TRYPANOSOMA CRUZI DNA IN CARDIAC LESIONS OF ARGENTINEAN PATIENTS WITH END-STAGE CHRONIC CHAGAS HEART DISEASE

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Abstract. The extent of inflammation, fibrosis, and progression of chronic Chagas heart disease (cChHD) was associated with persistence of parasite DNA in cardiac lesions of necropsies or explants from Argentinean cChHD patients. A Trypanosoma cruzi–based polymerase chain reaction showed a positive result in 1) 15% of cardiac sections with less than 10 mononuclear inflammatory cells/high-power field (440x) (MNC/HPF), 89% with 10–19 MNC/HPF, and 100% with more than 20 MNC/HPF (P < 0.0001); 2) 33% with less than 10% fibrosis, 79% with 10–19% fibrosis, and 100% with more than 20% fibrosis (P < 0.01); 3) 25% of specimens from patients classified in Kuschnir groups 0 and I, 70% in group II and 90% in group III (P < 0.01); and 4) 45% and 90% of the specimens from cChHD patients without or with heart failure, respectively (P < 0.01). These findings stress the role of the parasite in pathogenesis and disease progression of cChHD.

INTRODUCTION
Chagas disease is the main cause of chronic myocarditis in Latin American countries, where the disease is endemic, affecting approximately 20 million people.1 Fifty thousand chagasic patients die every year, mainly due to a chronic cardiomyopathy that is clinically evident only 10–30 years after the initial infection.2

Chronic Chagas heart disease (cChHD) evolves gradually from an asymptomatic period with radiographic or electrocardiographic manifestations known as the indeterminate phase, and progresses slowly to a dilated cardiomyopathy manifested by arrhythmias, left ventricular dysfunction, embolic episodes, and autonomic dysfunction.2,3 The apical aneurysm is found to be a distinctive pathologic marker in more than 50% of symptomatic patients.4

In general, the cause of death is heart failure or thromboembolic phenomena. Anatomically, the heart of a patient with cChHD is characterized by myocardial damage associated with mononuclear inflammatory foci scattered throughout the organ.2,4 The coexistence of areas of myocytic degeneration, inflammatory infiltration, and fibrosis suggests a chronically evolving process. The lesions are progressive, self-perpetuating, and cumulative.

Since the intracellular forms of the parasite (Trypanosoma cruzi) that cause this disease are rarely found at the sites of the heart lesions, the hypothesis of an autoimmune process has been proposed as a leading mechanism of cChHD pathogenesis.5,6 However, polymerase chain reaction (PCR) amplification and immunohistochemical techniques showed the presence of parasite DNA and proteins close to the inflammatory foci in lesions found in cardiac and digestive tissue from patients infected in endemic areas in Brazil and Venezuela.6–11

In this study, we applied the PCR technique to analyze the proportion of sections containing parasite DNA in left ventricular free walls or cardiac apexes collected from heart necropsies or explants in cChHD patients from Argentina who died at different stages of heart disease progression. The combination of clinical, electrocardiographic, histologic and PCR-based analysis enabled us to demonstrate a significant association between the detection of parasite DNA with inflammation, fibrosis, and clinical progression of cChHD.

MATERIALS AND METHODS

Study groups. Hearts from three groups of patients collected at necropsy and from transplant recipients were studied. Group A included hearts from six cChHD patients without symptoms of heart failure (HF). Group B included hearts from 10 patients with severe cChHD (New York Heart Association functional classes III and IV) who had died or were treated with heart transplants. Group C (control group) included hearts from six patients with non-chagasic cardiomyopathy (DCM) with HF (New York Heart Association functional classes III and IV) at the time of death or heart transplantation. Chronic ChHD and DCM patients were followed-up by the Service of Chagas Disease of the Department of Cardiology, Hospital Eva Perón (San Martín, Buenos Aires, Argentina). The patients had undergone heart transplantation at the Instituto de Cardiología y Cirugía Cardiovascular, Fundación Favaloro in Buenos Aires. The diagnosis of Chagas disease relied on positive results in at least two of three conventional serologic assays: complement fixation, indirect hemagglutination, and indirect immunofluorescence. This study was reviewed and approved by the Biomedical Ethics Committee of the Instituto de Cardiología y Cirugía Cardiovascular de la Fundación Favaloro and that of the Eva Perón Hospital. Patients undergoing heart transplants gave informed consent to have their explanted hearts analyzed. The other heart specimens included in the study were obtained from necropsy specimens that were retrospectively analyzed.

