# MITOCHONDRIAL DISORDERS IN CHAGASIC CARDIOMYOPATHY

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# 1. ABSTRACT

The mitochondria play a complex multi-factorial role in the cell. Along with their primary role in energy (ATP) production, mitochondria generate reactive oxygen species (ROS) that directly or indirectly affect several cellular functions. In this article, I review the molecular, structural and functional mitochondrial abnormalities reported in chagasic cardiomyopathy. I highlight current information about the potential etiology and the pathophysiological significance of mitochondrial dysfunction in chagasic cardiomyopathy and provide a brief background of mitochondrial biogenesis and bioenergetic pathways in cardiac growth and development.

# 2. INTRODUCTION

Biochemical and molecular studies have identified two primary bases for the development of cardiomyopathies; namely disorders of a) myocardial structural and contractile proteins, and b) myocardial energy metabolism. Disorders of myocardial contractile and structural proteins are usually linked to hypertrophic cardiomyopathy (HCM) (1-6). Energy metabolism disorders that may contribute to cardiac dysfunction include alterations of the mitochondrial oxidative phosphorylation (OXPHOS) pathway and/or of fatty acid (FA)  $\beta$ -oxidation (7-11). Current studies have advanced our knowledge of the specific genetic, molecular, and biochemical alterations that may contribute to metabolic

disorders causing cardiomyopathies and have provided new tools for classification and diagnosis of patients predisposed to cardiomyopathy development (12).

In recent years, mitochondrial metabolic deficiencies have also been recognized in cardiomyopathies of infectious etiology (13-15). In particular, defects of OXPHOS pathway are recognized as the major metabolic alterations in chagasic cardiomyopathy (16, 17). In this review, I summarize the literature on cardiac mitochondrial abnormalities in response to the stress of *Trypanosoma cruzi* infection and disease development. I briefly discuss the possible consequences of mitochondrial dysfunction in the pathogenesis of chagasic cardiomyopathy.

# 3. MITOCHONDRIA IN NORMAL CARDIAC GROWTH AND DEVELOPMENT

# 3.1. Mitochondrial bioenergetics

The provision of cellular energy by mitochondria is essential for a multitude of cellular functions, including intermediary metabolism, cell mobility and cell proliferation, ion regulation, and active transport processes. The heart is a highly oxidative tissue and essentially is dependent on mitochondria for the energy required for its contractile and other metabolic activities. Mitochondria represent 30% of the total volume of cardiomyocytes and provide  $\sim 90\%$  of the cellular energy (11, 18). The  $\beta$ -

oxidation of FA, tricarboxylic acid (TCA) cycle, and respiratory chain-mediated OXPHOS pathway, the three linked metabolic pathways of energy importance, are all carried out in mitochondria (19, 20). The FA β-oxidation and the oxidation of carbohydrates via the TCA cycle generate a majority of the intra-mitochondrial, reduced high-energy electron carrier nicotinamide adenine dinucleotide (NADH) and reduced flavin adenine nucleotide (FADH<sub>2</sub>). The OXPHOS pathway, consisting of five large-enzyme complexes, couples NADH and FADH<sub>2</sub> oxidation to phosphorylation, leading to ATP generation. All complexes are located in the inner mitochondrial membrane and designated as CI (NADH-ubiquinone oxidoreductase), CII (succinate-ubiquinone (ubiquinol-cytochrome oxidoreductase), CIII oxidoreductase), CIV (cytochrome c oxidase), and CV (F<sub>1</sub>F<sub>0</sub> ATP synthase). Respiratory complexes (CI-CIV) catalyze a series of redox reactions utilizing the reducing equivalents (NADH and FADH<sub>2</sub>) generated by the degradation of energy substrates. Specifically, electrons from NAD<sup>+</sup> are transferred to the CI complex and then to CoO. The electrons from FAD+, generated from succinate oxidation in the TCA cycle, are transferred to CII complex and then to CoQ. From CoQ, electrons are transferred to the CIII, cyt C and CIV, and finally released to ½ O to give H<sub>2</sub>O. The electron energy liberated during this process is utilized to pump the protons (H<sup>+</sup>) out of the mitochondrial inner membrane, resulting in the formation of an electrochemical gradient  $(\Delta \Psi)$  that is positive and acidic on outside and negative and basic on the mitochondrial matrix side. The electron energy stored in the proton gradient is finally captured by F<sub>1</sub>F<sub>0</sub> ATP synthase to drive the condensation of ADP and Pi for ATP synthesis (19, 20). ATP is transported to cytosol in exchange for the spent ADP by adenine nucleotide translocator (ANT) (21). Consequently, a defect in any component of the three metabolic pathways could potentially impair the energy availability, and subsequently affect the cardiac performance (22-26).

