

RICHARD MARCEL BRUNO MOREIRA GIRARD

Role of Alanine and Alanine Racemase in the metabolism of the

Trypanosoma cruzi

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RESUMO

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Os aminoácidos participam de vários processos importantes na biologia dos tripanossomatídeos, como osmorregulação, diferenciação celular e invasão de células hospedeiras. Alguns deles fornecem poder redutor para a síntese de ATP mitocondrial. Foi anteriormente demonstrado que a alanina, que é formada principalmente pela aminação do piruvato, é um produto final metabólico quando os parasitas estão proliferando em um meio rico em glicose e aminoácidos. Mostrou-se também que este aminoácido também pode ser usado para a regulação do volume celular e resistência ao estresse osmótico. Curiosamente, o *Trypanosoma cruzi*, agente etiológico da doença de Chagas, possui genes putativos para uma Alanina racemase (AR) que catalisam a interconversão entre L e D-alanina. Aqui mostramos, pela primeira vez, que os genes putativos TcAR_A em *T. cruzi* codificam a enzima recombinante funcional (rTcAR_A) bioquimicamente caracterizada e localizada no citoplasma. A atividade da AR foi detectada através do ciclo de vida dos parasitas. Demonstramos também que a TcAR_A racemiza a serina com parâmetros cinéticos semelhantes aos da Ala. Também demonstramos que ambos isômeros da Ala podem ser transportadas e através de um sistema ativo não estereosseletivo de baixa especificidade. Ambas, L-Ala, e D-Ala, podem ser completamente oxidadas em CO₂, fornecendo elétrons para a cadeia de transporte de elétrons, sustentando OXPHOS em epimastigotas de *T. cruzi*. Como não tem sido descrita em hospedeiros mamíferos uma AR, investigamos a atividade antiparasitária das tiadiazolidinonas, uma nova classe de inibidores de AR. Todos os inibidores testados exibiram uma inibição da replicação dos epimastigotas dependente da dose. Esses compostos também inibiram a atividade da rTcAR_A. Como o inibidor C3 mostrou uma menor concentração inibitória de 50% (IC₅₀) contra o crescimento de epimastigotas, o mecanismo de ação deste fármaco foi estudado em maior detalhe. C3 induz marcas típicas de morte celular programada em *T. cruzi*. De facto, os parasitas tratados exibiram uma exposição de fosfatidilserina na fase externa da membrana celular, diminuição do potencial de membrana mitocondrial, um aumento da concentração intracelular de ROS, e fragmentação de DNA. C3 apresentou um efeito inibitorio sobre o ciclo de infecção celular a concentrações na faixa submicromolar, com um alto índice de seletividade. Estes compostos também mostraram um interessante efeito anti-*T. brucei*, com similares características de ação. Em conjunto, nossos dados demonstram o papel versátil de Ala na bioenergética do parasita podendo ser secretado, ou transportado para o meio intracelular para ser oxidado pelos parasitas. Além disso, o catabolismo da D-Ala, através da AR, chama a atenção sobre a flexibilidade metabólica de *T. cruzi*, bem como sobre a relevância do metabolismo dos D-aminoácidos nesses organismos. Nossos resultados também mostraram que o AR pode ser um alvo promissor para a quimioterapia.

Palavras-chave: Transporte. L-Alanina. Metabolismo. Bioenergética. *Trypanosoma cruzi*. Alanina racemase. D-Alanina.

ABSTRACT

GIRARD, RMBM. **Role of Alanine and Alanine Racemase in the metabolism of the *Trypanosoma cruzi***. 2018. 167 p. Ph.D. Thesis (Parasitology) – Instituto de Ciências Biomédicas, Universidade de São Paulo, São Paulo 2018.

