

Monocyte glycolysis determines CD8+ T-cell functionality in human Chagas disease

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Research

In-Press Preview

Immunology

Metabolism

Chagas disease is a life-long pathology resulting from *Trypanosoma cruzi* infection. It represents one of the most frequent causes of heart failure and sudden death in Latin America. Herein we provide evidence that aerobic glycolytic pathway activation in monocytes drives nitric oxide (NO) production, triggering tyrosine nitration (TN) on CD8 T cells and dysfunction in patients with chronic Chagas disease. Monocytes from patients exhibited higher frequency of hypoxia inducible factor (HIF)-1 α and increased expression of its target genes/proteins. Non-classical monocytes are expanded in patients' peripheral blood and represent an important source of NO. Monocytes entail CD8 T cell surface nitration since both the frequency of non-classical monocytes and that of NO-producing monocytes, positively correlated with the percentage of TN⁺ lymphocytes. Inhibition of glycolysis in (in vitro) infected peripheral blood mononuclear cells decreased the inflammatory properties of monocytes/macrophages diminishing the frequency of IL-1 β - and NO-producing cells. In agreement, glycolysis inhibition reduced the percentage of TN⁺CD8 T cells improving their functionality. Altogether, these results clearly evidence that glycolysis governs oxidative stress on monocytes and modulates monocyte-T cell interplay in human chronic Chagas disease. Understanding the pathological immune mechanisms that sustains inflammatory environment in human pathology is key to design improved therapies.

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42 **Abstract**

43 Chagas disease is a life-long pathology resulting from *Trypanosoma cruzi* infection. It
44 represents one of the most frequent causes of heart failure and sudden death in Latin
45 America. Herein we provide evidence that aerobic glycolytic pathway activation in
46 monocytes drives nitric oxide (NO) production, triggering tyrosine nitration (TN) on CD8 T
47 cells and dysfunction in patients with chronic Chagas disease. Monocytes from patients
48 exhibited higher frequency of hypoxia inducible factor (HIF)-1 α and increased expression of
49 its target genes/proteins. Non-classical monocytes are expanded in patients' peripheral
50 blood and represent an important source of NO. Monocytes entail CD8 T cell surface
51 nitration since both the frequency of non-classical monocytes and that of NO-producing
52 monocytes, positively correlated with the percentage of TN⁺ lymphocytes. Inhibition of
53 glycolysis in (in vitro) infected peripheral blood mononuclear cells decreased the
54 inflammatory properties of monocytes/macrophages diminishing the frequency of IL-1 β - and
55 NO-producing cells. In agreement, glycolysis inhibition reduced the percentage of TN⁺CD8 T
56 cells improving their functionality. Altogether, these results clearly evidence that glycolysis
57 governs oxidative stress on monocytes and modulates monocyte-T cell interplay in human
58 chronic Chagas disease. Understanding the pathological immune mechanisms that sustains
59 inflammatory environment in human pathology is key to design improved therapies.

60

61 **Introduction**

62 Monocytes are critical components not only of the innate immune system but also of
63 adaptive immune response development. Based on the relative surface expression of LPS
64 co-receptor CD14 and of FcγIII receptor CD16, they have been classified into three
65 subtypes: “classical monocytes” (CD14⁺⁺CD16⁻), “non-classical monocytes” (CD14⁺CD16⁺⁺),
66 and “intermediate monocytes” (CD14⁺⁺CD16⁺) (1, 2). So far, however, there is poor
67 understanding of the effector functions of each monocyte subset and numerous reports
68 show contradictory results (3).

69 Under hypoxic or inflammatory conditions, monocytes activate transcriptional
70 responses, which are governed by the transcription factor hypoxia-inducible factor (HIF)-1α.
71 The accumulation of HIF-1α protein requires the metabolism of glucose into pyruvate that
72 prevents the aerobic degradation of HIF-1α protein. HIF-1α-target genes include glucose
73 transporters GLUT-1 and GLUT-3 (4-6). Glucose can be used throughout two integrated
74 pathways, the first of which, the glycolytic pathway, involves the cytoplasmic conversion of
75 glucose into pyruvate, with the consequent generation of 2 ATP molecules and, in anaerobic
76 conditions, lactate. Extracellular ATP (eATP) and lactate activate HIF-1α (7, 8), thus
77 resulting in a positive feedback. The second pathway, the tricarboxylic acid cycle, generates
78 the reducing equivalents nicotinamide adenine dinucleotide (NADH) and flavin adenine
79 dinucleotide (FADH₂), which donate electrons to the electron transport chain to fuel
80 oxidative phosphorylation (OXPHOS), the process by which 32 ATP molecules are
81 generated in the mitochondria.

82 In inflammatory settings, the OXPHOS is inhibited by nitric oxide (NO) production in
83 monocyte-derived inflammatory dendritic cells (moDC) in an autocrine manner. In the
84 absence of active respiratory chain, sustained glycolytic metabolism is essential for moDC
85 survival and function (9). Furthermore, NO production seems to be central in orchestrating
86 HIF-1α responses by inducing its stabilization and transcriptional activation (10).

87 Chagas disease, a complex pathological condition resulting from *Trypanosoma cruzi*
88 infection, has become one of the most frequent causes of heart failure, cardio-embolic
89 stroke and sudden death in Latin America (11). The acute phase lasts 2 to 3 months and is
90 characterized by detectable parasitemia and active parasite replication within target tissues.
91 However, clinical symptoms are usually mild and non-specific and the vast majority of acute
92 infections are never detected. During this phase, cell-mediated immunity controls parasite
93 levels, but it is insufficient to completely clear the infection and most individuals remain
94 infected for life. People who survive the acute phase enter a chronic asymptomatic phase
95 (indeterminate stage), which is generally symptomless and may last from 10 to 30 years.
96 Approximately 30% of patients in this period, also recognized as “silent”, may develop heart
97 abnormalities (12) that could give rise to the cardiac form of chronic infection. Although anti-
98 parasitic therapy is clearly recommended for acute Chagas disease, the treatment of
99 patients in the chronic stage is controversial. This is largely due to a lack of large,
100 randomized trials and incomplete understanding of pathological immune mechanisms
101 developed during this stage. After decades of controversies, it is widely accepted nowadays
102 that parasite persistence is a necessary and sufficient condition for the sustained
103 inflammatory responses underlying the progression of cardiac lesions of chronic Chagas
104 disease (13-18). Thus, one of the main challenges in understanding Chagas myocarditis
105 immunopathology is to find out why, despite a robust immune response during the acute
106 phase of the infection, the parasite is not completely eliminated, being able to sustain
107 pathological inflammatory environment.

108 Cell-mediated immunity involves activation of phagocytes and of cytotoxic T-
109 lymphocytes (CTLs). In this sense, we have recently reported increased IL-1 β plasma levels
110 concomitant with enhanced frequency of NO-producing leukocytes and the surface nitration
111 of CTLs associated with decreased functionality of this T cell compartment in the peripheral
112 blood from patients with Chagas disease in the indeterminate phase (19). In this study we

113 went deeper by exploring how metabolism affects the monocyte compartment and T cell
114 functionality during this human infectious disease. We have found that the non-classical
115 monocyte subpopulation expanded in the peripheral blood of both asymptomatic and
116 symptomatic chronic Chagas disease patients, being this subset an important source of NO
117 production. Additionally, total monocytes from Chagas disease patients exhibited higher HIF-
118 1 α expression, glucose uptake and glycolytic activity relative to control donors. In
119 agreement, glycolysis inhibition decreased IL-1 β and NO production in *T. cruzi*-infected
120 peripheral blood mononuclear cell (PBMCs) cultures and diminished T-cell nitration. Thus,
121 the CTLs dysfunction observed in infected individuals is associated to the metabolic pathway
122 activated in the monocyte compartment.

Results

Chagas disease patients have increased frequencies of NO⁺ and HIF-1 α ⁺ monocytes

Peripheral blood samples from 40 patients with Chagas disease and 55 from control donors of both sexes were collected and tested for *T. cruzi*-specific antibodies by ELISA and IHA (Table 1). The median value for anti *T. cruzi* antibody titer was 1/256 (local cutoff titer 1/32) detected by IHA. Patients were grouped according to Kuschmir classification (20): The 88% (35/40) of patients were grouped into group 0, 10% (4/40) into group 1, and 2% (1/40) into group 3.

To identify the main cellular source of NO from circulating leukocytes, we measured NO production in polymorphonuclear cells (PMNCs) and monocytes by flow cytometry following the gating strategy depicted in Figure 1A. Patients with Chagas disease exhibited higher frequency of NO-producing monocytes but no differences were detected in the percentage of NO-producing PMNCs relative to control donors (Figure 1B). Furthermore, the production of ROS by monocytes and PMNCs was similar between both groups (Supplementary Figure 1). Notably, no significant differences were found in the percentages of NO- and ROS-producing monocytes comparing patients in the asymptomatic phase (G0) versus symptomatic patients (G1-G3) ($p = 0.83$ and $p > 0.99$ respectively). Since NO production results from inducible NO synthase (iNOS) activity and this enzyme is a HIF-1 α -target molecules, we evaluated HIF-1 α protein expression in the monocyte population by flow cytometry. We have found that patients with Chagas disease exhibited increased frequency of HIF-1 α ⁺ monocytes in comparison with control donors, although the molecular expression levels per cell (MFI) remained unchanged (Figure 1C).