# 3.2. Mitochondrial biogenesis

Human mitochondrial DNA (mtDNA) encompassing 16,569 base pairs is a circular doublestranded DNA and consists of a total of 37 genes (12). The 13-mt mRNAs encode for proteins essential for the assembly of the four of the five complexes involved in the OXPHOS pathway, and are translated on a mitochondriaspecific ribosome/protein synthesis apparatus. The mtDNA also encodes part of the mitochondrial protein synthesis machinery, including 22 tRNAs, as well as 12S and 16S rRNAs. More than 95% of the mitochondrial proteins are, however, encoded in the nucleus, synthesized in cytosol, and transported into mitochondria. The nuclear DNA (nDNA) encodes proteins involved in mtDNA replication and transcription, protein components of mitochondrial ribosomes, and multiple structural and transport mitochondrial membrane proteins (27). In addition, nDNA encodes the pyruvate dehydrogenase enzyme complex, metabolic enzymes of the FA β-oxidation pathway and TCA cycle, and the peptide subunits of the respiratory enzyme complexes (other than the 13 mtDNA-encoded peptide subunits) (28). All four subunits of the complex II

are encoded by nDNA (28). The mitochondrial respiratory chain is unique from a genetic point of view as it is under the dual regulation of the nDNA and mtDNA.

Distinct genetic features that differentiate mtDNA from nDNA include a) maternal inheritance, b) polyploidy, and c) mitotic segregation. During fertilization, mtDNA are contributed by oocytes only. As a consequence, genetic disorders of mitochondria resulting in cardiomyopathy and other diseases are transmitted in a maternal fashion (29). In general, a cardiac cell consists of 100-500 mitochondria, each containing multiple copies (2-10) of mtDNA. The mtDNA are randomly distributed to progeny cells at cell division (30). The mechanisms that regulate mtDNA levels per mitochondria or the number of mitochondria per cell have yet to be elucidated (30). It is, however, well established that pathogenic point mutations and deletions in the mitochondrial genome, generalized depletion of mtDNA, or mutations in nuclear genes, all may affect mitochondrial biogenesis/and or function (29, 31). The physiological effects of mitochondrial dysfunction are expected to be severe in tissues with high-energy demand, such as the heart that is essentially dependent on mitochondrial generation of ATP to maintain contractility and other metabolic functions.

The adult heart predominantly utilizes aerobic metabolism, with the majority of ATP energy supplied by oxidative phosphorylation (32). Under normal conditions, the heart preferentially oxidizes FA as a reduced energy source (33). At the fetal stage and just after birth, the heart functions in a relatively hypoxic environment, utilizing glucose and lactate as the predominant fuel substrates for glycolysis and lactate oxidation, respectively (34). Several factors are suggested to contribute to preferential glucose oxidation in fetal hearts. For example, extremely high concentration of lactate along with limited free FA in fetal circulation is suggested to cause inhibition of FA uptake coupled with high level of lactate oxidation. Malonyl CoA, a metabolite produced during FA biosynthesis, is a potent, non-competitive inhibitor of carnitine-palmitoyl transferase I (CPT-I), an enzyme essential for transport of long chain FAs into mitochondria (35). The sensitivity of fetal CPT-I to malonyl CoA is greater in new-born hearts than adult hearts which could lead to efficient inhibition of CPT-I and decreased long chain FA oxidation (36). L-carnitine, a cofactor of CPT-I, is also produced at lower levels in fetal hearts, thus limiting FA transport/metabolism. After birth, a switch occurs so that FAs become the primary energy substrate in the heart (37). This shift correlates with decreased levels of malonyl CoA, and increased L-carnitine expression and FA delivery to mitochondria (38, 39). Two isoforms of CPT-I, CPT-Ia and CPT-IB, have been identified in the heart (40). CPT-I $\alpha$  is expressed in the fetal heart and declines after birth (41). The expression of CPT-Iβ, though detectable in fetal myocytes, is up regulated after birth and in later cardiac development. The specific activity of CPT-II also increases after birth (37, 41, 42). Differential expression and sensitivity of CPT isoforms to malonyl CoA is suggested to regulate cardiac fatty acid oxidation during development.

Concerning the pre-and post-natal changes in levels of cardiac-mitochondrial OXPHOS complex activities, Marin-Garcia et al (43) showed coordinated up regulation of the CIV and CV complex activities, polypeptide content (COX-II, COX-IV and ATP synthaseα subunits), and mtDNA copy number during early fetal cardiac development. In other studies, no changes were observed in the level of CIV and CV specific activities, COXII subunit content, and mtDNA copy number during progression from early neonatal period (<1 month after birth) to adult age (67 yrs) (44). The interpretations from these studies have, however, been limited because mitochondrial OXPHOS complexes are markedly affected by a variety of interrelated physiological, biochemical, and genetic factors during progression from early childhood to older adult.

# 4. MITOCHONDRIAL ABNORMALITIES IN GENETIC CARDIOMYOPATHIES

Since the early finding of a defect in mitochondrial respiratory activity associated with the accumulation of a large number of abnormal mitochondria in the skeletal muscle of a patient with hypermetabolism (45), impairment of mitochondrial function has been documented in a wide range of human diseases, including cardiomyopathies and heart failure (31, 46, 47). Mitochondrial dysfunction in dilated and hypertrophic cardiomyopathies is often due to a defect within respiratory chain complexes, each of which contain subunits encoded by mtDNA and/or nDNA. Accordingly, genetic defects in both genomes can contribute to mitochondrial cytopathies, although most of the known genetic mutations are identified in mtDNA (48). Appropriately, the diagnosis of mitochondrial defects is confirmed by biochemical assay of the respiratory chain activities and/or by molecular genetic analysis of mtDNA (49, 50).