On admission, cChHD patients were clinically classified according to the criteria of Kuschnir into four groups: 0 (positive serology only), I (abnormal electrocardiogram [ECG]), II (radiologic heart enlargement), and III (overt signs of heart failure).12 At the time of death or heart transplantation the patients were reclassified based on the progression of the cardiomyopathy. Such progression was determined according to 1) development of new electrocardiographic changes (NEC): right bundle branch block (RBBB), left anterior fascicular block (LAFB), RBBB plus LAFB, left bundle branch
right auricular enlargement. AVB1° enlargement; RVH/LVH block; VPC

Table 2). From each selected histologic section, a 5 μm–thick slice was stained with hematoxylin and eosin and Masson’s trichrome. Twenty high-power fields (HPFs) were examined at 400× magnification: five of the subepicardial myocardium, five of the outer mesocardium, five of the inner mesocardium, and five of the subendocardium.

The number of mononuclear cells (MNC) and the percentage of fibrosis were determined on each HPF using an eye piece mounted grid with a surface of 0.05 mm². The degree of myocarditis was defined for each heart according to the Dallas criteria. Samples were fixed in 10% buffered formaldehyde and embedded in paraffin. After evaluation of all histologic heart tissue sections, we selected two from each heart, one with the lowest degree of inflammation (section a, Table 2) and the other one with the highest degree (section b,

### Collection of histologic heart sections

Transmural sections at the apex, atrium and the whole circumference of the third cut were collected in all hearts, according to the procedures of Edwards and others. Samples were fixed in 10% buffered formaldehyde and embedded in paraffin. After evaluation of all histologic heart tissue sections, we selected two from each heart, one with the lowest degree of inflammation (section a, Table 2) and the other one with the highest degree (section b,

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The histologic sections were classified in three categories, those with mild fibrosis (less than 10%), those with moderate fibrosis (between 10% and 20%), and those with severe fibrosis (more than 20%).

To compare the number of MNC/HPF and the volume fraction of the fibrosis between patient groups, we analyzed one section of the left ventricular free wall region from each heart. In cases where two sections of the left ventricular free wall were previously selected, we analyzed the one with the highest degree of inflammation.

**Polymerase chain reaction.** Two to five 10 μm–thick serial tissue specimens consecutive to the section stained for histology analysis were transferred into sterile polypropylene microtubes (Eppendorf AF, Hamburg, Germany) for isolation of DNA. To avoid cross-contamination between samples, sterile disposable instruments and gloves were used during handling. The DNA was extracted using the QiAmp tissue kit (Qiagen, Valencia, CA) following the manufacturer’s recommendations for paraffin-embedded tissues, as previously reported.

Because the tissues were obtained from archival specimens, some of them from necropsies collected more than 10 years ago, the integrity of the purified DNA was firstly verified by the amplification of a human β-globin gene fragment, as reported previously. Accordingly, we searched for *T. cruzi* DNA only in those samples that were found to be positive by a β-globin gene-based PCR.