Amino acids participate in several critical processes in the biology of trypanosomatids, such as osmoregulation, cell differentiation and host cell invasion. Some of them provide reducing power for mitochondrial ATP synthesis. It was previously shown that alanine, which is formed mainly by the amination of pyruvate, is a metabolic end-product when parasites are replicating in a medium rich in glucose and amino acids. It was shown as well that this amino acid can also be used for the regulation of the cell volume and the resistance to osmotic stress. Interestingly, *Trypanosoma cruzi*, the etiological agent of Chagas's disease, possess putative Alanine racemase (AR) genes that catalyze the interconversion between L- and D-alanine. Here we describe, for the first time, that the putative TcAR_A genes in *T. cruzi* encode a functional recombinant enzyme (rTcAR_A) that was biochemically characterized and localized in the cytoplasm. AR activity was detected through parasites life cycle. We demonstrated that TcAR_A, also racemize serine with similar kinetic parameters. In this work, we also show that both isomers can be taken up and through a low specificity non-stereoselective active transport system. We show that L-Ala and as well D-Ala, through it conversion to the L-isomer by TcAR_A, can be completely oxidized to CO₂, supplying electrons for OXPHOS in *T. cruzi* epimastigotes. As AR had not been described in mammalian host, we investigated the anti-*T. cruzi* activity of the thiadiazolidinones, new class of potential AR inhibitors. All, the compounds exhibited dose-dependent inhibition of epimastigote replication and also inhibited the rTcAR_A activity. As C3 had shown a lower 50% inhibitory concentration (IC₅₀) against epimastigote growth, the mechanism of action of this drug was studied in more detail. C3 induces typical programmed cell death (PCD) hallmarks in *T. cruzi*. Indeed, treated parasites exhibited a phosphatidylserine exposure in the external leaflet of the plasma membrane, a decrease of the mitochondrial membrane potential, an intracellular ROS concentration deregulation, and nuclear DNA fragmentation. C3 exhibits a submicromolar range in the intracellular cell cycle infection with a high selectivity index. These compounds also induced an interesting anti-*T. brucei* with a similar mechanism of action. Taken together, our data demonstrate the versatile role for Ala in the parasite's bioenergetics being secreted as well taken up and oxidized by the parasites. Moreover, the catabolism of D-Ala, through AR, underlines the parasites outstanding parasites metabolic flexibility as well the relevance of the D-amino acids metabolism in these organisms. Our results also showed that AR could be a promising target for chemotherapy.

Keywords: Transport. L-Alanine. Metabolism. Bioenergetics. *Trypanosoma cruzi*. Alanine racemase. D-Alanine.

1. Introduction

1.1 Chagas' disease

The American Trypanosomiasis was also named Chagas Disease in honor of its discoverer Carlos Ribeiro Justiniano Chagas. Remarkably, in the article published in a medical journal in 1909 (2), Carlos Chagas described the etiological agent as well the vector and wild reservoirs of this disease. This parasite was named *Trypanosoma cruzi* in honor of Oswaldo Cruz. Over 100 years after its discovery, the disease is estimated to affect approximately 6 million to 7 million in all American countries and has been recognized by the World Health Organization as one of the world's neglected tropical diseases (3). Chagas disease is endemic of the Americas, from the South regions of USA to the south of Argentina and Chile. Its transmission parallel largely that of the vector insect geographical distribution (Figure 1) (3). Human population movements also spread the disease in non-endemic regions such as Europa, Asia or Oceania turning Chagas disease into a global health problem (4).

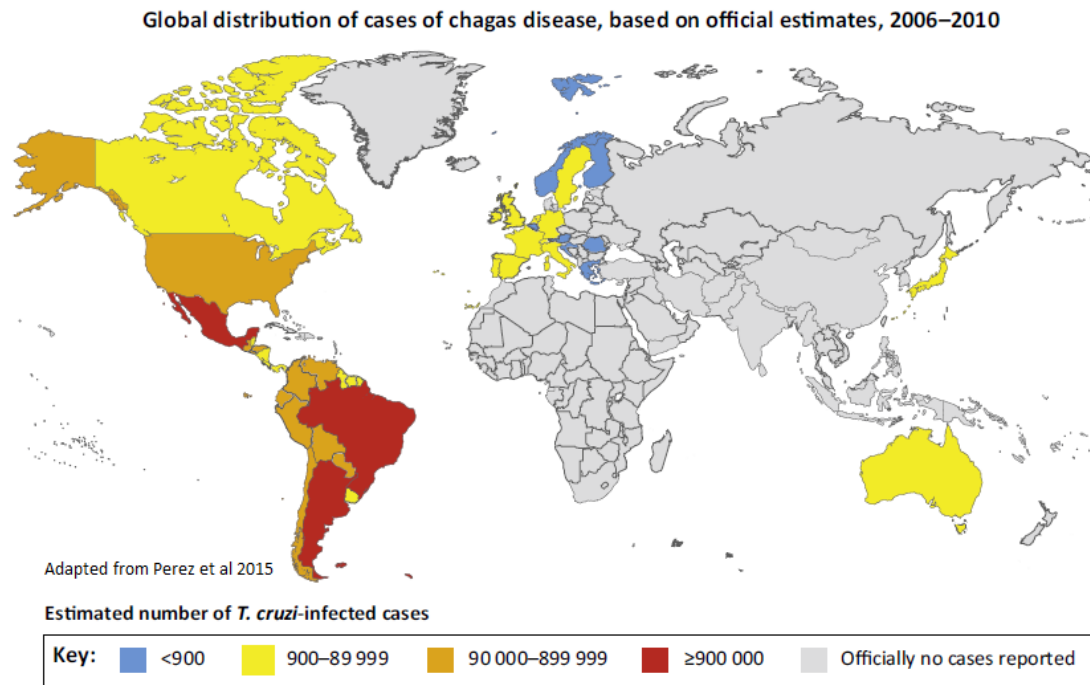


Figure 1 Global distribution of Chagas Disease. Data from World Health Organization (3).