Excellent dscussion of the mtDNA mutations identified in association with genetic cardiomyopathies can be found in recent reviews (26, 29, 31, 51). In brief, several pathogenic point mutations in mitochondrial tRNA genes have been associated with defects in mitochondrial protein synthesis and respiratory complex activities in cardiomyopathies (52-54). Other mtDNA point mutations in the protein-encoding genes are found to be heteroplasmic in DCM patients (53, 55, 56). Mis-sense mutations in cytochrome b have been reported in a wide spectrum of dilated and hypertrophic cardiomyopathies (57, 58). There is now a consensus view linking the mutations in mtDNA with ischemic heart disease and DCM (51, 59, 60). The multi-systemic, often maternally inherited, mitochondrial diseases present a variable cardiac phenotype, e.g., ventricular hypertrophy, cardiomegaly, and dysrhythmia, together with other syndromes (47). In addition, large-scale deletions in mtDNA that may or may not be inherited have also been detected in cardiomyopathy and cardiac conduction abnormalities. An accumulation of the mtDNA deletions in the myocardium is frequently linked to cardiac hypertrophy (61, 62), conduction block (63, 64), or heart failure (65). These abundant mtDNA deletions that may range up to 95% of total mtDNA are detectable by

Southern blot analysis. Specific, less abundant but largescale mtDNA deletions are also found by PCR analysis of cardiac tissue in many primary cardiomyopathies (66, 67).

Despite advancement in characterization of the genetic defects associated with mitochondrial disorders, the pathomechanisms in progression of clinical diseases are not well understood. In particular, the relationship between a given mtDNA mutation/deletion and the occurrence of specific clinical symptoms remains unresolved. Indeed, one is likely to observe the same clinical effects caused by different mtDNA mutations and conversely, the same genetic defect in mitochondria, leading to different clinical manifestations (50). Functional studies have also shown that biochemical defects in the same respiratory chain complex can lead to different clinical manifestations. It is likely that the physiological effects of mtDNA mutations/deletions are modulated by additional genetic, biochemical, or environmental cofactors and their identification in future studies would provide a better understanding of the outcome of the mtDNA mutations/deletions in various diseases.

## 5. CHAGASIC CARDIOMYOPATHY

# 5.1. Historical perspective

Chagasic disease is a pathological process induced by human infections with the hemoflagellate protozoan T. *cruzi* and is a major health problem in the southern parts of the American continent (68). The parasitological, serological and diagnostic non-invasive cardiological measures (electrocardiography (ECG), echocardiography (EKG), X-ray analysis) suggest that in a majority of acutely infected patients (>95%), parasitemia is controlled by the immune system and hence they exhibit no symptoms of clinical disease until several years later, when >40% of seropositive patients develop chronic heart disease (69). These observations have led to the proposal of an indeterminate phase between the acute infection and chronic disease phases during which patients remain seropositive but have no or sub-clinical cardiac involvement. Invasive ventricular angiography and light and electron microscopic analysis of myocardial biopsies or necropsies from seropositive patients have, however, detected the very early signs of myocardial damage in acute patients that progressively increase with disease severity (70, 71). In several independent studies, 40-60% of the seropositive patients exhibiting asymptomatic subclinical left ventricular systolic dysfunction by routine clinical diagnostic methods were found to show myocardial damage by microscopic analysis of myocardial biopsies (70, 72, 73) or by invasive ventricular angiography (74, 75). The long-term clinical follow-up records of seropositive patients or patients exhibiting variable severity of disease in association with survival analysis has shown that ventricular arrhythmia most significantly increase mortality in the chagasic patients (76-78). These studies, while underscoring that an indeterminate phase clinically defined as an asymptomatic phase may actually be a progressive phase of biochemical, molecular, and functional alterations that contribute to clinical disease, also suggest that preservation of cardiac function should be the most critical measure in treating chagasic patients.

# 6. MITOCHONDRIAL ABNORMALITIES IN CHAGASIC CARDIOMYOPATHY

#### 6.1. Human studies

The early insights suggesting mitochondrial alterations as an underlying cause for cardiac dysfunction in chagasic disease were provided by quantitative light and electron microscopic analysis of the myocardial biopsies obtained from seropositive chagasic patients exhibiting none to a variable degree of clinical disease symptoms (70). Microscopic examination of biopsy samples from the patients showed that degenerative myocardial changes occur very early during the indeterminate phase and excerbate with severity of clinical disease (70, 72, 73). Importantly, nuclei and mitochondria were noted to be maximally affected in indeterminate patients (70). As the disease progressed, an advanced degree of myocardial degenerative changes with increased involvement of nuclear and mitochondrial structural abnormalities was commonly noted. In experimental models of chagasic disease, the ultrastructural evaluation of the morphological alterations in the myocardium has illustrated an accumulation of large, irregular nuclei, swollen and displaced mitochondria, and myofibrillar degeneration, that becomes evident and more severe with the progression of chronic disease (79). These studies have elucidated two important observations, one, that nuclear and mitochondrial structural damage occurs much earlier than do the clinical symptoms of disease, and two, the severity of these aberrations increase with the evolution of chronic disease, thus implying a correlation between the extent of specific organelle abnormalities and clinical severity of chagasic disease.