Despite the fact that hypoxia could activate an inflammatory response, HIF-1 α activation leads to increase extracellular adenosine production as an essential endogenous anti-inflammatory mediator to protect tissue damage (21). Adenosine is originated from the sequential dephosphorylation of eATP, mainly by the subsequent action of CD39 and CD73

ecto-enzymes (22, 23). In line with this, we observed increased plasmatic ATP levels (Figure 1D), associated with higher frequency of circulating monocytes expressing CD39 in *T. cruzi*-infected patients compared to control donors but, we found similar expression of this ecto-enzyme per cell (MFI) in both studied groups (Figure 1E). Although we did not observe differences in the percentage of CD73⁺ monocytes, interestingly a higher MFI of this enzyme was detected in monocytes from seropositive patients (Figure 1F).

Monocytes from *T. cruzi*-infected patients exhibit increased functional activity

Following the gating strategy described in Figure 2A, we found that monocytes from patients showed increased frequency of IL-1 β , IL-6 and IL-10 production compared to control donors in response to in vitro stimulation with the pro-inflammatory stimulus (LPS). Moreover, the amount of IL-1 β and IL-6 (measured as MFI), were also significantly increased in monocytes from *T. cruzi*-infected patients but no differences were observed in IL-10 levels (Figure 2B). Strikingly, under parasite lysate stimulation, intracellular production of IL-6 and IL-1 β was higher in monocytes from patients than the control counterpart (Figure 2C).

The monocyte subpopulations were defined by the expression of CD14 and/or CD16 (Figure 3A). The percentage of circulating CD14⁺⁺CD16⁻ (classical) monocytes decreased, while the frequency of CD14⁺CD16⁺⁺ (non-classical) subset increased in seropositive patients when compared to control donors (Figure 3B) as was observed for bacterial and viral infections (24-26). The percentages of NO⁻ and ROS⁻-producing monocytes were significant higher in the non-classical monocyte subset than in classical monocyte subpopulation in both groups, patients and control donors (Figure 3C-D). Conversely, the proportion of non-classical monocytes producing IL-10 or IL-6 was lower than the frequency of IL-10⁺/IL-6⁺ classical monocytes (Figures 3E and F) in both studied groups. We found no differences in the frequency of non-classical monocytes from asymptomatic patients (G0)

and from those in the cardiac chronic stage (G1-G3) ($p > 0.99$). Altogether, the results clearly demonstrate that the non-classical subset of monocytes displays pro-oxidative properties.

Strikingly, Glut-1 expression exhibited a dichotomist pattern in classical and non-classical monocyte subsets between both groups. In seropositive patients non-classical monocytes exhibited increased Glut-1 expression while the main Glut-1+ subset in healthy control was classical monocytes (Figure 3G). Although CD39 expression did not show significant difference in both monocyte subpopulations (Figure 3H), increased CD73 expression was detected in non-classical monocytes in comparison with classical monocytes, in control as well as in patient samples (Figure 3I).

Monocytes from *T. cruzi*-infected patients showed increased glycolysis and mitochondrial damage

HIF-1 α drives multiple immune cell effector functions, including energy metabolism. Indeed, HIF-1 α -dependent glycolytic pathway orchestrates a metabolic checkpoint for the differentiation of Th17 profile (27), Tr1 cells (28) and classically-activated macrophages (29). To determine whether monocytes from patients with Chagas disease have enhanced glycolytic metabolism, we measured extracellular acidification rate (ECAR), and oxygen consumption rate (OCR), as measures of glycolysis and OXPHOS, respectively.

Higher glycolysis, glycolytic capacity and glycolytic reserve was observed in monocytes from seropositive patients compared to control donors (Figure 4A and B). Consistent with these findings, *T. cruzi*-infected patients exhibited higher frequency of Glut-1+ monocytes relative to controls (Figure 4C). Of note, monocytes from asymptomatic (G0) seropositive individuals did not exhibit differences in the glycolytic activity compared to monocytes from patients in cardiac chronic G1-G3 stages ($p > 0.99$ glycolytic activity).

Moreover, monocytes from patients showed lower respiration driving-ATP synthesis OCR and higher respiration driving proton leak in comparison with control donors (Figure 4D

199 and E). Consequently, monocytes from infected individuals exhibited a significant decrease
200 of the bioenergetic health index (BHI), a proposed functional biomarker of oxidative stress in
201 patients suffering metabolic disorders (30) (Figure 4F). To distinguish between mitochondria
202 with altered or unaltered mitochondrial potential (31) we stained monocytes with a
203 combination of MitoTracker Green ($\Delta\psi$ -independent mitochondrial stain) and MitoTracker
204 Orange ($\Delta\psi$ -dependent mitochondrial stain). A significant increase in the number of
205 dysfunctional mitochondria (MitoTracker Green^{high}, MitoTracker Orange^{low}) and in
206 mitochondrial mass (MitoTracker Green staining) was found in monocytes from seropositive
207 patients compared to monocytes from control donors (Figure 4G).

208 **Monocyte glycolysis is necessary for *T. cruzi*-induced lymphocyte nitration and** 209 **dysfunction**

210 Since glycolytic activity has been extensively associated with pro-inflammatory
211 activities of immune cells, we characterized the effect of glycolysis on monocyte effector
212 function during *T. cruzi* infection. To this aim in vitro infected PBMCs were pre-treated with a
213 synthetic glucose analog 2-DG that inhibits glycolysis and compared with non-treated
214 infected PBMCs from the same donor. We found that 2-DG treatment did not modify M1-
215 marker (CD64) expression, but increased the M2-marker mannose receptor (CD206)
216 expression on infected monocytes/macrophages (Mo/Ma) (Figure 5A). Moreover, glycolysis
217 inhibition decreased the frequency of IL-6- and of IL-1 β -producing Mo/Ma, as well as the
218 amount of IL-1 β released to the culture supernatant (Figure 5B and C). In contrast,
219 glycolysis inhibition raised the percentage of IL-10-producing Mo/Ma (Figure 5D).

220 To evaluate the effect of monocyte glycolysis on T cell nitration, we measured NO
221 production and TN⁺ lymphocytes in infected PBMCs cultures subjected to 2-DG treatment.
222 The glucose analog lowered the frequency of NO-producing Mo/Ma (Figure 5E), NO levels
223 in culture supernatant (Figure 5F) as well as the frequency of T cell nitration (Figure 5G). To
224 further define the link between monocyte glycolytic metabolism and T-cell nitration, in vitro

225 infected monocytes were pre-treated with 2-DG. After 3 h the monolayers were washed and
226 co-cultured with sorted CD3⁺ lymphocytes. The inhibition of glycolysis decreased the
227 percentage of TN⁺ T-cells (Figure 5H). Furthermore, T-cell nitration is cell contact
228 dependent since the disruption of physical contact between infected monocytes and T-cells
229 abrogated the nitration of lymphocytes (Figure 5H).

230 To confirm that NO production by monocytes induces CTLs dysfunction during *T.*
231 *cruzi* infection, we treated PBMCs from control donors with NO production-inhibitor L-NAME
232 previous to infection. We observed that L-NAME reduced NO levels (Figure 6A),
233 lymphocytes nitration (Figure 6B) and re-established the effector function measured by IFN-
234 γ and TNF production by CTLs (Figure 6C) compared to untreated infected cells. Altogether,
235 these results clearly evidence that glycolysis governs oxidative stress on monocytes and
236 consequently regulate T cell function in the context of *T. cruzi* infection.

237 Our hypothesis was further confirmed by the fact that both the frequency of non-
238 classical monocytes and the frequency of NO-producing monocytes positively correlated
239 with the percentage of TN⁺ lymphocytes in peripheral blood samples from *T. cruzi* infected
240 patients and control donors (Figure 6D).

241

242 **Discussion**

243 Monocytes are key players in anti-parasite immune response since they produce
244 inflammatory cytokines, inflammation-accelerating chemokines, and microbicidal species.
245 The present study demonstrates that during human chronic *T. cruzi* infection monocytes
246 exhibit long-lasting functional phenotypic changes, since they are more prone to produce
247 cytokines under stimulation and they exhibited increased production of NO compared to
248 monocytes from control donors, contrasting with the impaired effector function of the CTLs
249 compartment (19). Cytotoxic CD8⁺ T cells from seropositive patients are more susceptible to
250 apoptosis and exhibit high levels of nitrated tyrosine residues on their surface. Naïve cells
251 constitute the main subpopulation that undergoes tyrosine nitration, and the majority of NT⁺
252 cells are effector memory CD8⁺ T cells. Notably, TN⁺CTLs are less functional than TN⁻
253 population as TN⁺CTLs exhibit deactivation of the cytotoxic function with lower expression of
254 CD107a (a degranulation marker) and decreased production of cytokines (IFN- γ , TNF and
255 IL-2). The nitration of surface proteins on T cells is promoted by peroxynitrites, which are
256 induced by the reaction of NO with the superoxide anion (32-34). In the present work, we
257 identified non-classical monocytes as an important cellular source of NO, which promotes
258 CD8⁺ T cell nitration/dysfunction in this human infectious disease.