A hot-start PCR procedure targeted to the 330-basespair minicircle fragment of the *T. cruzi* kinetoplast genome was performed in 50-μL reactions using PCR tubes containing wax beads (Molecular BioProducts, Inc., San Diego, CA). The 12-μL lower mixture carried 2 μL of 25 mM MgCl₂, 5 μL of 2.5 mM of each deoxynucleotide triphosphate (Promega, Madison, WI), 1.5 μL of 50 μM of primers 121 (5′-AAATAATGTCAGGG(T/G)GAGATGCATGA-3′) and 122 (5′-GGTTCATTGGGTT GGTGTAATATA-3′), and 1.2 μL of 10× *Taq* buffer ( Gibco-BRL, Gaithersburg, MD). The 33-μL upper mixture contained 4 μL of 25 mM MgCl₂, 3.3 μL of 10× *Taq* buffer, 1.25 units of *Taq* DNA polymerase (Gibco-BRL), and 5 μL of specimen DNA. Amplification was performed in a MJR PTC-100 thermocycler (MJ Research, Inc., Waltham, MA) under the conditions previously reported. The PCR products were analyzed by 3%
agarose gel electrophoresis followed by Southern hybridization, as previously reported.\textsuperscript{18} The results obtained by the kinetoplast DNA (kDNA)–PCR on the serial tissue specimens consecutive to the histologic heart section were scored as 1 if at least one of them amplified \textit{T. cruzi} kDNA or as 0 if all the tested specimens were PCR negative (Table 2).

In addition, a nested PCR procedure targeted to the 435-basepair short interspersed repetitive element (SIRE)\textsuperscript{19} of the nuclear genome of \textit{T. cruzi} was assayed in the heart sections obtained from two group B patients (cases 9 and 12, Table 1). The first round of the SIRE PCR was carried out in a 50-\mu L volume reaction containing 15 pm of primers SIs (5'-GGAGAGCTGGCTAACTTAAT-3') and SIna (5'-GGGGTCCTCCTCAACACAGAC-3') using the following cycling conditions: one cycle at 94°C for five minutes and 58°C for two minutes, followed by 35 cycles at 72°C for one minute, 94°C for one minute, and 58°C for one minute, and a final step at 72°C for seven minutes. The second round of SIRE PCR was carried out in a 50-\mu L volume reaction with 15 pm of primers Slns (5'-GTATGAATCTTTTGGGAA-GAAC-3') and SIna (5'-TTACTTACGAAGTGGCA-GACT-3') using the following cycling conditions: one cycle at 94°C for five minutes and 55°C for two minutes, followed by 35 cycles at 72°C for one minute, 94°C for one minute, and 55°C for one minute, and a final step at 72°C for 10 minutes. The SIRE PCR products were visualized by UV light after electrophoresis in ethidium bromide–stained 3% agarose gels.

Negative controls for each PCR consisted of specimen preparation reagents without DNA. Positive specimen controls consisted of 10-\mu m serial brain tissue specimens obtained from a necropsy of a patient with acquired immunodeficiency syndrome who died of chagasic meningoencephalitis. Purification of DNA from tissue specimens, assembling of reagent mixtures, cycling, gel electrophoresis, and hybridization procedures were carried out in different laboratory working areas. The PCR was carried out blinded to the clinical and/or the histologic findings.

**Statistical analysis.** Continuous variables were analyzed by one-way analysis of variance (ANOVA) and unpaired \textit{t}-tests when appropriate. Categorical variables were compared by the chi-square test and Fisher's exact test. The number of inflammatory cells and the area of fibrosis in the histologic heart sections were expressed as median values. The agreement between inflammation and fibrosis was studied using the Spearman correlation coefficient. The Kruskal-Wallis one-way ANOVA was used to test the differences between groups. The Mann-Whitney \textit{U} test was used to evaluate the agreement between the median value of inflammatory cell counts and the median percentage of fibrosis with the PCR scores in each heart tissue block. \textit{P} values < 0.05 were considered statistically significant. The pathologic and clinical data were analyzed using the SPSS\textsuperscript{\textregistered} 6.1 statistical analysis software for Windows (SPSS, Inc., Chicago, IL).

**RESULTS**

**Clinical features of the study groups.** Group A was composed of six cChHD patients, four males and two females, with a mean ± SD age of 54.83 ± 11.58 years, without evidence of HF at the moment of death. The mean ± SD time of follow-up was 864.2 ± 981.9 days (Table 1).