The direct evaluation of mitochondrial metabolic functions in the myocardium of chagasic patients is limited by the ethical aspects of obtaining large tissue biopsies that are required for the mitochondrial isolation for these studies. Histochemical staining of small tissue biopsies is, therefore, the method of choice for monitoring biochemical and enzymatic changes in the myocardium. For the detection of the early signs of myocardial damage, Carrasco et al (70) recruited seropositive chagasic patients at various stages of infection and disease development. The severity of cardiac disease in seropositive patients was determined on the basis of abnormalities of ECG and hemodynamic parameters, extent of myocardial damage. and congestive heart failure, with the indeterminate patients showing none of these clinical signs, followed by patients exhibiting myocardial damage only, patients exhibiting abnormal ECGs and myocardial damage, leading to advanced patients exhibiting all clinical signs of cardiac damage and dysfunction. Small endomyocardial biopsies obtained from the patients were subjected to histochemical staining for lipids and polysaccharide deposits, and for a variety of enzymes involved in maintaining the myocardial structure and organelle function. They showed a reduction in the activities of succinate dehydrogenase and myosine ATPase in chagasic patients (70). The histochemical alteration index was evident in seropositive patients in the so-called "indeterminate" phase, suggesting that chagasic patients were predisposed to very early mitochondrial

functional defects. The chronic chagasic patients with clinical disease symptoms exhibited highest histochemical myocardial alteration index. These results are in agreement with the ultrastructural studies (discussed above) demonstrating myocardial cellular and organelle abnormalities in indeterminate patients and the increased involvement of mitochondrial structural abnormalities with disease evolution and suggest that myocardial alterations are likely to be associated with functional defects of mitochondria in chagasic disease.

The notion of mitochondrial functional abnormalities in chagasic patients is also supported by indirect observations. Alarcon-Corredor et al (80) indexed the changes in the serum pattern of metabolic enzymes in chagasic patients categorized according to clinical severity of disease (as above). Blood samples from the coronary sinus, superior vena cava, and pulmonary and femoral arteries were analyzed. The main finding in this study was a substantial increase in the serum level of the enzymatic activity of glutamate-oxaloacetate transaminase (GOT) and 3-hydroxy butyrate dehydrogenase (HBDH), specifically in the blood collected at the coronary sinus, the draining site for blood metabolized by the heart. Importantly, high serum levels of GOT and HBDH were detected in indeterminate patients, and remained consistently high in patients advancing to clinical cardiac dysfunction. In comparison, an increased serum level of glutamate-pyruvate transaminase (GPT, a cytosolic enzyme) activity was found only in chagasic patients at advanced stages of heart dysfunction. It is usually assumed that an increase in activity of the metabolic enzymes in serum is related to cellular damage. Clinical studies have invariably demonstrated an increase in the serum level of these enzymes in the event of cardiac injury. Considering the site (coronary sinus) and the extent of release of GOT and HBDH in indeterminate-to-chronic patients, it was surmised that mitochondrial and cell membrane injuries are the earliest events in chagasic disease, and the degenerative mitochondrial and cellular events persist with advanced disease. The serum detection of GPT in advanced patients is then most likely due to extensive cellular injuries, also evident by the clinical documentation of abnormal ECG and severe myocardial damage.

Utilizing a similar approach to determine the extent and type of cellular damage in chagasic disease, others (81) determined the concentration or activity of a variety of electrolytes, glycoproteins, and enzymes related to cardiac metabolism in the blood of chagasic patients. The important biochemical changes observed in this study were the detection of inorganic phosphorus and isocitrate dehydrogenase at the coronary sinus in all patients. The detection of these molecules in the serum of indeterminate patients, followed by a positive coronary sinus-femoral artery inorganic phosphate gradient with advancement of chronic disease, supports the hypothesis of very early and progressive manifestations of mitochondrial metabolic abnormalities in chagasic myocarditis.

# 6.2. Studies in experimental models

Experimental models have proven valuable in elucidating the molecular and biochemical alterations

associated with mitochondrial dysfunction in chagasic cardiomyopathy. Recent molecular studies have profiled the changes in mitochondrial function-related gene expression in experimental models of T. cruzi infection and disease development (17, 79, 82) and in the cardiac biopsies obtained from seropositive human patients (unpublished data). These studies utilized global and custom-designed arrays and confirmed the array data by traditional and real-time RT-PCR and Northern blotting approaches. The overall picture that emerged from these studies was that the myocardial transcripts encoding metabolic enzymes involved in FA β-oxidation were up regulated, while the mRNAs for a majority of the subunits of the complexes of the OXPHOS pathway were repressed in response to infection. For instance, the expression profiling with custom-designed mito-arrays showed an increased level of transcripts for long chain acyl-CoA dehydrogenase (ACADL), dodecenoyl-CoA δ-isomerase (DCI), and carnitine-o-acetyltransferase (CRAT) in the myocardium of T. cruzi-infected mice (17). Increased myocardial level of mRNAs for ACADL, DCI and 3hydroxyacyl-CoA dehydrogenase were also detected by global profiling of cardiac gene expression in murine models of *T. cruzi* infection and disease development (79). Others (83) have demonstrated alterations in the protein levels of enzymes involved in β-oxidation of FA in chagasic and hypertrophic hearts. The mRNAs for the enzymes involved in the  $\beta$ -oxidation of FA were, in general, increased in acutely infected hearts and normalized during the chronic disease phase, thus suggesting that chagasic hearts most likely are not compromised in their capacity to generate reduced energy. In similar studies, the nDNA-encoded transcripts for subunits of the OXPHOS complexes were found to be differentially expressed, i.e. while some transcripts were shown to be increased, others were noted to be decreased in infected myocardial tissue (17, 79, 82). It is important to note that the mtDNAencoded transcripts for the subunits of the OXPHOS complexes were diminished very early during the acute phase of infection (16), before the alterations in nDNAencoded transcripts were detected, suggesting that the expression from the mitochondrial genome might be more severely affected in response to T. cruzi infection. The expression level of mtDNA-encoded OXPHOS components that were examined (9 of 13) was substantially reduced (up to 80%) with progression to chronic disease phase. A loss in mtDNA-encoded transcripts (and presumably proteins) below the threshold level is likely to result in a deficiency of respiratory complexes in chagasic hearts.

