iron as cofactor. These isoforms are expressed in different organelles; FeSOD-B is distributed between cytoplasm and glycosomes of *T. cruzi* and *T. brucei*, whereas FeSOD-A and FeSOD-C are found in *T. brucei* mitochondrial matrix and intermembrane space, while only the first isoform was described in *T. cruzi* [220–223]. FeSOD-D was described in the three pathogenic trypanosomatids, being its activity related with apoptotic-like death in *T. cruzi* and *L. donovani*, while in *T. brucei*, it is considered nonessential [57, 224, 225]. The downregulation of FeSOD-A in *Leishmania* spp. increased the parasite sensitivity to menadione, a $O_2^{\cdot-}$ producer, whereas this enzyme overexpression protects the parasite from the oxidative stress. Furthermore, the SOD expression is related to differentiation and replication processes in *Leishmania* spp. Promastigotes in stationary phase showed increased resistance to oxidative stress and higher SOD activity during amastigote differentiation. In contrast, low SOD activity and ROS accumulation were found during promastigote logarithmic phase [226, 227]. In *T. cruzi*, the enzyme also has an important role in vertebrate host adaptation, with the enzymatic levels increasing during metacyclogenesis [92].

8.3.2 Antioxidant Defenses in the Hosts

8.3.2.1 Glutathione/Glutathione Reductase System

GSH (L-glutamyl-L-cysteine-L-glycine) is the most abundant low molecular mass thiol in eukaryotic cells [228, 229]. Its reduced form is also the active form (GSH) that is oxidized to glutathione disulfide (GSSG) in the oxidative stress. GSH is synthesized in cytosol and is transported into mitochondrion by dicarboxylate carrier protein and 2-oxoglutarate carrier protein [230]. Glutathione reductase (GR) is the enzyme responsible for maintain glutathione in its reduced form since the abundance of its oxidized form leads to a decrease in GSH/GSSG ratio, which serves as a warning of oxidative stress [229]. GR has been found in all organisms analyzed thus far, being a highly conserved enzyme in highly divergent organisms, such as *Homo sapiens* and *E. coli* [231]. GR has two cysteines in the catalytic domain and two other domains that bind to FAD and NADPH. Glutathione is found in cytoplasm, nucleus, mitochondria, and endoplasmic reticulum, as well as it seems to be present in lysosomes [232]. The formation of disulfides between GSH and protein cysteine residues constitutes a protective mechanism for thiols, which prevents their further oxidation, protecting cells from oxidative stress [233]. However, the formation of protein disulfides can alter the function of thiol-based proteins, such as receptors, protein kinases, and transcription factors, impairing cell signaling. In this context, GSSG is able to play a role in a nonspecific cell

signalization [230]. GSH is considered the most important redox molecule present in organisms, above all, mammals. This molecule is able to play several roles, such as a redox buffer, acting as cofactor scavenger for antioxidant enzymes such as GPx. This enzyme is able to detoxify H_2O_2 and lipid peroxidation products by the reaction of selenocysteines (presents in its active site) with peroxide group, forming GSSG and H_2O [228, 230, 233, 234].

GSH is not only found in cytosol but also in endoplasmic reticulum, nucleus, and intermembrane space. The transport of this molecule to nucleus is thought to be facilitated by passive diffusion via nuclear pores [235], and nuclear pool of GSH is responsible for regulating the redox state of protein sulfhydryls, in order to prevent DNA oxidative damage [229, 230]. The regulation of cytosolic GSH transport to the nucleus appears to follow cell cycle progression, balancing the GSH cytosolic/GSH nuclear according to cellular proliferation [236]. Reaching the endoplasmic reticulum, GSH is responsible for maintaining the homeostasis and the thiol levels in catalytic sites for PDI (protein disulfide isomerase) protein folding. Besides endoplasmic reticulum capacity to produce ROS, other oxidative inducers can lead to an unbalanced environment, impairing natural protein folding [237, 238]. Inside mitochondria, GSH is able to control mitochondria ROS generation by ETC and preserve mitochondrial proteins and lipids integrity [239, 240]. GSH also prevents toxic effects of free intracellular metals, such as iron, preventing its reaction with O_2 and Fenton reaction [228].