259 The expanded non-classical monocyte subset has been previously described in the
260 context of different inflammation-related diseases (35-37). Regarding Chagas disease, our
261 results are in full agreement with a recent report from Dr. Laucella's group. They
262 demonstrated that "*T. cruzi*-infected subjects with mild or no signs of cardiac disease
263 showed increased levels of non-classical monocytes compared to healthy controls" (38).

264 In the present work, we have also found increased monocyte-expressing HIF-1 α , a
265 transcription factor that could be promoting the enhanced amount of plasmatic IL-1 β
266 observed in Chagas disease patients (19). In fact, it was recently demonstrated that
267 activated macrophages produce IL-1 β because of HIF-1 α stabilization in a mechanism

268 supported by glycolysis (29). The metabolism of glucose into pyruvate prevents aerobic
269 degradation of HIF-1 protein, allowing HIF-1 accumulation. Accordingly, total monocytes
270 isolated from patients showed activated glycolytic metabolism in comparison with their
271 control counterpart.

272 HIF-1 is the master regulator of metabolic adaptation to hypoxia with a broad range of
273 effector functions. Among these, NO production is a recognized downstream effect of HIF-
274 1 α , since this transcription factor stimulates the expression of iNOS. Interestingly, although s
275 *T.cruzi*-infected patients exhibited higher frequency of NO-producing monocytes, this
276 mediator is not augmented in plasma from infected patients (19), which is consistent with
277 data from the literature (39). Regarding cellular NO effector functions, Everts and coworkers
278 demonstrated an autocrine NO effect on dendritic cell metabolism (9). They postulated the
279 notion that NO inhibits mitochondrial electron transport by the nitrosylation of iron-sulfur-
280 containing proteins from complex I (NADH-ubiquinone oxidoreductase), complex II
281 (succinate-ubiquinone oxidoreductase) and complex IV (cytochrome C oxidase), thereby
282 blocking oxygen consumption and ATP production (40-42). The direct connection between
283 reduced respiratory rate and inflammation has been recognized for some time (43). In this
284 sense, cells with mitochondrial damage activate the glycolytic metabolism to produce the
285 ATP necessary to survive. Our results suggest that oxidative stress disrupts mitochondrial
286 potential in monocytes from seropositive individuals. In turn, these cells enhance the
287 activation of glycolytic metabolism supporting their inflammatory state.

288 Mitochondria are sub-cellular organelles that play vital roles into the eukaryotic cells.
289 Even though their function in energy metabolism is extensively recognized, only few years
290 ago several evidences have demonstrated the relevance of mitochondria in immunity (29,
291 44-46), and put these organelles as a platform for immune regulation (47, 48). Mitochondria
292 function could be assessed by respiration driving ATP production, respiration driving proton
293 leak, maximal respiration and spare respiratory capacity, among others. Each of these

parameters is sensitive to different free radicals or oxidants, clearly indicating that mitochondria are particularly susceptible to oxidative stress. In agreement with our results, a high percentage of cardiac and skeletal muscle mitochondria exhibiting structural and functional alterations was reported in Chagas disease patients even in those without clinical criteria of cardiomyopathy (49, 50). In this sense, *T. cruzi* infection provokes a significant decline in mitochondrial membrane potential (51).

Recent studies indicate mitochondrial damage products (mROS production, cytosolic release of mtDNA, and the dissipation of mitochondrial membrane potential) as common factors to trigger NLRP3 inflammasome activation (52, 53). In line with these findings, we observed altered mitochondrial potential with decreased BHI in monocytes from infected individuals. Therefore, the accumulation of damaged mitochondria might give rise to the activation of NLRP3 inflammasome with the consequent induction of IL-1 β production, which would account for the increased levels of this potent inflammatory cytokine observed in plasma from patients with Chagas disease. On the other hand, the release of ATP can also promote inflammasome activation. Here we have also found increased ATP plasmatic levels in *T. cruzi*-infected patients concomitant with higher monocyte expression of CD39 and CD73 ecto-enzymes, which are in charge of eATP metabolic degradation to adenosine. Thus, it is plausible that monocytes promote eATP degradation to dampen the inflammatory microenvironment. In this sense, it was described that ATP promotes HIF-1 α expression (54), with the consequent ecto-nucleotidases up-regulation (55).

In vitro studies confirmed our hypothesis. Glycolysis inhibition of infected PBMCs (obtained from controls donors) suppresses *T. cruzi*-induced inflammatory Mo/Ma profile, diminishing inflammatory cytokine production and increasing IL-10⁺ cells. Of note, the increased frequency of IL-10⁺ Mo/Ma could be an indirect effect of glycolysis inhibition and could be the consequence of IL-1 β diminution induced by 2-DG. In accordance with our previous observations, which revealed that IL-1 β induces NO production (19, 56), 2-DG

320 reduced IL-1 β production and this reduction could lead to lower cellular secretion of NO. In
321 turn, glycolysis inhibition of infected monocytes decreased nitration of lymphocytes, an effect
322 that depend on cell-cell contact. Supporting the in vitro results, the frequency of NO-
323 producing monocytes positively correlated with the percentage of TN⁺ lymphocytes in
324 peripheral blood samples from control donors and patients. Through well designed
325 experimental strategies, Koo and co-workers have recently delineated the metabolic
326 regulation of the macrophage response to *T. cruzi*. By studying in vitro assay murine
327 systems they found that upon infection macrophages maintain a Krebs cycle linked oxidative
328 metabolism that allow only a partial iNOS activation. Strikingly, IFN- γ treatment “lead to
329 complete metabolic shut down of oxidative metabolism, and enhanced the glycolytic source
330 of energy availability in infected macrophages”. This shift activates the production of optimal
331 NO and ROS levels dampening the lack of effective microbicidal response (57).

332 The major achievement of the present work was to establishe that glycolysis could be
333 a key factor that sustains the pro-oxidative monocyte profile in seropositive patients, even in
334 those in the indeterminate (asymptomatic) chronic form of Chagas disease, also known as
335 “silent” stage. Etiological treatment of Chagas disease is currently based on two compounds,
336 nifurtimox and benznidazole, which have significant activity in congenital and acute *T. cruzi*
337 infections (> 95 and 60–80% of parasitological cures, respectively). However, a major
338 limitation of these drugs is their limited and variable curative activity in the chronic form of
339 the disease, the most prevalent clinical presentation. Even when etiological treatment is
340 clinically recommended, the evidence-based medicine has not been fully validated, and its
341 use in the chronic phase of the disease is still controversial. The effect of benznidazole
342 treatment on patients with Chagas cardiomyopathy was recently reported in a well-
343 conducted BENEFIT trial (58). After 5 years of follow up, the results evidence that treatment
344 with benznidazole is unlikely to have a major preventive effect on the progression of heart
345 disease in chronic Chagas disease patients, even though the parasite load significantly

346 diminished. Although the exact cause-effect relation for cardiomyopathy development has
347 not yet been revealed, the results described in the present work point out that a sustained
348 pro-oxidative monocyte profile could be accounting for chronic state described in these
349 patients.

350 In summary, altogether the results of the present study demonstrate that chronic *T.*
351 *cruzi* infection sustains monocyte glycolytic metabolism and HIF-1 α /NO pathway activation
352 and expands non-classical circulating monocytes with increased oxidative potential that may
353 induce nitration of CTLs affecting their functionality. In concert, the described mechanisms
354 could explain the inefficient parasite clearance, concomitant with a sustained inflammatory
355 environment that underlies the characteristic lesions of chronic Chagas disease.

356

357 **Methods**

358 **Subjects and ethics statement**

359 A total of 95 subjects were recruited at the “Hospital Nuestra Señora de la
360 Misericordia”, Córdoba and at the Instituto Nacional de Parasitología “Dr. Mario Fatale
361 Chabén” Buenos Aires, Argentina. *T. cruzi* infection was diagnosed by indirect
362 hemagglutination (IHA) and enzyme-linked immunosorbent assay (ELISA). Subjects positive
363 on these two tests were considered infected. Chronic Chagas disease patients (n=40) were
364 evaluated clinically including electrocardiogram (ECG) and chest X-rays. Subjects were
365 grouped according to the Kuschnir grading system (20). Group 0 (G0) included seropositive
366 individuals having a normal ECG and a normal chest X-rays; group 1 (G1) comprised
367 seropositive patients with a normal chest X-rays but abnormalities in the ECG; group 2 (G2)
368 encompassed seropositive patients with ECG abnormalities and heart enlargement as
369 determined by chest X-rays and group 3 (G3) involved seropositive patients with ECG
370 abnormalities, heart enlargement and clinical or radiological evidence of heart failure. The
371 control group (n=55) consisted of age-matched individuals who were serologically negative
372 for *T. cruzi*. All donors with chronic or inflammatory diseases, erythrocyte sedimentation rate >30
373 mm or white blood cells count <4,000 or >10,000/mm³ were excluded from the study.

374 **Blood collection**

375 Approximately 15-30 mL of peripheral blood were drawn from each individual. PBMCs
376 were isolated through density gradient centrifugation using Ficoll-Hypaque PLUS (GE
377 Healthcare Bioscience).

378 ***T. cruzi* lysate**

379 Protein lysate from *T. cruzi* trypomastigotes was obtained by 4 freeze/thaw cycles,
380 which were followed by sonication. In brief, trypomastigotes from the Tulahuen strain were
381 collected from a monolayer of infected Vero cell cultures. After washing, the parasites were

382 frozen and thawed 4 times. Thereafter, the sample was sonicated and the supernatant of a
383 12,000 g centrifugation was collected and filtered. Protein concentration was determined by
384 Bradford technique.