Not surprisingly then, alterations in the activities of the respiratory complexes in chagasic hearts was demonstrated. We have employed catalytic staining and spectrophotometric approaches to determine the changes in the activities of the respiratory complexes in response to *T. cruzi* infection and disease development (16). This study found the earliest and strongest repression of CI activity, i.e. a 38% loss at 3 days post-infection (dpi) and a 47-57% decline during the acute phase in infected murine hearts. The specific activity of CIII and coupled activity of CII+CIII were diminished consistently, albeit at different

levels (32-60% and 23-42% respectively) throughout the infection and disease phase. Minimal, but statistically significant, alterations in CV activity have been reported in infected murine and rat hearts (16, 84, 85). It is important to note, that along with a decline in total specific activity of respiratory complexes (determined by spectrophotometry assays), activities of the assembled complexes (determined by catalytic staining on blue-native gels) were also affected, suggesting that multiple mechanisms are likely to be involved in the inactivation of the respiratory complexes in the chagasic myocardium (16). The skeletal muscle mitochondria of the infected mice, except for a decline in CI activity, presented no statistically significant impairment of CII, CIII, and coupled CII+CIII activities at all stages of infection and disease progression (16). The observation of the heart-specific progressive and sustained deficiencies of respiratory chain complexes implies pathophysiological significance of mitochondrial dysfunction in CCM.

To summarize, electron microscopic, molecular, and biochemical studies discussed above suggest that abnormalities of mitochondria occur in early stages of *T. cruzi* infection and are indicative of the presence of an active, ongoing process of organelle and myocardial degeneration with progressive severity of chronic chagasic cardiomyopathy.

# 7. FACTORS CONTRIBUTING TO MITOCHONDRIAL DYSFUNCTION IN CHAGASIC CARDIOMYOPATHY

Considering the complexity of the information available in the literature, it is likely that a number of interrelated mechanisms may contribute to mitochondrial dysfunction in chagasic disease. Many of these pathways appear to be an outcome of constant oxidative damage to mitochondria and may also contribute to oxidative stress generation. I, therefore, focus on the source and site of action of oxidative stress as it relates to mitochondrial dysfunction in chagasic disease.

# 7.1. ROS generation

Infection by *T. cruzi* generally induces inflammatory cytokines (TNF-α, IL-1, and IL-6) that participate in parasite control through activation of cytotoxic agents, including ROS and reactive nitrogen species (86-89). These reactive species, while necessary in limiting T. cruzi replication and survival (89), also affect the host cellular and organelle function (90, 91). These observations have led to the suggestion that immunemediated responses might be the primary source of oxidative stress in acute hearts. Others have suggested that chagasic myocardium may be predisposed to sustained oxidative stress with progressive disease severity as a consequence of mitochondrial dysfunction. This idea is based upon the fact that mitochondrial generation of ROS as a by-product of respiratory chain is the major source of free radicals in the heart (26, 92, 93). Under normal conditions, as much as 2-4% of the reducing equivalents escape the respiratory chain, leading to the formation of superoxide  $(O_2)$ .  $O_2$  is dismutated by manganese superoxide dismutase (MnSOD) to H<sub>2</sub>O<sub>2</sub> that may then be converted to highly reactive and harmful hydroxyl radicals (HO·) (26, 94, 95). The CI and CIII complexes of the respiratory chain are the prime site for electron leakage to oxygen, and free radical production in mitochondria (26, 92, 93). ROS release may exponentially increase when CI and CIII function at a sub-optimal level (96). Further, CI and CIII are redox sensitive, as they contain Fe<sub>4</sub>S<sub>4</sub> clusters that when oxidized; release one iron atom, resulting in the inactivation of important functional Fe-S centers and enzyme activity (97-101). The released ferrous ions, when participating in the Fenton reaction, produce highly reactive HO<sup>-</sup> radicals. The importance of these findings in chagasic disease is that an early and consistent repression of CI and/or CIII activities associated with sustained ROS production was observed in mitochondria isolated from the myocardium of mice infected by T. cruzi (16) (unpublished data). A consistent decline in manganese superoxide dismutase (MnSOD) activity, the major oxygen radical scavenger in the mitochondrial matrix (102), with progression of infection and disease in chagasic myocardium was also shown (103). These studies have led to a suggestion that a catastrophic cycle of mitochondrial functional decline and ROS generation, coupled with an inability to efficiently scavenge the mitochondrial ROS (due to MnSOD deficiency), predisposes the chagasic hearts to sustained oxidative stress during infection and disease development. This notion is supported by the observations of a decrease in complex I-mediated respiration and an increase in oxidative damage in MnSOD /+ mice (104), and the neonatal lethality associated with the development of DCM and mitochondrial dysfunction in MnSOD<sup>-/-</sup> mice (105). The morphologic abnormalities in mitochondrial structure associated with alterations in respiratory complex activities and increased ROS production have also been reported in ischemic hearts of experimental animals (98, 106, 107) and oxygen-depleted cardiomyocytes (99) upon reoxygenation.