8.3.2.2 Other Thiol-Dependent Enzymes

Trx is part of a major system called TRX system, which includes, besides the Trx, the thioredoxin reductase (TrxR) and NADPH. Trx is a ubiquitous protein with a redox-active dithiol/disulfide site [241]. As GSH/GSSG, Trx appears in a reduced form [$Trx(SH)_2$], with a dithiol group, and in an oxidized form ($TrxS_2$), with a disulfide bound. Trx contains a conserved site Cys-Gly-Pro-Cys found in all organisms. In mammalian cells, Trx is described by having two isoforms, known as Trx-1 and Trx-2. Trx-1 is localized in cytosol, being transported to the nucleus during oxidative stress [229], while Trx-2 is the exclusive mitochondrial Trx isoform, regulating mitochondrial homeostasis. As in GSH/GSSG system, the maintenance of reduced and oxidized Trx ratio is extremely important in TRX system. TrxR is an oxidoreductase, responsible for regulating $Trx(SH)_2/TrxS_2$ [241, 242].

PRXs are ubiquitous thiol-dependent enzymes, known as an ancient family of proteins, being evolutionarily conserved and present in all kinds of organisms [243]. This peroxidase was first observed in *Saccharomyces cerevisiae*, demonstrating an antioxidant activity [244]. Unlike GSH and Trx, PRXs are selenium and heme-free molecules, with a peroxidatic cysteine (Cp) conserved in N-terminal domain. PRX mechanism of action consists in Cp attack to O–O bonds present in peroxide (reaction 3), which is oxidized into cysteine sulfenic acid [245]. PRX uses Trx as a hydrogen donor, creating an electron flow. Besides the H_2O_2 , PRXs are able to act as a scavenger for peroxynitrite and lipid peroxidation products. The ability to

scavenge peroxides protects prokaryotic and eukaryotic cells from DNA, lipids, and proteins oxidative damages, caused by ROS and RNS [243, 245]. Some groups have been demonstrating the relation of H_2O_2 signaling with PRX inactivation, describing new roles for this protein. Low concentrations of H_2O_2 appear to generate PRX inactivation by hyperoxidation, a reversible reaction promoted by sulfiredoxin [246, 247]. This reaction appears to follow a circadian rhythm, whereas the H_2O_2 signaling is required for different cell functions [248]. In structural terms, PRXs are divided in two subcategories: 1-Cys and 2-Cys peroxiredoxins, depending on the quantity of Cys residues involved in the reaction. There are six PRX isoforms present in mammalian: PRX I, II, III, and IV (2-Cys PRX), PRX V (atypical 2-Cys PRX), and PRX VI (1-Cys PRX) [242, 243, 245, 249]. PRX I and II are found in cytosol and nucleus. PRX III has an affinity to mitochondria, while PRX IV is found at endoplasmic reticulum. PRX V has been already detected at cytosol, mitochondria, and peroxisomes [250].

Glutaredoxin (GRX) is a small dithiol protein, also known as thioltransferase, required at the redox system. GSH is able to reduce GRX, and it has been described the potential role of its sensing changes in GSH/GSSG ratio [251]. GRX has the Trx family motif Cys-X-X-Cys, and it is able to form a disulfide bond within GSH. GRXs are also under two forms, an oxidized and a reduced form, and its reduction reaction is done by GSH, GR, and NADPH [249]. GRX is also found inside the intermembrane space, endoplasmic reticulum, and cytosol. It has been described that GRX can also display a sensing role at GSH-dependent glucose deprivation, as its interactions result in mediated cell death [251]. GRX-GSH is extremely important when TRX system decreases its activity under circumstances such as lack of selenium or Trx/TrxR inhibition, acting as a backup redox system [252, 253]. It has been described that mitochondrial GRX serves as TrxR substrate, maintaining mitochondrial redox homeostasis.