Classically, Chagas disease is transmitted to humans through the contact of contaminated faeces from the vector insect (bugs from the *Reduviidae* family) with the mucosa or injured skin, (5). In addition to insect transmission, Chagas disease can be transmitted by ingestion of food or drinks contaminated with the vector feces containing *T. cruzi* oral or by the ingestion of raw meat from infected sylvatic reservoir (5). Alternatively, the transmission can occur by transfusions, transplants, laboratory accident and congenital mechanisms (5).

Chagas disease presents an acute and a chronic phase. In the acute phase most patients are asymptomatic. However, when symptoms are present, usually they are unspecific such as fever, headache, muscle or abdominal pain, difficulty in breathing, inflammation at the inoculation site (inoculation chancre) or unilateral palpebral oedema (Romaña sign). The acute phase lasts about lasts about 2 months after infection. In the chronic phase, two main forms of

the disease are distinguished: indeterminate (about 60–70% of the patient) and determinate or symptomatic (about 30–40% of the patient). The symptomatic form of the disease is in turn subdivided into three main forms: cardiac, digestive or cardiodigestive forms. During the indeterminate form, the patients are positive to serological tests with undetectable parasitemia; No signs and symptoms of the disease can be detected. The determinate phase is generally suspected from clinical findings, mainly in the cardiac and digestive systems, and diagnosis should be confirmed by the results of laboratory tests (3-7). The chronic phase persists for the entire host's lives and the determinate form of chronic disease usually appears 10–30 years after the initial infection (6).

Benznidazole and nifurtimox are the only drugs with proven efficacy against Chagas disease (5, 7). Both drugs, despite various side effects, are effective during the acute phase, however their efficiencies during the chronic phase, when most cases are diagnosed, remain controversial (6, 7). These facts underline the urgent need to intensify the search of therapeutics targets against *T. cruzi*. In this sense, it is relevant to study in detail the unique features of the *T. cruzi* biology. Studies on metabolism, drugs resistance, action of new class of compounds and other general biological functions of *T. cruzi* helped to understand and to identify potential compounds against *T. cruzi*-specific targets (8-14). These finding allowed proposing new therapeutic strategies such as drug repositioning or new compounds which could result in an adequate treatment for the acute and chronic forms of Chagas disease.

1.2 Biology of *T. cruzi*: a brief revision

1.2.1 *T. cruzi* organelles linked to the energy metabolism

T. cruzi possess unique structures/organelles, characteristic of the Trypanosomatidae family (Figure 2). Herein, we briefly described some of them that are relevant to understand its metabolism.

T. cruzi possess a unique and branched **mitochondrion** which has the classical compartments: the outer and inner membrane and between them the inter membrane space and the mitochondrial matrix. The mitochondrial inner membrane forms the typical invaginations known as mitochondrial cristae (Figure 2). Studies on mitochondrial functions in *T. cruzi*, indicate that this organelle shares similar bioenergetics properties with its mammalian counterpart. Indeed, several biochemical parameters were analyzed such as respiration rates at different energy states oxidizing different metabolites, mitochondrial membrane potential, as well ions fluxes and the redox state (12, 15)(12, 15)(12, 15)(12, 15)(12, 15)(12, 15). Regarding the electron transfer system (ETS), the presence of complex II to V, in the inner membrane of the mitochondrion, has been demonstrated (Figure 3). (15, 16). In spite of the presence of a variable quantity of subunits of complex I in the ETS, there is a controversy on the contribution of complex I to energy metabolism in *T. cruzi* (Figure 2). Indeed, *T. cruzi* complex I appears to be insensitive to rotenone and *T. cruzi* naturally mutant strains for some complex I subunits did not present OxPhos alterations (12, 16-20). This facts suggest that NAD^+ regeneration occurs through a fumarate reductase (21).

Inside the mitochondrial matrix, **the kinetoplast is a structure containing the mitochondrial genome, and** situated in the region proximal to the nucleus. The kinetoplast is

made of kinetoplastid DNA (kDNA) composed by two type of interlocked and concatenated circular DNA: the minicircles and the maxicircles. There are several thousand minicircles (0.5 to 2.5 kb), and a few dozen maxicircles (20 to 40 kb) (22). The kDNA is a remarkable complex feature of the Trypanosomatidae family, which needs to be replicated and then equally segregated between daughter cells along the parasites life cycle. The kDNA replication is independent from the nucleus and possess a complex machinery to perform this process (22). Another special characteristic is that it presents approximately 60 % of AT-rich regions (23). These unique characteristics of kDNA has been a widely studied for potential chemotherapeutic target.