## 7.2. Mitochondrial oxidative damage

ROS can cause damage to biological macromolecules, i.e. lipids, proteins and DNA. Lipid peroxidation (LPO) is the major biochemical consequence of an oxidative attack on unsaturated FA, abundantly present in cell and mitochondrial membranes (108). The aldehydic products of LPO, e.g. malonyl dialdehyde (MDA) and 4-hydroxy-2-nonenal (4-HNE), are highly reactive and able to diffuse and attack targets in the near vicinity as well as those distant from their site of origin (109). 4-HNE reacts with Cys, His or Lys residues via a Michael addition that results in irreversible alkylation and introduction of carbonyl groups into proteins (110). The direct oxidative attack by ROS on Arg, Lys, Pro, and Thr residues can also derivatize the proteins and lead to the formation of protein carbonyls (111, 112). The first indication of mitochondrial oxidative damage in chagasic disease was reported in a recent study. Utilizing an experimental model of infection and chronic disease, Wen et al (113) measured the changes in the mitochondrial level of LPO derivatives (i.e. MDA) by TBARS assay (114) and validated these findings by the quantitation of the triphenylphosphine (TPP)-specific lipid hydroperoxide

(LHPO) contents (115). TPP is a specific reductant of hydroperoxides and allows definitive identification of LHPO (115).The specific binding dinitrophenylhydrazine (DNPH) with oxidized and carbonylated proteins was exploited to detect the protein carbonyl-DNP complexes by immunoblotting with anti-DNPH antibody (116). The finding of a substantial increase in LPO and PCO derivatives in cardiac mitochondria of infected mice, compared to controls, led to the suggestion that mitochondria were exposed to oxidative stressmediated damage in chagasic hearts. The LPO derivatives of mitochondrial membranes were detectable as early as 3 days post-infection, and gradually increased by >2-fold during the course of disease development. In comparison, the PCO content in cardiac mitochondria became evident during the acute infection phase and remained consistently enhanced throughout the chronic phase of disease progression. Given that the LPO derivatives preceded PCO formation, it was proposed that modification of protein residues by HNE/MDA-mediated cross-linking and Michael adduct formation may contribute to an elevated PCO level in cardiac mitochondria. The role of mitochondrial oxidative modifications of membrane lipids and proteins in alterations of mitochondrial integrity, increased permeability and dissipation of the mt membrane potential and protonmotive force, and decreased activity of the respiratory chain complexes (RCC, CI-CV) in chagasic hearts would likely be addressed in future studies.

Direct oxidative modification of specific subunits of respiratory complexes may be an underlying mechanism in the inactivation of assembled mitochondrial complexes in chagasic hearts (113). Cardiac mitochondria from infected mice were subjected to two-dimensional bluenative gel electrophoresis to resolve the subunits of the respiratory complexes. Carbonylated subunits were then detected by immunoblotting with anti-DNP antibody and identified by N-terminal Edman sequencing. On the basis of the identity of subunits that were oxidatively modified, different mechanisms were proposed to participate in inactivation of CI and CIII respiratory complexes in chagasic hearts. Of the >42 subunits of CI, carbonyl adducts were primarily detected with NDUFS1, NDUFS2, and NDUFV1, the core subunits considered essential for electron transfer from NADH to ubiquinone and for the generation of protonmotive force (117, 118). NDUFS4, also oxidatively modified in infected murine hearts, plays an important role in regulating the enzymatic efficiency of CI (117). Considering that genetic mutations in genes encoding NDUFS1 (119), NDUFS2 (120), NDUFS4 (121) NDUFV1 (122) in human patients and oxidation/nitration of NDUFS2 and NDUFS8 in human and bovine hearts (123) are linked to CI deficiencies, it was surmised that oxidatively modified structural subunits contribute to the inactivation of the assembled CI complex in chagasic hearts. Among the 11 components of CIII, consistent carbonylation of core proteins (UQCRC1 and most likely UQCRC2) and CYC1 was shown in the cardiac mitochondria of infected mice. Core proteins constitute the matrix portion of the CIII complex. Based upon the highsequence similarity with soluble matrix-processing peptidases (MPP) (124), core proteins are thought to be