8.3.2.3 Superoxide Dismutase and Catalase

In the enzymatic redox system, SOD and catalase appear as the main enzymes in cellular detoxification. SOD is the first defense against superoxide, converting $O_2^{\cdot-}$ in H_2O_2 and O_2 . This enzyme is dependent on metal as a cofactor, and in mammals, there are three different isoforms: SOD1, a Cu/ZnSOD found in cytoplasm, nucleus, and plasma membrane; SOD2, a MnSOD found in mitochondrial matrix; and SOD3, a Cu/ZnSOD found in extracellular compartments, scavenging $O_2^{\cdot-}$ released in inflammatory cascades [254, 255]. High H_2O_2 concentrations are very dangerous for the cells, being necessary its elimination. Catalase is an enzyme that works directly connected with SOD, in order to complete $O_2^{\cdot-}$ detoxification, converting H_2O_2 into H_2O and O_2 [256]. The catalase types include Fe (heme)/Mn dependent [257]. These enzymes are largely found in all mammalian tissues, especially in red blood cells, and have been described as a cardiac and neural aging protectors [255, 258, 259].

8.4 Role of Oxidative Metabolism in Hosts/Trypanosomatid Infection

These parasites must thrive endogenous toxic metabolites produced by its aerobic metabolism and deal with the oxidative burst derived from the host immune system, which include ROS production. Once some antioxidant machinery in trypanosomatids such as catalase and classical GSH/GPx system is lacking, many authors suggested that ROS production by the hosts is a defense against parasite infection. However, it is well described the ability of trypanosomatids to overcome this situation, using ROS and RNS as important signaling molecules for their survival [260–262].

Both *Leishmania* spp. and *T. cruzi* have an intracellular stage inside the vertebrates. Macrophages and neutrophils are phagocytic cells, responsible for recognizing, internalizing, and destroying pathogens, being the first contact of infective metacyclic forms, performing a key role in infection control [263, 264]. For a successful infection, *T. cruzi* metacyclic trypomastigotes must invade macrophages and survive to oxidative burst found inside the phagosome. Previous data showed that cruzipain, an immunogenic glycoprotein, induces an increase in ROS production in murine cells during parasite invasion [265]. $O_2^{\cdot-}$ is produced by an associated-membrane NADPH oxidase, contributing to the formation of an oxidative environment during phagocytosis [266]. Besides that, the increase in H_2O_2 formation is also related with NADPH oxidase activation, once that spontaneous reactions (enzymatic or not) can convert $O_2^{\cdot-}$ in this molecule [267]. When the parasite is phagocytosed, a signaling cascade is triggered, culminating in the oxidative burst. The complex NADPH oxidase, known as NOX family, is a transmembrane multimeric protein able to transfer electrons to O_2 by NADPH oxidation [268, 269]. Cytochemical data demonstrated $O_2^{\cdot-}$ production when the parasite is attached to the macrophage surface, due to NADPH oxidase activation [270]. These enzymes need calcium or cytosolic proteins to be activated and thus lead to ROS production. In early stages of infection, NADPH oxidase is activated and its subunits are directed to phagosome membrane. Seven NADPH oxidase homologues have been identified in several cells types, being the NADPH oxidase 2 (NOX 2) the homologue present in phagocytic cells [269, 271].

Other important reactive species found during macrophages infection is NO. This RNS is a highly reactive free-radical produced by the oxidation of L-arginine by nitric oxide synthase (NOS) [272], participating in trypanosomatids killing, both directly or through the interaction with other free radicals, such as $O_2^{\cdot-}$, forming ONOO⁻ [273, 274]. NO is not a strong reactive species by itself, being unlikely to account for a direct damage to the parasite. The NO can inhibit the respiratory chain in mammalian via interactions with cytochrome c oxidase, which is accompanied by a steady-state level of reduced respiratory complexes, which favors intramitochondrial $O_2^{\cdot-}$ formation [275–277]. Proinflammatory cytokine production by macrophages, such as IL-12, INF- γ , and TNF- α , activates the inducible nitric oxide synthase (iNOS), generating high amounts of NO, which is maintained by 24 h during infection [264, 278]. The upregulation of iNOS expression in BALB/c mice