Group B was composed of 10 cChHD patients, five males and five females, with a mean ± SD age of 50.60 ± 14.37 years, with evidence of HF as cause of death or indication for heart transplantation. The mean ± SD time of follow-up was 968.6 ± 925.8 days and the mean ± duration of the clinical symptoms of heart failure was 17.80 ± 9.55 months (Table 1).

Group C was composed of six patients with DCM, four males and two females, with a mean ± SD age of 47.50 ± 13.68 years, with HF at the moment of death or heart transplantation. The mean ± SD time of follow-up was 426.67 ± 319.2 days and the mean ± SD duration of the clinical symptoms of heart failure was 25.67 ± 17.47 months (Table 1). The mean ages, time of follow-up, and period with heart failure were similar among groups B and C (Table 1).

During monitoring of the cChHD patients, new electrocardiographic changes (NECs) were detected in two of six cases in group A and in all patients in group B (\textit{P} = 0.008). Conversely, an NEC occurred only in one of six cases in control group C, a significant difference when compared with the NECs found in group B (\textit{P} = 0.001). No deterioration of the clinical group was detected in group A; however, a clinical deterioration occurred in 3 of 10 patients in group B (\textit{P} not significant). The causes of death or heart transplantation for all patients are shown in Table 1.

**Histopathologic findings.** The mean ± SD heart weight was 467.5 ± 170.0 grams, 490.5 ± 114.7 grams, and 587.5 ± 200.0 grams in groups A, B, and C respectively (\textit{P} not significant) (Table 2). We observed borderline myocarditis in three of 16 hearts and active myocarditis in 12 of 16 hearts from cChHD patients. In contrast, only two of six DCM hearts presented borderline myocarditis and none had active myocarditis (Table 2). The morphometric data for inflammation and fibrosis are shown in Table 2. There was a positive correlation between the inflammation and fibrosis measured in the histologic heart sections of patients with Chagas disease (Spearman correlation coefficient = 0.388, \textit{P} < 0.001).

A comparison between the median intensity of heart tissue inflammation and the percentage of fibrosis, as measured in the left ventricular free wall sections of the hearts from groups A, B, and C is shown in Figure 1. The median number of MNC/HPF in left ventricular wall specimens in group A (11, range = 11–16) was significantly lower than in group B (31, range = 17–53) (\textit{P} = 0.039) (Figure 1A). The percentage of fibrosis in the same left ventricular wall sections was 15.5% (range = 6–18%) in group A and 20.5% (range = 15–30%) in Group B (\textit{P} not significant) (Figure 1B). The comparison of inflammation between sections from groups B and C showed significant differences; we observed a median value of 31 (range = 17–53) MNC/HPF in group B compared with 7 (range = 6–11) MNC/HPF in group C (\textit{P} = 0.005) (Figure 1A). The percentage of fibrosis in group C was 10.5% (range = 9–12%), which was significantly lower than that measured in group B (\textit{P} = 0.005) (Figure 1B). No significant differences in inflammation and fibrosis were observed between groups A and C (Figure 1A and B).

The intensity of inflammation and fibrosis was also evaluated in the four layers of the myocardium (Figure 1C and D). In the subepicardium, group B showed higher MNC/HPF counts and a higher percentage of fibrosis than groups A and C (\textit{P} < 0.001). In the outer myocardium, group B specimens showed higher counts of MNC/HPF than those in groups A or C (\textit{P} < 0.001) and a higher percentage of fibrosis than those in groups A or C (\textit{P} < 0.001). In the inner myocardium,
group B specimens showed higher counts of MNC/HPF than those in groups A or C ($P < 0.001$) and a higher percentage of fibrosis than those in groups A ($P < 0.01$) or C ($P < 0.001$). Interestingly, sections from the outer and inner mesocardium of group A patients contained a higher number of MNC/HPF than group C ($P < 0.001$ and $P < 0.01$, respectively), but there were no differences in the percentage of fibrosis. In the subendocardium, group B specimens showed slightly more inflammation than group C ($P = 0.045$), but there were no differences when compared with group A ($P$ not significant) (Figure 1C). Group B samples showed more fibrosis than those from groups A ($P < 0.01$) or C ($P < 0.01$), but there were no differences between groups A and C (Figure 1D). As shown in Figure 1D, in cChHD, the fibrosis was higher in the mesocardial layers, whereas in DCM the subendocardium was more involved.