385 Monocyte isolation and bioenergetics studies

386 Monocytes were purified by positive selection from PBMCs using CD14 Microbeads
387 (EasySep, StemCell Technology), following manufacturer's instructions. Then, 300,000
388 cells/well were plated in triplicate of XFp cell culture microplates (Seahorse Agilent) pre-
389 coated with polyethylenimine and centrifuged to attach monocytes. RPMI medium was
390 replaced with 180 μ L of assay medium (DMEM XF base supplemented with 2 mM
391 glutamine, pH 7.4) for extracellular acidification rate (ECAR) measurements or with 175 μ L
392 of assay medium (DMEM XF base supplemented with 4 mM glutamine, 5.5 mM D-glucose
393 and 1 mM pyruvate, pH 7.4) for oxygen consumption rate (OCR) determination. Plates were
394 kept at 37°C for 45 min and loaded into Seahorse XFp extracellular flux analyzer. OCR was
395 determined at the beginning of the assay (basal OCR) and after the sequential addition of 1
396 μ M oligomycin, 1 μ M FCCP and 0.5 μ M rotenone plus antimycin A. Monocytes were titrated
397 with 0.125-2 μ M FCCP and 1 μ M FCCP rendered the maximum OCR, so this concentration
398 was used for the experiments. Non-mitochondrial OCR was determined after the addition of
399 0.5 μ M rotenone plus antimycin A and subtracted from all other values before calculating the
400 respiratory parameters, as previously described (59). Respiratory parameters were obtained
401 as follows: basal respiration, baseline OCR; respiration driving proton leak, OCR after
402 oligomycin addition; respiration driving ATP synthesis, basal respiration–respiration driving
403 proton leak; maximum respiration, OCR after FCCP addition; spare respiratory capacity,
404 maximum respiration–basal respiration. Values were expressed as a percentage of OCR
405 corresponding to the last baseline rate (100%). ECAR was determined at the beginning of
406 the assay and after the sequential addition of 10 mM d-glucose, 1 μ M oligomycin and 100
407 mM 2-deoxy-D-glucose (2-DG). Glycolytic parameters were obtained as follows: glycolysis,

408 ECAR after glucose addition–basal ECAR; glycolytic capacity, ECAR after oligomycin
409 addition–basal ECAR; glycolytic reserve, glycolytic capacity–glycolysis. Values were
410 expressed as a percentage of ECAR corresponding to the last basal rate (100%). Non-
411 glycolytic ECAR was determined after the addition of 100 mM 2-DG and subtracted from all
412 other values before calculating the glycolytic parameters.

413 The bioenergetic health index (BHI) was estimated according to the equation from Chacko et
414 al. (60)

$$BHI = \frac{\text{Spare respiratory capacity} \times \text{ATP production}}{\text{Non – mitochondrial respiration} \times \text{Proton leak}}$$

415 Ex Vivo flow cytometry

416 Peripheral blood was lysed with ACK lysing buffer to remove erythrocytes, cells were
417 blocked with Fc block and stained with anti-CD14-PECy5 (eBioscience; Cat:15-0149-41,
418 Clone:61D3), anti-CD16-PECy7 (eBioscience; Cat: 25-0168-41, Clone:CB16), anti-CD39-
419 biotin (Biolegend; Cat: 328204, Clone:1A) and Streptavidin-APC (eBioscience; Cat: 17-
420 4317), anti-CD73-PE (Biolegend; Cat: 344003, Clone:A2D), anti-Glut-1-PE (R&D Systems;
421 Cat: FAB1418P, Clone: 202915), anti-NT rabbit (Sigma-Aldrich; Cat: N 0409) and anti-rabbit-
422 Alexa 647 (ThermoFisher, Cat: A-21244). To determine HIF-1 α expression, cells were
423 permeabilized with FOXP3 staining buffer set (eBioscience) and labeled with anti-HIF-1 α
424 rabbit (Abcam; Cat: AB51608, Clone: EP1215Y) followed either by anti-rabbit-Alexa 488
425 (ThermoFisher, Cat: A11034) or anti-rabbit-Alexa 647 (ThermoFisher, Cat: A21244)
426 antibodies. Data was acquired with a FACS Canto II flow cytometer (Becton Dickinson) and
427 analyzed using the FlowJo software.

428 ATP quantification

429 ATP levels were quantified in plasma from individuals by ATP Determination Kit
430 (Invitrogen™), according to the manufacturer's instructions. Briefly, samples were incubated

431 with luminescent reaction mix at room temperature for 30 min in a 96-well white plate
432 protected from light. Luminescence was measured at 560 nm in a Synergy 2 Multi-Mode
433 Reader (BioTek). A standard curve was plotted to calculate the ATP concentration and a
434 regression analysis was applied. It is important to stress that plasma samples were
435 separated from formed elements 35 min after blood collection.

436 Measurement of mitochondrial contents

437 PBMCs were stained with anti-CD14-PECy5 (eBioscience; Cat:15-0149-41,
438 Clone:61D3), anti-CD16-PECy7 (eBioscience; Cat: 25-0168-41, Clone: CB16) and then
439 MitoTracker Green and MitoSpy Orange stainings were performed, according to
440 manufacturer's instructions (Biolegend) and analyzed by flow cytometry.

441 Intracellular cytokine measurement

442 PBMCs were cultured with monensin (GolgiStop; 0.6 µl/ml; BD Biosciences), brefeldin
443 A (Golgiplug; 1µl/ml; BD Biosciences) and parasite lysate (10µg/mL) for 16h or LPS (100
444 ng/mL; Sigma) for 4 h (61), and stained with anti-CD14-PECy5 (eBioscience; Cat:15-0149-
445 41, Clone:61D3), anti-CD16-PECy7 (eBioscience; Cat: 25-0168-41, Clone: CB16). After
446 staining of surface markers, cells were fixed and made permeable according to the
447 manufacturer's instructions BD Cytofix/Cytoperm™ Kit (BD Biosciences). Then the cells
448 were stained with anti-IL-1β-FITC (eBioscience; Cat: BMS127, Clone:B-A15), anti-IL-6-PE
449 (Immunotools; Cat: 21670064, Clone: 8C9), and anti-IL-10-APC (Biolegend; Cat: 501419,
450 Clone: JES3-9D7) antibodies, and analyzed by flow cytometry.

451 Measurement of reactive oxygen (ROS) and nitrogen species

452 ROS and NO production were evaluated using the molecular probes: H2DCF-DA and
453 DAF-FM DA (10 µM), respectively and analyzed by flow cytometry. After surface staining,
454 the cells were re-suspended in 100 µL of RPMI and 100 µL of 2',7'
455 dichlorodihydrofluorescein diacetate 20 µM (H2DCFDA) or 100 µL of DAF-FM DA 20 µM

456 (Molecular Probes, Eugene, OR, USA) were loaded onto cells in clear bottom, black walled
457 plates (Fisher Scientific). Cells were incubated for 30 min at 37°C, washed twice with PBS,
458 and then loaded with 300 µL of PBS. Fluorescence of oxidized product was measured at
459 excitation/emission of 488/520 nm using the FACs Canto II (BD Bioscience). The
460 nitrite/nitrate content, indicative of NO production, was monitored by the Griess reagent
461 assay (62).

462 Culture of PBMCs and glycolysis inhibition

463 Vero cell monolayers were infected with *T. cruzi* Tulahuen trypomastigotes for 3 h,
464 washed and maintained in RPMI at 37°C in a 5% CO₂ atmosphere. After 7 days, the
465 parasites were collected from the supernatant of infected cells and harvested by
466 centrifugation and washed. PBMCs from 8 control donors were seeded at 2.5 x 10⁵ cells/well
467 and treated with 2-DG (11mM, R&D Systems) or maintained in medium for 1 h, and then
468 washed and cultured with *T. cruzi* Tulahuen trypomastigotes (1:1 rate) for 3 h; then, the cells
469 were washed. After 24 h, culture supernatants were evaluated for NO levels, and the cells
470 stained with anti-CD14-PECy5 (eBioscience; Cat:15-0149-41, Clone:61D3), anti-CD64-
471 APCCy7 (Biolegend; Cat: 305026, Clone: 10.1), anti-CD206-Alexa 647 (Biolegend; Cat:
472 321116, Clone: 42050), anti-IL-1β-FITC (eBioscience; Cat: BMS127, Clone:B-A15), anti-IL-
473 6-PE (Immunotools; Cat: 21670064, Clone: 8C9), anti-IL-10-PECy7 (Biolegend; Cat:
474 501419, Clone: JES3-9D7) antibodies, anti-Nitrotyrosine antibody produced in rabbit
475 (Sigma-Aldrich; Cat: N 0409) and anti-rabbit-Alexa 647 antibody (ThermoFisher, Cat: A-
476 21244), and NO production (Molecular Probes; Cat: D23842) by flow cytometry.