is protected from infection by *Leishmania major*. Furthermore, *T. cruzi* infection-resistant C57BL/6 mice produced larger amounts of NO, which is correlated with a better control of acute-phase parasitemia [279, 280]. In addition to NADPH oxidases and iNOS, myeloperoxidase (MPO) is another enzyme present in phagocytic cells, mainly neutrophils, which is pointed out as responsible for oxidative burst. MPO is able to catalyze the reaction of hypochlorite production, one of the major neutrophil antimicrobial responses [269]. This enzyme is a lysosomal hemoprotein, member of cyclooxygenase superfamily, stored in neutrophils azurophilic granules [281, 282]. When neutrophils are activated, the MPO is released in cytoplasm during degranulation, which also releases H_2O_2 . The MPO- H_2O_2 system is able to convert halide ions such as Cl^- , Br^- , and I^- , producing their oxidized forms of hypohalous acids (HOX), potent antimicrobial molecules [283, 284].

The levels of parasite antioxidant defenses during macrophage invasion may improve pathogen survival [285]. Chronic chagasic cardiomyopathy is characterized by the presence of pseudo cysts of amastigotes nests in the cardiac fiber. During *T. cruzi* invasion in cardiomyocytes, there is an increase in the production of inflammatory mediators, such as TNF- α and IL-1 β , and the induction of iNOS, with subsequent NO generation [286, 287]. The biochemical and genetic heterogeneity among *T. cruzi* strains is, in part, responsible for the diverse clinical manifestations of the disease, controlling several pathogenesis aspects [288]. Taking into account the establishment of a nitroxidative stress during the acute and chronic stages of Chagas disease, *T. cruzi* antioxidant enzymes are important virulence factors and become decisive for the infection success. In this context, several proteomic analyses showed an overexpression of *T. cruzi* antioxidant machinery in the infective metacyclic trypomastigotes compared with noninfective epimastigotes [92]. Such increase, found during metacyclogenesis of different *T. cruzi* strains, may act as a general preadaptation process to allow the parasite survival in the nitroxidative environment found in the vertebrate host. Piacenza et al. [289] showed a positive association between parasite virulence and levels of antioxidant enzymes *in vivo*.

In *Leishmania* spp. infection, some strategies to escape the oxidative burst present in phagocytic cells were demonstrated. Lipophosphoglycan (LPG), a molecule widely distributed in promastigotes surface, plays an important role in intracellular survival of these parasites. The protective effect of LPG is restricted to the establishment of infection during differentiation of promastigotes into amastigotes. *In vitro* experiments showed that LPG decreased oxidative burst in activated monocytes through inhibition of p67phox and p47phox recruitment to NADPH oxidase complex in phagosomes [290, 291]. LPG is also able to reduce NO \cdot production, regulating the iNOS expression in macrophages [292]. Additionally, $O_2^{\cdot-}$ generation after the infection by promastigotes and amastigotes is substantially different [272]. The hypothesis for this difference is the deficiency of NADPH oxidase activity after amastigote infection. Monocytes of patients with visceral leishmaniasis produce lower levels of $O_2^{\cdot-}$ and H_2O_2 and have a decreased NADPH activity when compared with healthy controls [293, 294]. To accomplish the successful NADPH oxidase complex assembly, the maturation of gp91phox is necessary, which is dependent on heme availability. During the infection, *Leishmania pifanoi*

amastigotes induces the heme oxygenase-1 expression, an enzyme responsible for heme degradation, thereby blocking gp91phox maturation and preventing NADPH activity [295, 296]. Amastigotes also induced lower levels of p47phox phosphorylation mediated by protein kinase C, decreasing the phagosomal recruitment of p67phox and p47phox to NADPH oxidase complex. Interestingly, unlike promastigotes, such effect is not attributed to LPG in amastigotes and remains unclear [291, 297, 298].