The appearance of NECs in all patients (groups A, B, and C) correlated with inflammatory infiltration in the LV wall samples (Spearman correlation coefficient = 0.578, $P < 0.01$), as well as with the percentage of fibrosis ($\rho = 0.620$, $P < 0.005$).

Detection of *T. cruzi* DNA by PCR. We tested for the presence of *T. cruzi* DNA in serial tissue specimens consecutive to the section stained for morphometric analysis from each selected heart tissue block (sections a and b, Table 2). One hundred nineteen specimens were processed for PCR analysis; 82 were positive for amplification of the human $\beta$-globin gene (Table 2) and were further analyzed by the kDNA-based PCR. Parasite kDNA amplicons were obtained from 53 (75.7%) of 70 tissue specimens tested (Table 2) from 15 of the 16 hearts from patients with Chagas disease analyzed in this study. The only heart sections for which no parasite DNA could be amplified were those from case 1, a patient with positive serologic test results for Chagas disease but without clinical or histologic signs of myocarditis (Table 2 and Figure 2A and lane 1). None of the 12 heart specimens from hearts of DCM patients were positive for *T. cruzi* kDNA (Table 2).

The PCR results observed after agarose gel electrophoresis (I) and hybridization with a *T. cruzi* kinetoplast radioactive probe (II) are shown in Figure 2. Nucleic acids were obtained from preparations of tissue specimens consecutive to the
stained sections shown in Figure 2. Two cases from group A are shown in Figure 2A, B, and C. Figure 2, lane 1 shows the only example in which no parasite DNA could be amplified from heart sections of case 1 (Tables 1 and 2 and Figure 2A), a patient who died in the indeterminate phase of Chagas disease, without any evidence of myocarditis. Figure 2, lanes 2 and 3 show that for patient 3 (Table 1) parasite DNA was amplified only from the tissue section with the highest degree of inflammation (Figure 2C and Table 2, histologic section 3b).

Four PCR results from patients in group B are shown in Figure 2D–H. Patient 7 was a 48-year-old man admitted into clinical group I who had clinical deterioration and was reasigned to Kuschnir’s group III (Table 1). The histologic analysis of the heart tissue sections from the left ventricular free wall (Figure 2D and Table 2, histologic section 7b) showed evidence of active myocarditis; parasite kDNA was obtained from all the tested serial tissue specimens (Figure 2, lane 4).

Case 9 was a 54-year-old woman who was admitted into clinical group II, progressed to clinical group III, and died after a rapid onset of symptoms of HF. The histologic sections from her heart showed active myocarditis (Table 2, histologic section 9b and Figure 2E) with evidence of T. cruzi kDNA (Figure 2, lane 5). Patient 14 died of heart failure at age 27 (Figure 2F). In the left ventricular free wall from his heart necropsy, all tested serial samples were PCR positive (Table 2, histologic sections 14a and 14b and Figure 2, lane 6). Interestingly, amastigote nests were detected in another histologic section, adjacent to the ones analyzed by the PCR. Case 16 was a 46-year-old woman who underwent a heart transplant. Her explanted heart showed regions with very low counts of inflammatory cells (Figure 2G and H); however, parasite DNA was found in specimens consecutive to the histologic section with myocarditis (Figure 2H, lane 8). In Group C, parasite kDNA was not detected in any DCM control specimen, as shown in Figure 2I, lane 9 (case C in Table 2). The result of the kDNA PCR was negative for DNA samples extracted from archival specimens of brain, lung, kidney, and liver collected at necropsies from cases 3, 6, 14, and 16.