477 Transwell co-culture assay

478 PBMCs obtained from buffy coats from healthy donors were diluted 1:2 times with
479 supplemented RPMI and layered on Ficoll Hypaque (Sigma Aldrich). Lymphocytes and
480 monocytes were further purified from PBMCs by sorting. To obtain highly purified T
481 lymphocytes and monocytes, PMBCs were labeled with anti-CD3 Alexa Fluor 488 (BD

482 Biosciences Cat: 557694, Clone: UCTH1) and anti-CD14 PECy5 (eBioscience; Cat:15-0149-
483 41, Clone:61D3) for 20 min at 4°C and sorted using FACS Aria II (Beckton Dickinson).
484 Monocytes were seeded in the lower chamber of 24-well plate at a concentration of 500.000
485 cells/well and were treated with 2-DG (11 mM; R&D Systems) or maintained in medium for 1
486 h. The monolayers were washed and monocytes were infected with *T. cruzi* trypomastigotes
487 (1:1 rate) for 3 h, and then washed. CD3+ cells (3.5×10^5 cells/well) were plated on top of
488 the transwell inserts or directly co-cultured with infected monocytes and incubated overnight
489 at 37°C, 5% CO₂ incubator. The cells were then harvested and stained with anti-CD14
490 PECy5 (eBioscience; Cat:15-0149-41, Clone:61D3), anti-CD3 Alexa Fluor 488 (BD; Cat:
491 557694, Clone: UCTH1), anti-CD8 APCCy7 (BD; Cat: 557834, Clone: SK1), anti-Glut-1 PE
492 (R&D Systems; Cat: FAB1418P, Clone: 202915), rabbit anti-Nitrotyrosine (Sigma Aldrich;
493 Cat: N0409) and anti-rabbit Alexa 647 (ThermoFisher, Cat: A-21244) antibodies, for flow
494 cytometry.

495 Statistical analysis

496 Statistical analysis was performed with GraphPad Prism 5.0 software. Student *t-test*
497 or Mann-Whitney test were used according to data distribution for statistical analysis when
498 independent two groups were analyzed. For paired samples, parametric paired *t-test* or non-
499 parametric Wilcoxon test were used, according to data distribution. For comparison between
500 more than 2 groups the data obtained were analyzed by ANOVA with post-hoc Tukey test.
501 Pearson correlation coefficient was used to evaluate the association between two parametric
502 variables. Statistical significance was set at **p-values* <0.05.

503 Study approval

504 This study was reviewed and approved by the Comité Institucional de Ética de la
505 Investigación en Salud del Adulto, Ministerio de Salud de la Provincia de Córdoba (Act #
506 194/2014) and by the Comité de Ética del Instituto Nacional de Parasitología “Dr. Mario
507 Fatała Chaben”, Buenos Aires, Argentina. All studies were conducted according to the

508 principles expressed in the Declaration of Helsinki. Signed informed consent was obtained
509 from each donor included in the study.

510 **Author contribution**

511 Conceived and designed the experiments: LMS and MPA. Performed the experiments: LMS,
512 NE, GB, LPQP, PMA, LMV, EACS and MPA. Analyzed the data: LMS, NE, GB, LPQP, PMA,
513 LMV, ARM, EACS, YHV, LM, MP and MPA. Patients handling and human samples: LPQP,
514 LMV, ARM, YHV and MP. Wrote the paper: LMS and MPA.

515

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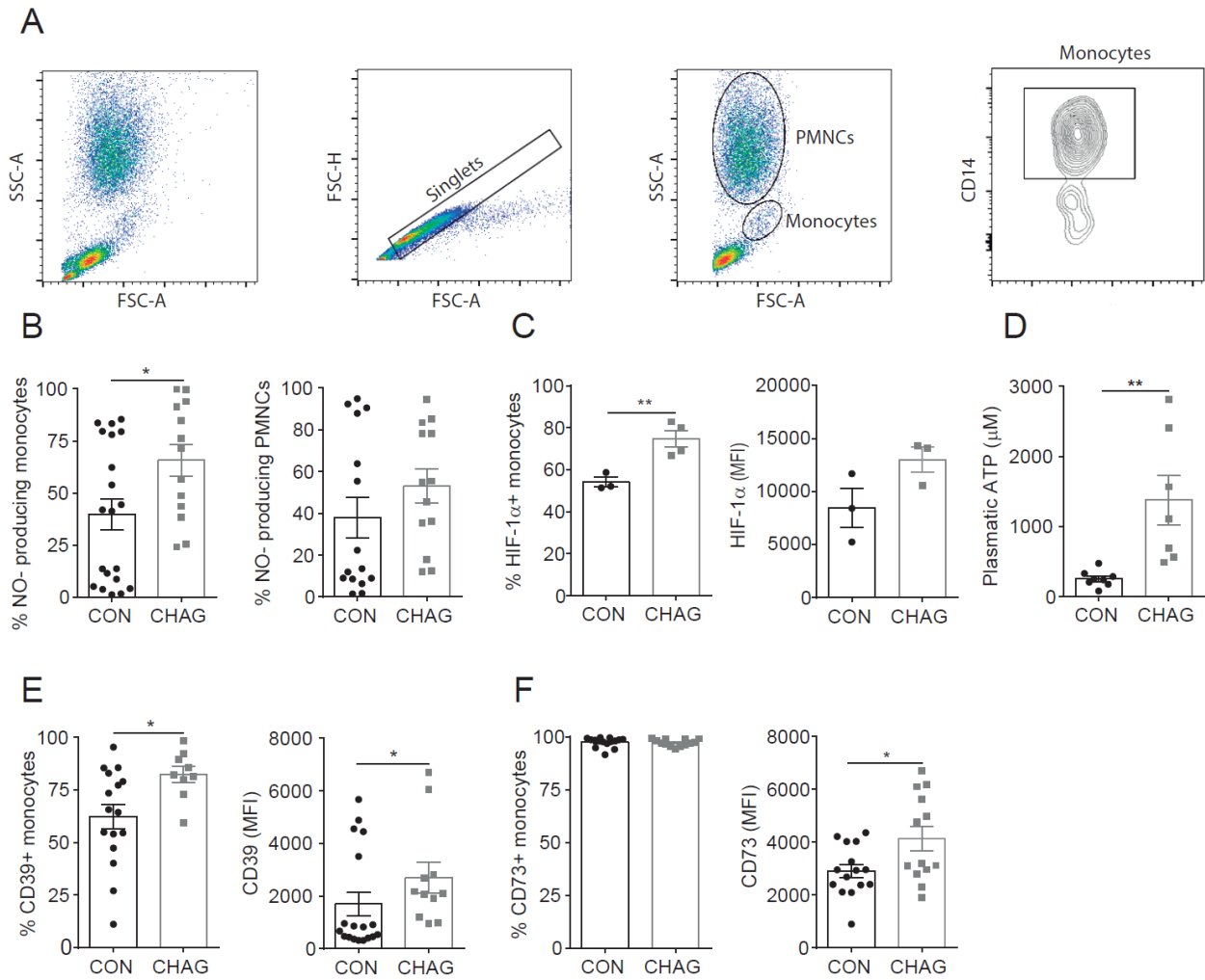


Figure 1: Patients with Chagas disease show increased frequency of NO+ and HIF-1α+ monocytes

(A) Flow cytometry gating strategy for leukocytes from peripheral blood samples. After exclusion of doublets and debris by using forward light scatter-height (FSC-H) vs. forward light scatter-area (FSC-A) density dot plots, polymorphonuclear cells (PMNCs) and monocytes were gated according to their FSC-A vs. SSC-A features. Monocytes were further identified by CD14-positive staining. **(B)** Frequency of NO-producing circulating monocytes and PMNCs from control donors (CON; n=20) and Chagas patients (CHAG; n=13). **(C)** Frequency and FMI of HIF-1α+ monocytes from CHAG (n=4) and CON (n=4). **(D)** ATP levels in plasma from CON (n=8) and CHAG (n=8). Frequency and MFI of **(E)** CD39+ and **(F)** CD73+ monocytes from CON (n=16) and CHAG (n=13). Data are presented as mean ± SEM. * p < 0.05, ** p < 0.01 (Student's t test or Mann-Whitney test).