Although ROS are expected to be responsible for pathogen elimination during oxidative burst as described above, evidences suggest that ROS production could also have a beneficial role to *T. cruzi* macrophage infection. Oxidative stress mobilizes iron from host intracellular storages, which is an essential for amastigote replication. Such process occurs by the regulation of eIF2 α kinase. In the absence of heme, eIF2 α kinase is active and promotes cell growth arrest, leading to the differentiation of proliferative amastigotes into nonproliferative trypomastigotes [299]. ROS also participate in *Leishmania* spp. differentiation in a process dependent on iron availability. In this case, changes in intracellular iron levels activate a ROS-dependent signaling pathway that induces promastigotes differentiation into infective amastigotes [300]. Trypanosomatids also have contact with ROS and RNS inside the invertebrate host, in which the blood digestion, derived from the hematophagic behavior, causes an increase of heme concentration and an oxidative burst [260, 301]. Heme-induced and mitochondrial ROS stimulates epimastigote proliferation, being the contribution of mitochondrial ROS in epimastigote growth confirmed by the use of mitochondrial-targeted antioxidant that impairs parasite proliferation [103, 104]. The contribution of mitochondrial ROS to epimastigote growth was confirmed using the mitochondrion-targeted antioxidant MitoTEMPO that decreased ROS and ATP production induced by heme, strongly impairing the cell proliferation.

8.5 Oxidative Mechanisms of Action of Anti-trypansomatid Drugs

Considering all mechanistic studies of preclinical compounds performed in trypanosomatids, mitochondrion stands out among the most recurrent targets in these parasites, and mitochondrial damage has been described as part of the mode of action of distinct drugs classes [83, 84, 149, 302–311]. Surprisingly, the components and molecular events involved in the mitochondrial susceptibility to drugs, usually detected by phenotypes such as swelling and/or depolarization of the organelle, are completely undescribed [312]. Such scarcity of molecular information about the mechanisms of action of the great majority of the compounds makes hard to prove the mitochondrial direct effect. The specificity of this organelle as a target is very controversial, representing its injury a secondary target, derived from primary effects on another biochemical processes in different cellular structures. Independently of the origin or intensity, the mitochondrial damage caused by drugs regularly promotes a calcium homeostasis and/or ROS production [313].

Additionally, the activity of mitochondrial-specific inhibitors has been evaluated in trypanosomatid parasites, essentially targeting ETC complexes. Due to the fact that the biological activity of complex I had not been demonstrated in trypanosomatids up to now, the effect of the classical inhibitor of NADH dehydrogenase, rotenone, is very debatable [68, 77, 83, 314]. On the other hand, ROS generation was stimulated in parasites treated with complexes II and III inhibitors (nonyltrifluoroacetone and antimycin A, respectively), being correlated to the mitochondrial depolarization and an apoptotic-like events in some cases [66, 75, 83, 94, 315]. Interestingly, the inhibition of complex II promoted a potentialization of leishmanicidal effect of the clinical drug pentamidine in vitro [83]. In *L. donovani*, 4,4'-bis((tri-n-pentylphosphonium)methyl)benzophenone dibromide and sitamaquine, complex II inhibitors, led to a ROS production and deep mitochondrial alterations, including reduction in oxygen consumption and ATP levels as well as the remarkable swelling of the organelle and consequent cell cycle arrestment [316, 317]. Similar alterations could also be observed after treatment of *L. donovani* with tafenoquine and miltefosine, which inhibited complexes III and IV, respectively [318, 319]. Furthermore, in almost all pathogenic trypanosomatids, complex IV activity was, at least partially, inhibited by KCN, a classical cytochrome c oxidase inhibitor in higher eukaryotes [84, 91, 94, 320–322]. The absence of AOX in humans makes this oxidase another interesting mitochondrial drug target [323]. In *T. brucei*, it was demonstrated that ascofuranone affects ubiquinol oxidase activity in vitro, producing an apoptotic-like phenotype [323–326]. The alkyl lysophospholipid analogue edelfosine interferes in ATP synthase activity in *Leishmania*, being suggested a correlation between this biological effect to the leishmanicidal mechanism of action [327].