Six tissue sections positive for T. cruzi kDNA from patients 8, 9, 10, 11, 12, and 14 were further tested for the presence of the nuclear, multicopy SIRE. A nested PCR procedure resulted in the amplification of a 230-basepair SIRE fragment from two heart samples (cases 9 and 12, Table 2). The amplicon from case 9 was sequenced and aligned with those from parasite strains CL-Brenner and Tulahuen II, as well as with SIRE sequences amplified from two endomyocardial biopsy specimens (Figure 3).

Association of inflammation and fibrosis with T. cruzi DNA in heart lesions. The degree of inflammation and fibrosis in the histologic sections was associated with the detection of T. cruzi kDNA by PCR (Figure 4). Heart sections were classified into three categories according to the MNC counts and the percentage of fibrosis (see Materials and Methods). Accordingly, the PCR result was positive in 1) serial tissue samples derived from only one (15%) of seven heart sections with low inflammation collected from hearts 1–4, 8, and 10 (Table 2), 2) eight (89%) of nine sections with moderate inflammation (Figure 2, lane 4 and micrograph D from case 7), collected from hearts 2, 4–7, 11, 12, and 16 (Table 2), and 3) all 14 (100%) sections with high inflammation (Figure 2, lane 3 and micrograph C; lane 6 and micrograph F), collected from hearts 3, 7, and 9–16 (Table 2) and Figure 4) (P < 0.0001).

The association of inflammation with detection of T. cruzi DNA was also observed when histologic sections with different degrees of inflammation from the same heart were compared. Accordingly, in cases 2 and 3 in group A and cases 10 and 16 in group B, parasite DNA was amplified only from...
those sections with the highest MNC counts (Figure 2, case 16, lane 7 and micrograph G; lane 8 and micrograph H).

Parasite DNA was also linked with the degree of fibrosis found in the same tissue sections. It was detected in serial samples from two (33.3%) of six sections with mild fibrosis collected from hearts 1, 2, 5, and 16, in 11 (78.6%) of 14 sections with moderate fibrosis collected from hearts 3–6, 10, 12, 13, and 16, and in all 10 sections (100%) with severe fibrosis collected from hearts 7–9, 11, 14, and 15 (P < 0.01) (Figure 4).

**Parasite DNA and apical aneurysm.** Heart sections from cardiac apexes of cases 1 and 2 of Group A (Kuschnir’s Group 0) as well as cases 7 and 15 from Group B (Kuschnir’s Group III) were tested by kDNA based PCR. In apical samples from Group A cases there were no evidences of parasite DNA, whereas in those from Group B cases the PCR results were positive (Table 2).

**Association of** *T. cruzi* **kDNA with cause of death or transplantation and disease progression.** The proportion of serial tissue specimens containing *T. cruzi* kDNA was 45% (10 of 22) in group A and 89.6% (43 of 48) in group B (P < 0.001) (Figure 5). Furthermore, the PCR result was positive in 25% (3 of 12) of the heart specimens from Kuschnir’s groups 0 and I, in 70% (7 of 10) of the samples from group II, and in 90% (43 of 48) of the samples from Group III (P < 0.001) (Figure 5). Moreover, parasite DNA was detected in all patients who showed clinical deterioration evolving to Kuschnir’s group III (Table 2).

**DISCUSSION**

We investigated the association between the clinical, ECG data, and heart histologic features of followed-up cChHD and DCM patients with the evidence of parasitic DNA at the sites of cardiac lesions. When histologic specimens from the hearts of cChHD and DCM patients with HF with similar mean ages, times of follow-up, and New York Heart Association classes (Tables 1 and 2) were compared, we confirmed the far more intense myocarditis and fibrosis in cChHD associated with parasitic DNA, in contrast to the scarcity of inflammation and negative *T. cruzi* PCR findings in DCM patients (Figure 1A and B).
the coronary vessels, contacting the epicardium (Figure 1C). The distribution of fibrosis in the myocardial layers of cChHD with HF followed the pattern of inflammation, which was clearly not the case for DCM. Indeed, heart sections from cChHD patients showed more fibrosis in the mesocardium, whereas in DCM patients the subendocardium seemed to be more involved (Figure 1D), probably as a consequence of the disturbance of oxygen supply and demand.25–27