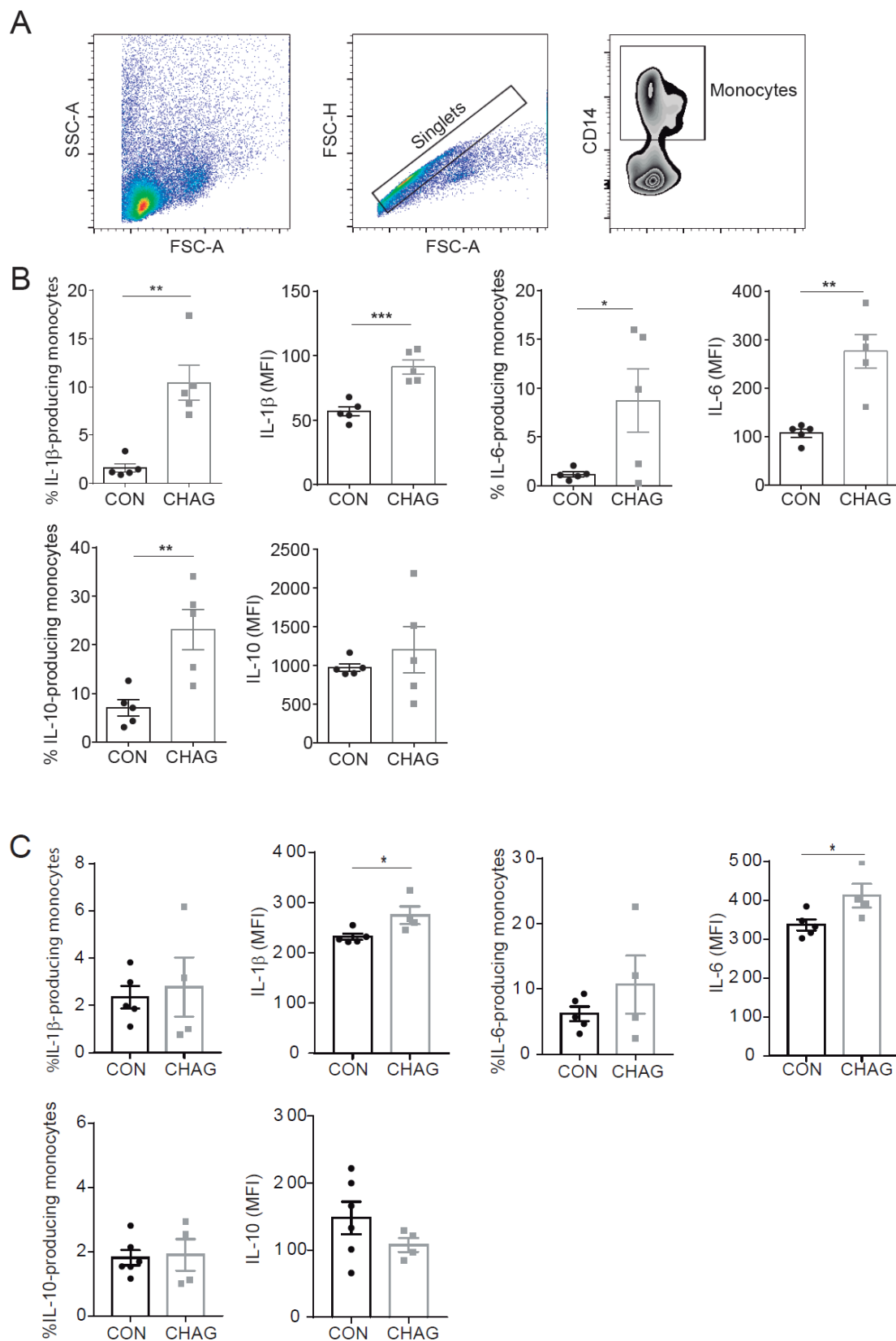
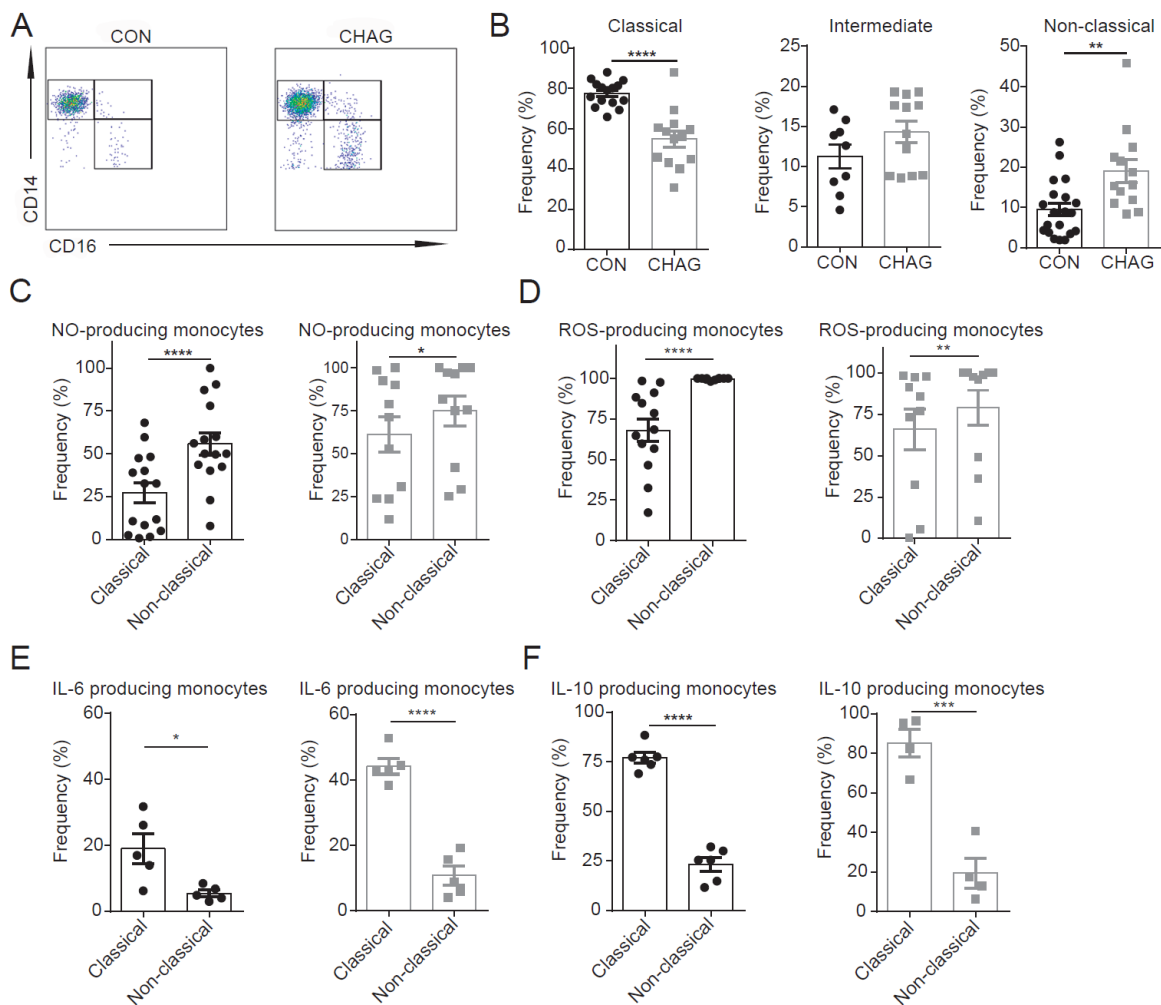


Figure 2: Monocytes from *T. cruzi*-infected patients exhibit higher functional activity potential
(A) For intracellular cytokine analysis PBMCs isolated from peripheral blood from control donors and from seropositive patients were cultured with monensin, brefeldin A and **(B)** LPS (CON, n=5; CHAG, n=5) or **(C)** parasite lysate (CON, n=6; CHAG, n=4) and stained with

731 anti-CD14-PECy5. After staining of surface markers, cells were fixed and made permeable.
732 Then the cells were stained with anti-IL-1 β , anti-IL-6, and anti-IL-10 antibodies, and
733 analyzed by flow cytometry. PBMCs were gated according to their CD14-positive staining
734 after exclusion of doublets and debris by using FSC-H/FSC-A dot plots. Frequency and
735 mean fluorescence intensity (MFI) of IL-1 β , IL-6 and IL-10-producing monocytes. Data are
736 presented as mean \pm SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ (Student's t test or Mann-
737 Whitney test).

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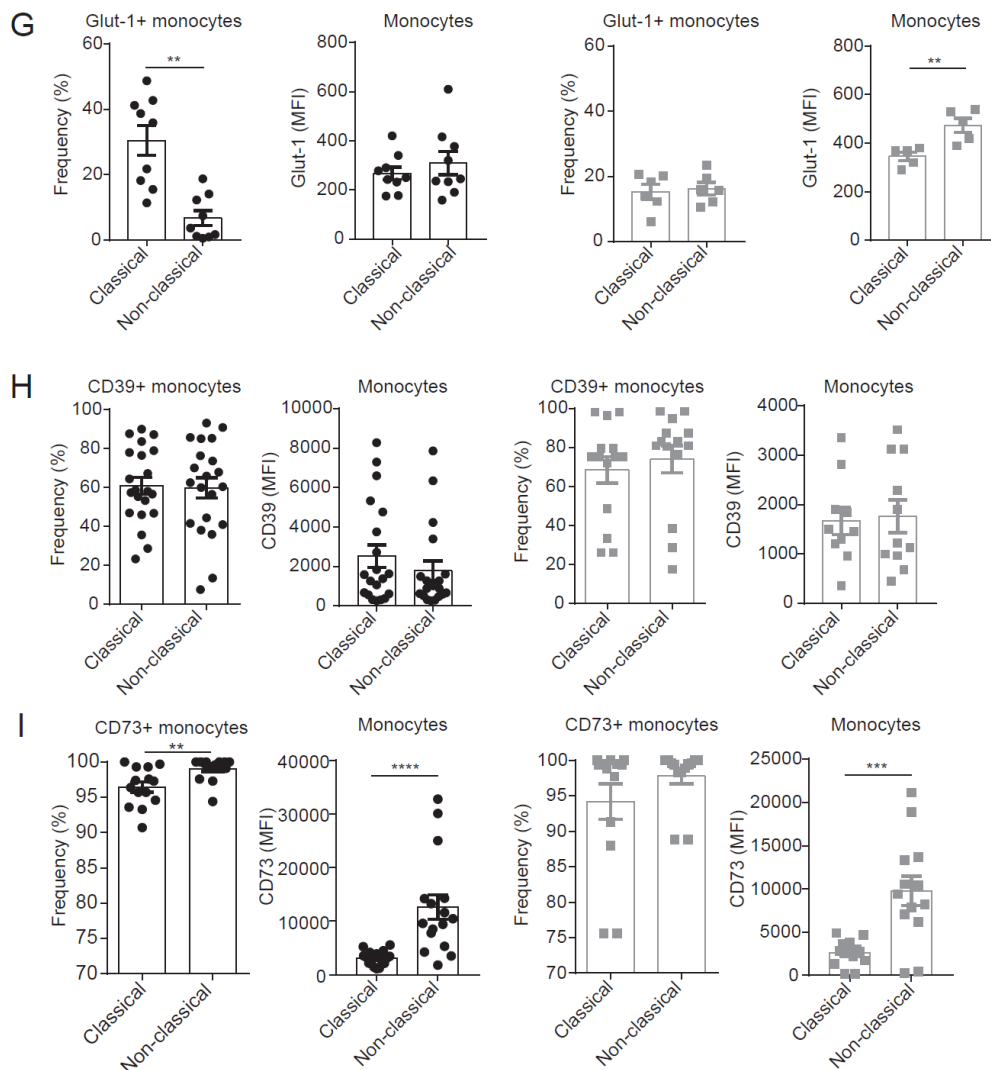