It is well-established that some chemical characteristics confer high redox potential to some compounds, leading to ROS generation [328, 329]. In this context, structural differences presented in the quinoidal nucleus directly influenced the oxidative capacity of quinones [330]. The effect of naturally occurring quinones and derivatives has been investigated in different *Leishmania* spp., *T. cruzi*, and *T. brucei*, and a promising activity was observed [331–339]. The first description of the oxidative effect of a quinone in trypanosomatids was performed in the late 1970s, demonstrating that beta-lapachone induced ROS generation in *T. cruzi* epimastigotes [340, 341]. More recently, other naphthoquinones also showed similar mode of action, producing considerable amounts of reactive species in this parasite [321, 342–344]. Almost a decade ago, a mechanistic proposal was raised by our research group, in order to explain the anti-*T. cruzi* effect of naphthofuranquinones. In 2009, our data pointed to the mitochondrial depolarization, derived from electron flow impairment, probably due to the electrons deviation from ubiquinone to the compounds. It compromises electron flux, producing ROS, leading to the impairment of the mitochondrial function, reflected by the reduction in respiratory rates, complexes I–III activity, and the dilation of the organelle [321]. Natural products also promoted mitochondrial damage/ROS production on different species of *Leishmania*. Quercetin, apigenin, and epigallocatechin-3-gallate are flavonoids working as potent ROS inducers in both *Leishmania* forms, causing mitochondrial dysfunction such as a decrease in ATP levels by altering mitochondrial membrane

potential [345–349]. Thiosemicarbazones, 1,3,4-thiadiazole, and triazoles derivatives, or even other classes of drugs such as LQB-118, Flau-A, clioquinol, and pyrazyl/pyridylhydrazones derivatives, also induced morphological injury in the mitochondrion and ROS production, suggesting the trigger of parasite cell death [350–356]. Interestingly, a trypanothione reductase inhibitor, cyclobenzaprime also increased ROS levels, which may be the mechanism of the antileishmanial effect caused by this compound [357].

After half century of the development of nifurtimox and benznidazole, the available clinical options for Chagas disease, their mode of action is still debatable. The first mechanistic hypothesis for the trypanocidal activity of both compounds was proposed in early 1980s, indicating $O_2^{\cdot-}$ and H_2O_2 generation induced by nifurtimox; however, such production was not observed after the treatment with benznidazole [358–361]. In this way, the effect of nifurtimox depends on the type-II nitroreductases activity that transforms nitroanion radical, producing ROS and their subsequent biological consequences such as lipids peroxidation [359, 362, 363]. Unfortunately, Boiani et al. [364] showed no correlation between anti-*T. cruzi* effect of nifurtimox and ROS production, which was demonstrated by the absence of redox cycling at trypanocidal concentrations together with low molecular weight thiol reduction. Recently, the trypanocidal activities of nifurtimox and also benznidazole were associated with type-I nitroreductase in oxygen-independent way, and nitroso and hydroxylamine intermediates would generate amine, using NADH as a cofactor [365–367]. Based on the nitroderivative, different reactions of these intermediates would take place. For example, furane ring would be cleaved, producing a highly reactive unsaturated open chain nitrile in case of nifurtimox [367, 368]. For benznidazole, such cleavage led to glyoxal and other metabolites production, which directly interacts with DNA [367].

Moreover, despite the current clinical drugs for sleeping sickness or leishmaniasis have not been associated with oxidative stress, a great variety of compounds leads to the mitochondrial functional impairment, increasing ROS production during the treatment. The molecular targets of anti-trypanosomatid drugs involved in these protozoa oxidative stress events reported experimentally were described in Fig. 8.3.

8.6 Conclusions

During the macrophage/parasite interaction, the host cell triggers a signaling cascade, recruiting immune cells to combat the infection. Macrophages induce NO production via iNOS and O_2 , which is also required in initial phagocytic steps; therefore, an oxidative burst against the parasites is developed [262, 369, 370]. Both superoxide and NO can also generate peroxynitrite, a toxic-free radical for pathogens [371]. Neutrophils, the first-line defense at pathogen infection, are also able to induce NO production in order to kill parasites, but in a smaller scale than macrophages [371, 372]. However, both leishmania and trypanosome parasites developed several evasion systems, being able to fool host oxidative burst mechanisms.