involved in the cleavage and processing of the targeting pre-sequence of Reiske [2Fe-2S] protein (ISP) (125) and other mitochondrial proteins (126). It was suggested that the inappropriate processing of ISP by oxidatively modified core proteins may result in incorporation of the mis-folded ISP in CIII, resulting in mis-assembly of the catalytic site and inhibition of the enzymatic activity of complex. CYC1, an essential component of the inter-membrane-associated, central catalytic domain of CIII (127), accepts electron from ISP and transfers it to soluble CYC (128). The inability to accept or transfer electrons by oxidatively modified CYC1 would disrupt the electron flow-coupled proton translocation by the protonmotive Q-cycle and thus directly affect the CIII activity. Future studies would confirm the mechanistics of oxidative stress-induced CI and CIII inactivation in CCM. Nevertheless, the observation of dose-dependent HNE-mediated inhibition of respiratory complexes in the same study supports the idea that oxidative modifications contribute to inactivation of respiratory complexes in chagasic myocardium.

In other studies, the detection of a substantial depletion of mtDNA in chronically infected murine hearts associated with compromised levels of mtDNA-encoded transcripts has led to the suggestion that a limited biosynthesis of mitochondria-encoded protein subunits may contribute to reduced assembly of respiratory chain complexes in chagasic myocardium (16). What may cause mtDNA depletion in chagasic myocardium is not known. Given the detection of similar numbers of mitochondria in cardiac sections of infected mice exhibiting increasing severity of chronic disease and in normal mice, by transmission electron microscopic analysis (79), it is likely that mitochondrial biogenesis defects may not be the probable cause of mtDNA depletion in infected mice. Instead, numerous studies strongly support reactive species as playing a prominent role in mtDNA deletions through oxidative damage. MtDNA is highly susceptible to damage by reactive oxidants due to a lack of protective histones (129). Accumulation of significantly higher levels of DNA oxidation product 8-hydroxy deoxyguanosine in mtDNA compared to nuclear DNA and increased degradation of the mutated mtDNA are shown in a variety of in vitro and in vivo conditions of oxidative stress (102, 130, 131). It was postulated that ROS-induced alterations resulting in deletions or degradation of oxidatively damaged mtDNA contribute to mtDNA depletion, and subsequently, to decreased assembly and activity of respiratory complexes in chagasic myocardium.

# 7.3. Structural abnormalities

The mutations in genes encoding structural and contractile proteins are frequently implicated in the pathogenesis of cardiomyopathies. Specific mutations in structural and contractile proteins, e.g. actin (132), desmin (133), sarcoglycan, and dystrophin (134), are identified in many cases of DCM and heart failure. Similarly, mutations in myofibrillar/sarcomeric proteins, e.g. β-myosin heavy chain (β-MHC), cardiac troponin T (cTnT), tropomyosin, and myosin binding protein C (MYBP-C) have been identified in cases of familial HCM (reviewed in (135)). *In vitro* and *in vivo* studies have confirmed mutations in β-

MHC, MYBP-C, actin and some other proteins are presented with excess production of mutated or normal protein that stimulate the phenotype of hypertrophy and fibrosis (135-137). In other cases, mutation in desmin and cTnT are shown to result in decreased protein expression, cardiac degeneration and impaired contractility (133, 138). Numerous ultrastructural studies have suggested potential association of intermediate filaments with mitochondria. The intracellular position and movement of mitochondria and meiosis-dependent mitochondrial rearrangement are suggested to be governed by cytoskeletal proteins (139). The interplay of mitochondrial defects with alterations in contractile and/or structural proteins is, therefore, worthy of note. For example, patients with defects in β-MHC expression are shown to exhibit a decline in respiration capacity consistent with a reduction in mitochondria number (140). Impaired energy metabolism is linked to gene mutations in β-MHC, cTnT and MYBP-C in hypertrophic cardiomyopathy patients (141). Intracellular distribution of mitochondria and respiratory function are profoundly altered with defects in desmin (142). In CCM patients, mutations in any of the structural and contractile proteins encoding genes are yet to be identified. However, studies document the morphological numerous modifications in the myofibers, and alterations in the expression of a variety of structural and contractile proteins in human patients and animal models of CCM development (79, 82) (unpublished results). The defective cellular location of mitochondria, a likely outcome of cytoskeletal have potential organizational abnormalities, may downstream effects on cardiac bioenergetic function and consequently contribute to cardiac pathophysiology in CCM patients.

# 8. PHYSIOLOGICAL EFFECTS OF MITOCHONDRIAL DYSFUNCTION

Three of the most important aspects of mitochondrial OXPHOS dysfunction for disease pathogenesis are i) energy depletion; ii) regulation of apoptosis or programmed cell death, and iii) oxidative stress. Whether mitochondrial dysfunction of OXPHOS pathway compromises the availability of energy for contractile and other metabolic functions in chagasic hearts, and whether mitochondrial release of ROS and/or cytochrome c contribute to apoptotic cell death in chagasic myocardium is not known and hopefully will be examined in future. I summarize the published literature addressing the sustenance of oxidative stress-induced damage in chagasic myocardium.