Figure 3: Chagas disease patients exhibit increased frequency of non-classical monocytes (A) Representative dot plots of CD14 vs CD16 monocyte subsets in peripheral blood from control donors (CON) and from seropositive patients (CHAG). (B) Frequency of classical (CD14++CD16-), intermediate (CD14++CD16+) and non-classical (CD14+CD16++) monocytes from CON (n=20) and CHAG (n=13). (C) Percentage and mean fluorescence intensity (MFI) of NO+ (CON, n=15; CHAG, n=11), (D) ROS+ (CON, n=13; CHAG, n=10), (E) IL-6+ (CON, n=5; CHAG, n=5), (F) IL-10+ (CON, n=5; CHAG, n=5), (G) Glut-1+ (CON, n=12; CHAG, n=6), (H) CD39+ (CON, n=21; CHAG, n=14), and (I) CD73+ cells (CON, n=15; CHAG, n=15) gated in classical vs. non-classical monocytes from CON (black plots) and CHAG (grey plots). For intracellular cytokine analysis, the cells were processed as in Figure 2 and stimulated with LPS. Data are presented as mean \pm SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ and **** $p < 0.0001$ (Student's t test or Mann-Whitney test).

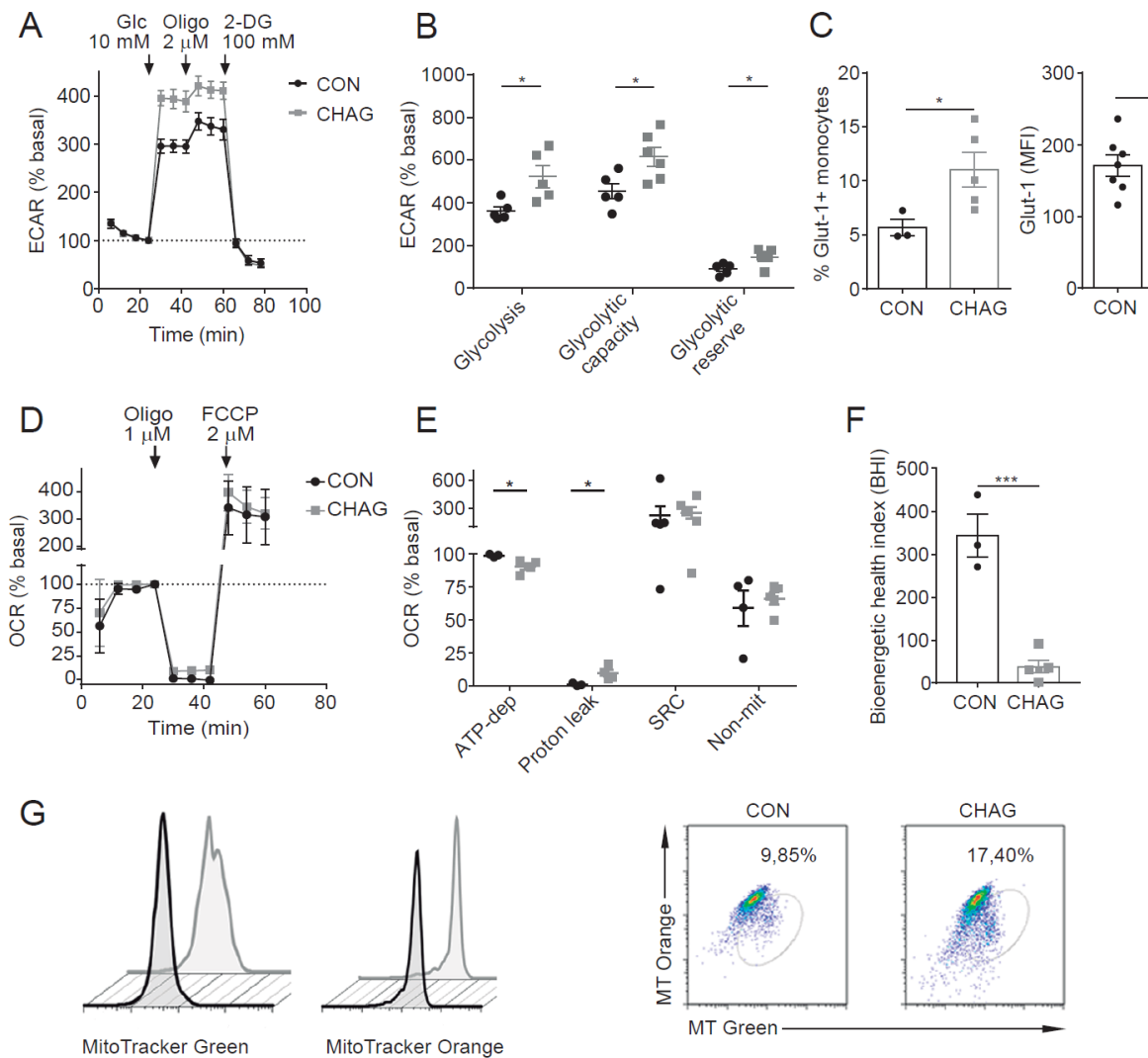


Figure 4: Monocytes from *T. cruzi*-infected patients show increased glycolysis and altered mitochondrial potential

(A) Monocytes from control donors (CON) or Chagas disease patients (CHAG) isolated by CD14 positive selection were seeded in a Seahorse XFp analyzer and real-time extracellular acidification rate (ECAR) was determined during sequential treatments with glucose, oligomycin (ATP-synthase inhibitor) and 2-deoxyglucose (2-DG) (glycolysis inhibitor). Data represent mean \pm SEM of 8 runs. (B) Bars show glycolytic rate, glycolytic capacity and glycolytic reserve of monocytes from CON (n=5) and CHAG (n=5). To analyze these parameters first non-glycolytic acidification was subtracted, and then the data were normalized to basal ECAR. (C) Frequency and MFI of Glut-1+ monocytes from CON (n=3) and CHAG (n=5). (D) Real-time mitochondrial respiration was analyzed starting from basal respiration and after the addition of oligomycin (complex V inhibition), FCCP (maximal respiration induction), and rotenone/antimycin A mixture (electron transport chain inhibition). Data represent means \pm SEM of 5 experiments. Bars show (E) respiration driving-ATP synthesis, respiration driving proton leak, spare respiratory capacity (SRC) and non-mitochondria OCR, and (F) bioenergetics health index (BHI) of monocytes from CON (n=4) and CHAG (n=5). To analyze these parameters first non-mitochondrial OCR was subtracted, and then the data were normalized to basal OCR. (G) Representative histogram of total mitochondrial mass analyzed by flow cytometry in monocytes from CON (black line) and CHAG (grey line) labeled with MitoTracker Green. Mitochondrial membrane potential ($\Delta\psi_m$) was analyzed in monocytes from CON (black line) and CHAG (grey line) labeled with MitoTracker Orange. Representative dot plot of mitochondrial mass vs. mitochondrial