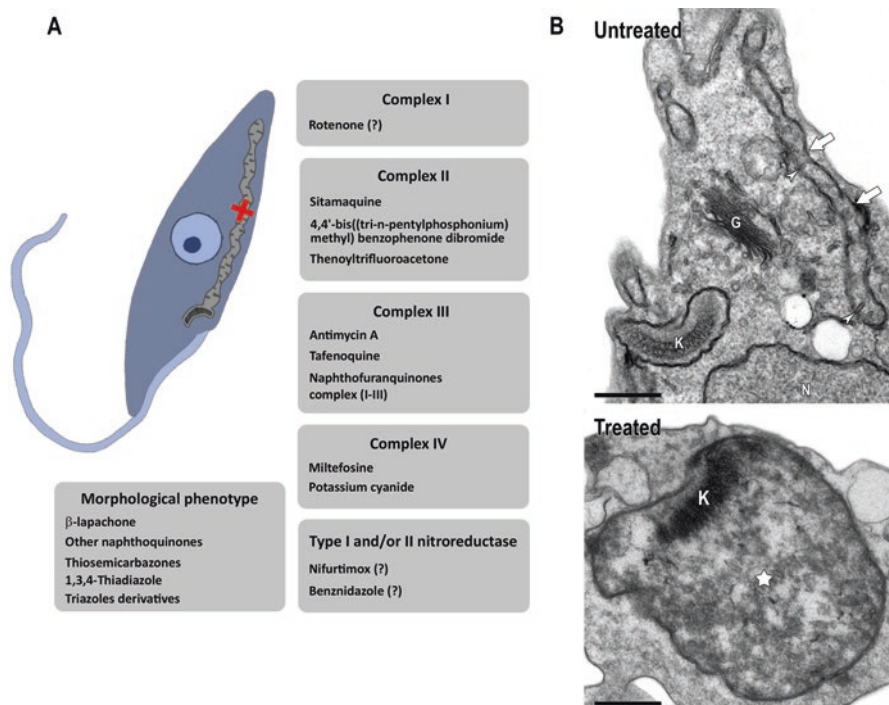


Fig. 8.3 Main mitochondrial molecular targets of anti-trypanosomatid drugs (a) and a recurrent morphological phenotype found in treated trypanosomatids are the mitochondrial swelling (b)

Antioxidant machinery of trypanosomatids, especially trypanothione/trypanothione reductase pathway, is considered an interesting drug target, and many efforts have been made to the design of novel-specific inhibitors that do not interfere with mammalian systems [184]. Trypanothione is the most characterized antioxidant system in these parasites, once glutathione/glutathione peroxidase pathway and classical enzymes such as catalase are absent [185, 373]. Unfortunately, up to now, no promising inhibitors of any antioxidant enzyme of pathogenic trypanosomatids were found, despite all the efforts employed [374]. The high susceptibility of these protozoa to ROS in relation to their hosts is an old-fashioned concept, due to the presence of efficient scavengers in trypanosomatids [51, 57, 375].

Several preclinical studies associated oxidative stress to the mode of action of anti-trypanosomatid compounds, being the parasites mitochondrion, the main ROS source [98]. Curiously, the participation of this organelle in pathogenic trypanosomatids treated with different drugs has been extensively demonstrated, but the molecular mechanisms involved are still unknown in a large number of cases. The mitochondrial injury could be derived from a randomic outcome of an indirect effect (probably in the great majority of the cases) or even resulted from ETC-specific inhibition that generates a redox imbalance [312]. Previous data published

showed high host toxicity of anti-trypanosomatid compounds with redox mode of action, suggestive of low drug specificity to these protozoa.

As it was mentioned, the significative role of ROS in cell signaling cannot be neglected. The pro-oxidant molecule heme triggers an oxidative stress, leading to calmodulin kinase II activation and consequent proliferation of *T. cruzi* epimastigotes [103]. On the other hand, ROS production also represents a crucial step for the success of these parasites in different hosts, and mitochondrial plasticity (morphological and molecular) has been postulated as an important adaptation, being ETC impairment directly associated to oxidative stress and loss of the redox balance [50]. The clinical correlation between the efficiency of mitochondrial antioxidant machinery (especially trypanothione synthetase and peroxiredoxins) of trypanosomatids and these parasites virulence was proposed, favoring the progression of the disease [277]. Studies about the molecular regulation of oxidative stress processes could base promising strategies for the development of new drugs.

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