As discussed above, chagasic hearts are likely to be exposed to ROS of inflammatory and mitochondrial origin. To cope with free radicals, the myocardium contains high concentrations of various non-enzymatic antioxidants such as reduced glutathione (GSH) and vitamins A, C, and E, and enzymatic scavengers of ROS including glutathione peroxidase (GPx), glutathione reductase (GSR) and SOD (143). GSH, GPx, and SOD have been shown to be most critical in cardiac antioxidant defenses (144). These enzymes work in tandem to scavenge ROS. SOD is present in the cytoplasm, as well as on the endothelial cell surface

(Cu or ZnSOD) and in the mitochondria (MnSOD). The SOD catalyzes the dismutation of superoxide anion (O<sub>2</sub>) to H<sub>2</sub>O<sub>2</sub> that is reduced to H<sub>2</sub>O and O<sub>2</sub> by GPx. GPx scavenges H<sub>2</sub>O<sub>2</sub> in the presence of GSH to form H<sub>2</sub>O and oxidized glutathione (GSSG). GSR complements the action of GPx by converting GSSG to GSH (145). Under conditions of increased ROS production, or when the antioxidant system is compromised, cells are unable to efficiently scavenge the free radicals, resulting in ROS-induced oxidative stress (90, 107, 143, 146). The myocardial cells, when oxidatively stressed, may exhibit saturation of the antioxidant defenses, loss of intracellular redox homeostasis, alterations in cellular signaling, and induction of pathological processes (90, 91, 147, 148).

In a series of recent studies, us and others have addressed the oxidative status and antioxidant defense capabilities during the course of infection and progression of chagasic disease in human patients and experimental models. The demonstration of a selenium deficiency that increased with severity of chronic disease in chagasic patients (149) was probably the first observation suggesting that antioxidant deficiencies may be related to the progression of disease pathology. Further studies in experimental CCM models showed that selenium-depletion was associated with increased susceptibility, myocarditis severity, and heart damage (150), leading to higher mortality rate (151). The myocardial damage in infected mice was arrested or reversed upon dietary supplementation with low doses of selenium (152). Considering no effect on parasite burden was observed in animals depleted or supplemented with dietary selenium, the direct beneficial effects of selenium in protecting heart from inflammatory and/or oxidative damage was concluded. In other studies, the detection of inflammatory cytotoxic mediators (TNF-α and NO) along with a reduction in plasma levels of GPx and SOD in patients led to a suggestion that an oxidant/antioxidant imbalance may drive the chagasic disease pathology (153). We have shown that when antioxidant defense responses (constituted by GPx, GSR, and GSH) were of sufficient magnitude (e.g. in skeletal muscle), T. cruzi-induced oxidative stress and damage was controlled (103). However, myocardium appeared to be poorly equipped with antioxidant defenses. In response to T. cruzi, though a transient increase in antioxidant enzyme activities (SOD, GPx, GSR) and reductant (GSH) level was noted in the myocardium of infected mice, these responses subsided or decreased with disease development. Consequently, myocardium of infected animals sustained oxidative damage evidenced by consistent increase in oxidative stress biomarkers (LPO, PCO, GSSG) during the course of infection and chronic disease (103). Altogether, these studies imply that sustained ROS generation (of inflammatory and mitochondrial origin, discussed in section 7.1) coupled with inadequate antioxidant response resulting in inefficient scavenging of ROS in the heart leads to sustained oxidative damage of the cardiac cellular components during chagasic disease. A passive antioxidant response to increased oxidative stress is shown in experimental models of ischemia/reperfusion (154) and dicroceliosis (155), and human end stage heart failure (156). Future studies would determine whether

treatment with antioxidant mimics or pharmacological agents capable of enhancing the endogenous antioxidant defense response along with anti-parasite drugs would be promising avenues in preventing myocardial pathology in chagasic patients.

# 9. SUMMARY

Several factors may contribute to the pathogenic outcome of chagasic disease. Host inflammatory and immune responses are activated to control the parasite burden. During the process of parasite destruction, inflammatory mediators may also injure the host cellular and organelle components. Mitochondria being particularly susceptible to stress-mediated damage are probably affected most, resulting in mitochondrial abnormalities at the molecular, biochemical and functional level. The deficiencies of CI and CIII enzyme complex activities is likely to create a positive feed back cycle, as these complexes in addition to being sensitive to stress, are also the primary site of oxygen radical production, leading to progressively greater levels of oxidative stress and lowered mitochondrial function. The major physiological effects of the mitochondrial disorders are energy deficit and sustained ROS production, both of which can contribute to CCM pathogenesis. The current literature suggest that oxidative damage of cellular components (DNA, lipids, and proteins) contributes to mitochondrial respiratory chain dysfunction and sustained ROS generation, and subsequently may drive cell death and tissue damage in CCM. The promising areas of research that may yield practical benefits related to treatment of CCM include a critical evaluation of the role of mitochondrial ROS in activation of the signaling cascades (e.g. MAPKs) that may be involved in instigation of cardiac hypertrophy and remodeling responses, and cellular damage. Future studies geared to testing the usefulness of therapies capable of enhancing mitochondrial function, antioxidant efficiency, or ROS scavenging in combination with antiparasite drugs will provide convincing evidence to link the oxidative stress as a causative mechanism in the development of CCM. These studies will also provide a clue to the upstream and downstream events in redox-induced cardiac pathology and suggest the usefulness of antioxidant therapies in arresting the severity of chagasic pathology.

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