779 membrane potential in CON (n=3) and CHAG (n=5) monocytes. Data are presented as
780 mean \pm SEM. * $p < 0.05$, *** $p < 0.001$ (Student's t test or Mann-Whitney test).
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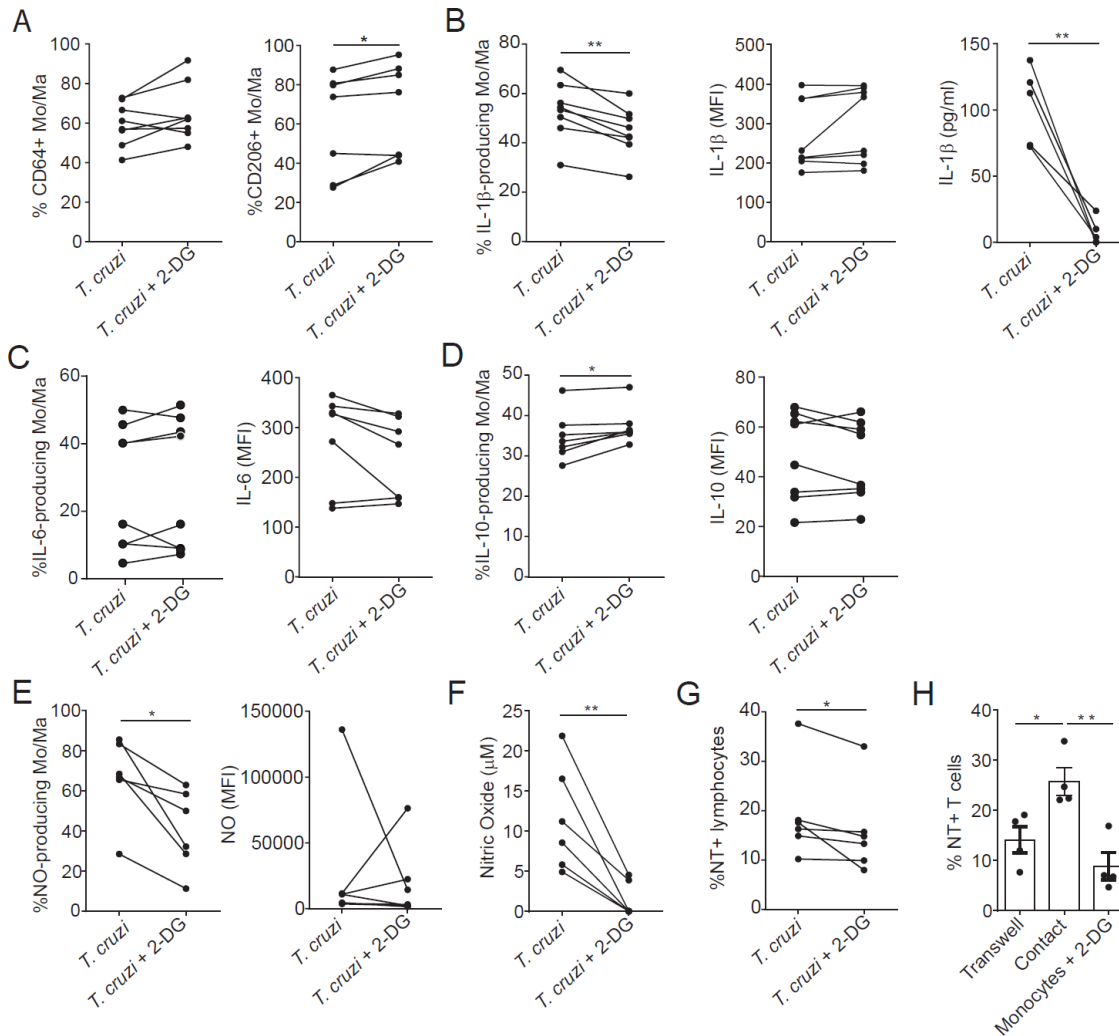


Figure 5: Glycolytic activity inhibition decrease NO-producing monocytes and lymphocyte nitration induced by *T. cruzi* infection

Infected PBMCs from control donors (8) were treated or not with 2-deoxyglucose (2-DG). **(A)** Frequency of CD64+ and CD206+ monocytes/macrophages (Mo/Ma). **(B)** Percentage and mean florescence intensity (MFI) of IL-1 β + Mo/Ma (left) and IL-1 β levels in culture supernatants measured by ELISA (right). **(C)** Percentage and MFI of IL-6+, **(D)** IL-10+ and **(E)** NO+ Mo/Ma. **(F)** NO levels measured in culture supernatants by Griess reaction. **(G)** Frequency of TN $^+$ CD3 $^+$ lymphocytes. * $p < 0.05$, ** $p < 0.01$ (paired Student's t test or Wilcoxon test). **(H)** Infected purified monocytes from control donor (buffy coat) were cultured with purified lymphocytes in independent chambers (transwell) or in the same chamber (contact), in some co-cultures monocytes were treated with 2-DG (monocytes+2DG), (ANOVA with post-hoc Tukey) (representative experiment (n=4); from 2 independent experiments).

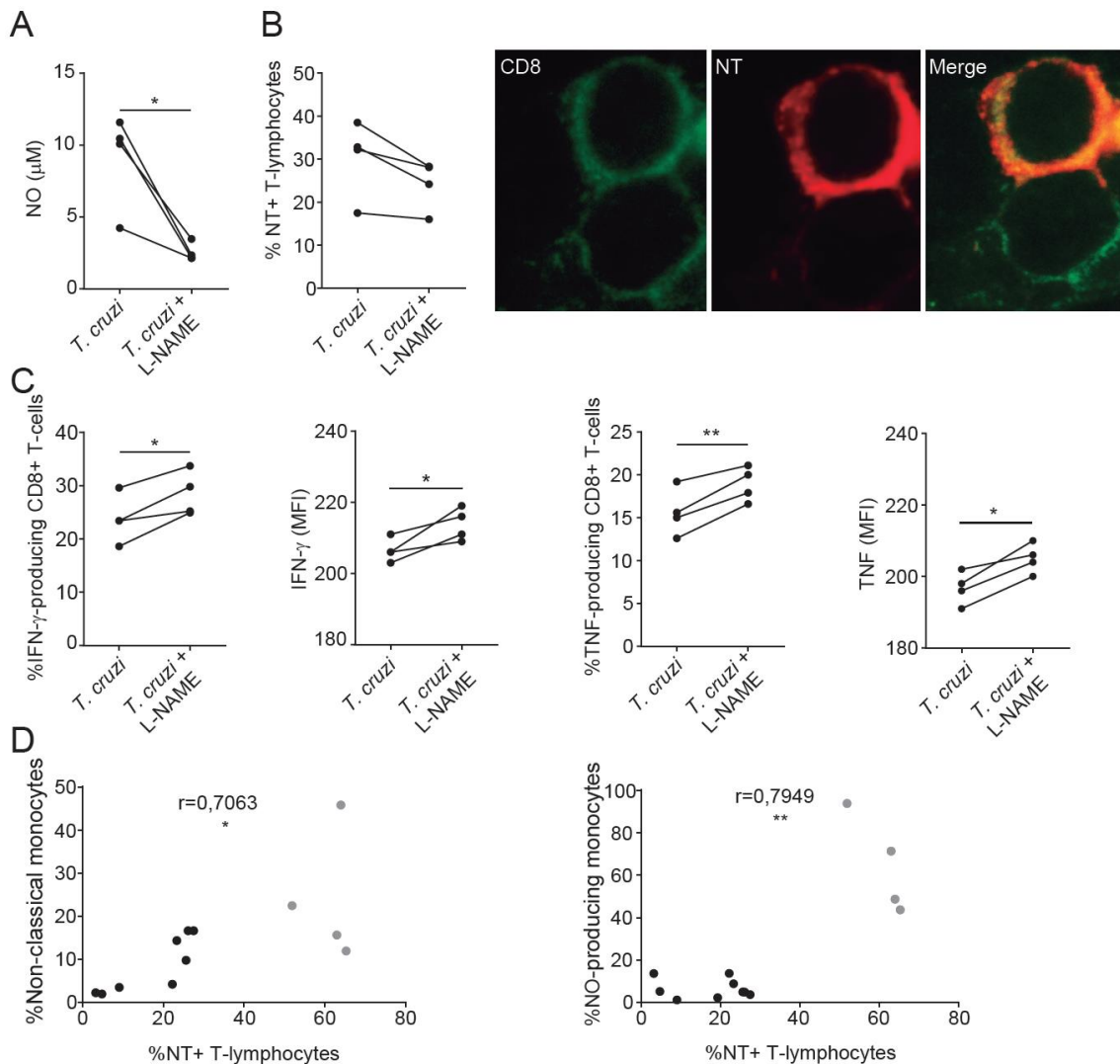


Figure 6: NO production drives tyrosine nitration on CTLs surface and CD8 T cell dysfunction

Infected PBMCs from control donors (4) were treated or not with L-NAME. **(A)** NO levels in culture supernatants measured by Griess reaction. **(B)** Frequency of TN⁺ CD3⁺ lymphocytes (left) and representative images of cells from seropositive patient peripheral blood labeled with anti-TN antibody (red) and anti-CD8 antibody (green) (1000x) (right). **(C)** Percentage and mean fluorescence intensity (MFI) of IFN-γ⁺ and TNF⁺ cells also positive for CD8 and CD3 expression. * p < 0.05, ** p < 0.01 (paired Student's t test or Wilcoxon test). **(D)** Pearson correlation analysis between the percentage of TN⁺ CD3⁺ lymphocytes vs. the frequency of non-classical monocytes (left) and between the percentage of TN⁺ CD3⁺ lymphocytes vs. the frequency of NO-producing monocytes (right) from control donors (black dots; n=8) and from seropositive patients (grey dots; n=4).

812 **Table 1: Demographic and clinical data**

	Control donors (CON) <i>n</i> =55	Chagas disease patients (CHAG) <i>n</i> =40
Age (years old)		
Range	19-60	20-60
Median	31	35
Gender		
Female	<i>n</i> =37	<i>n</i> =30
Male	<i>n</i> =18	<i>n</i> =10
Clinical evaluation		
Electrocardiographic changes	<i>NE</i>	<i>n</i> =5
Echocardiographic changes	<i>NE</i>	<i>n</i> =5
Chest X-rays abnormalities	<i>NE</i>	<i>n</i> =1

NE Not Evaluated

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