The appearance of NECs during follow-up is a striking characteristic of cChHD.2 The progression of ECG abnormalities was reported to be approximately 20–25% in longitudinal population studies of individuals chronically infected with T. cruzi for seven or more years.28–30 In this study, NECs were detected in 100% of cases in group B, in 30% of cases from group A, and in only 17% in group C. Remarkably, in group B the ECG evolution was associated with heart failure and death, with heart tissue necropsies showing diffuse and fibrosing myocarditis, which are typical signs of end-stage cChHD that all linked to the detection of parasite DNA.

The paucity of parasite nests in hearts of cChHD patients led several investigators to discard a role for the parasite in its pathogenesis.6,17,31 In certain series of necropsies, amastigote nests were identified in only 25–36% of the hearts.21,32,33 However, immunohistochemical analysis using monoclonal antibodies to T. cruzi allowed detection of T. cruzi antigens in 71% of the cardiac regions with moderate or severe myocarditis and in only 16.6% with mild or absent myocarditis.7 Moreover, a significant correlation between the presence of parasite antigens and increased CD8 T cell counts has been also reported.34

The PCR has shown the presence of nuclear and kinetoplastid sequences from the parasite in biopsy or necropsy specimens from hearts and digestive tissues of patients with
chronic Chagas disease from endemic regions of Brazil and Venezuela. In the present study, amastigote nests were detected in only one heart tissue block (case 14 in group B), whereas the PCR amplified the highly repetitive kinetoplastid minicircle sequence in 15 of 16 heart necropsy specimens (Table 2). For the first time, the middle repetitive nuclear element known as SIRE has been amplified from an eight-year-old heart preparation and sequenced (Figure 3). The characterization of T. cruzi nuclear DNA sequences from these archival necropsy specimens, as well as those from heart biopsy specimens, provide a starting point to determine the genomic structure of the parasite populations associated with the human tissue lesions.

Our study suggests that there is a strong association between the histologic evidence of heart tissue damage and T. cruzi amplicons. Indeed, there was a significant correlation between the number of tissue sections positive by PCR and the intensity of heart inflammation, as well as fibrosis at the corresponding cardiac lesions (Figure 4). The proportion of PCR-positive sections increased in patients who died or received a heart transplant due to HF (group B) compared with those from patients who had died of other causes (group A) (Figure 5). This finding suggests that the transition from a chronic asymptomatic period of the disease, represented by infected individuals with the clinical profile of group A patients, to manifest cChHD, the clinical profile of group B patients, is directly associated with the detection of parasite DNA in the affected tissues. Moreover, amplification of specific parasite DNA sequences was linked to clinical deterioration (Figure 5).

The absence of intact parasites at the sites of inflammation suggests that microorganisms invading the myocardium are rapidly destroyed, probably immunologically, whereas DNA
and antigens may be still detected at the sites of injury. Based on experimental evidence showing that parasite DNA did not persist for more than two days in murine-infected tissues, PCR findings appear to indicate intact or recently destroyed parasites, rather than mere residual DNA. The positive correlation between parasite DNA in tissue lesions and inflammation, fibrosis, and disease progression and severity suggests that during the chronic infection the parasite contacts the heart at different times and locations, invoking an immunologic response at these sites. As a direct consequence, parasites are lysed, the surrounding tissue is damaged, and replacement fibrosis ensues. The accumulation of these multifocal lesions, mainly in the left ventricular wall, leads to cardiac dysfunction. Moreover, heart damage may be also enhanced by the humoral immune response of the patient against intracellular parasite antigens, such as the T. cruzi ribosomal P proteins, which generates arrhythmogenic antibodies.

In conclusion, these results suggest not only a relevant role of the parasite in the pathogenesis and disease progression of cChHD, but also a need to develop novel anti-parasitic drugs, with sufficient efficacy to clear intracellular parasites, thus preventing the progression of heart disease.

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