Glycosomes are an unusual type of peroxisomes which contain most of the glycolytic enzymes. This compartmentalization is a hallmark of the kinetoplastids since in most organisms this metabolic pathway is essentially cytosolic. The first six enzymes involved in the glycolytic pathway are compartmentalized within the glycosome (24). Another peculiarity is the lack the typical allosteric regulation presents in hexokinase (HK) and phosphofructokinase (PFK), which, classically tightly regulate the glycolytic pathway in many organisms (25-28). Furthermore, glycolysis only function properly with an individual pool of cofactors (NAD(H), ADP and ATP) separated from the cytosolic pool. Interestingly, the number and/or the compositions of glycosomes vary from species to species and even among developmental stages of the same species. In addition, other metabolic pathways occur within this organelle such as: purine salvage and *de novo* pyrimidine biosynthesis, fatty acid elongation, isoprenoid biosynthesis, and sterol biosynthesis (29, 30).

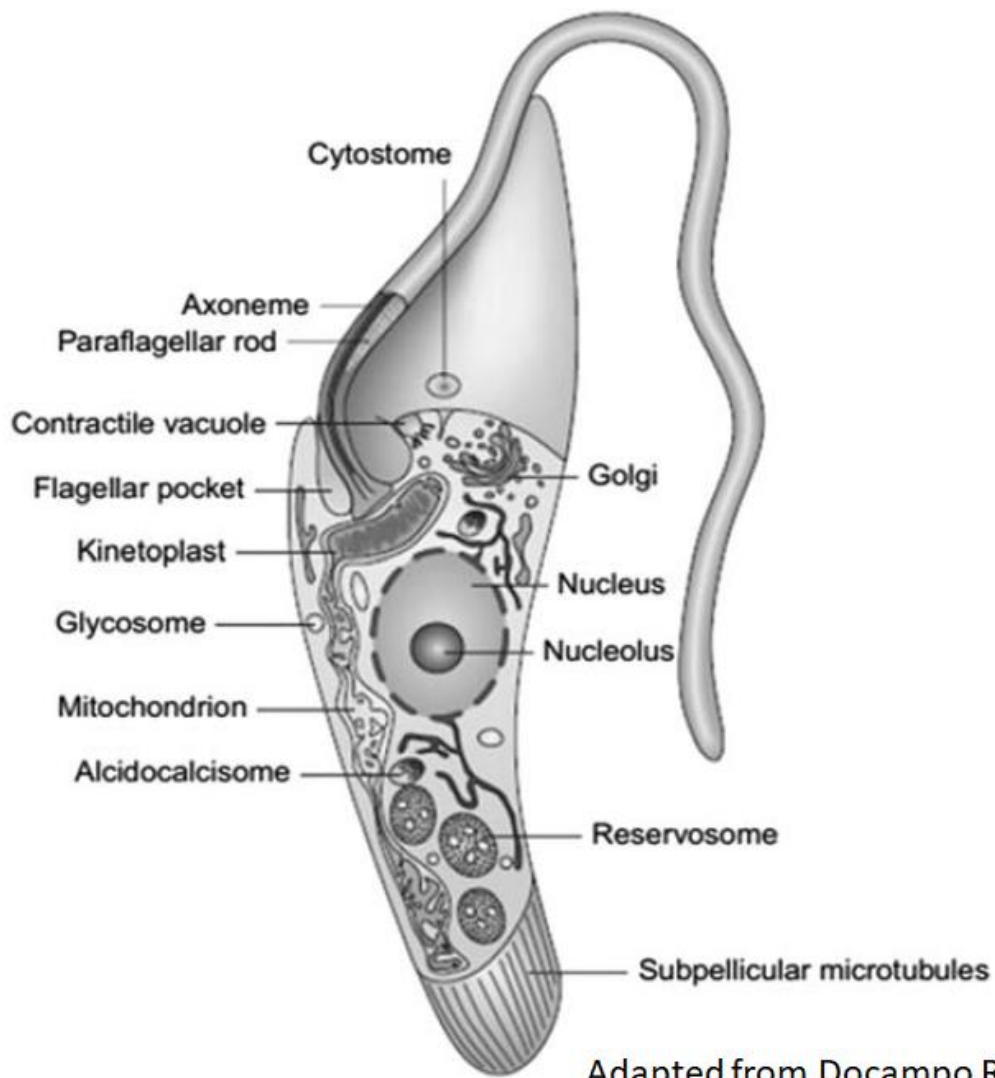


Figure 2 Schematic representation of longitudinal section of an epimastigote showing the main structures and organelles found in *T. cruzi*.

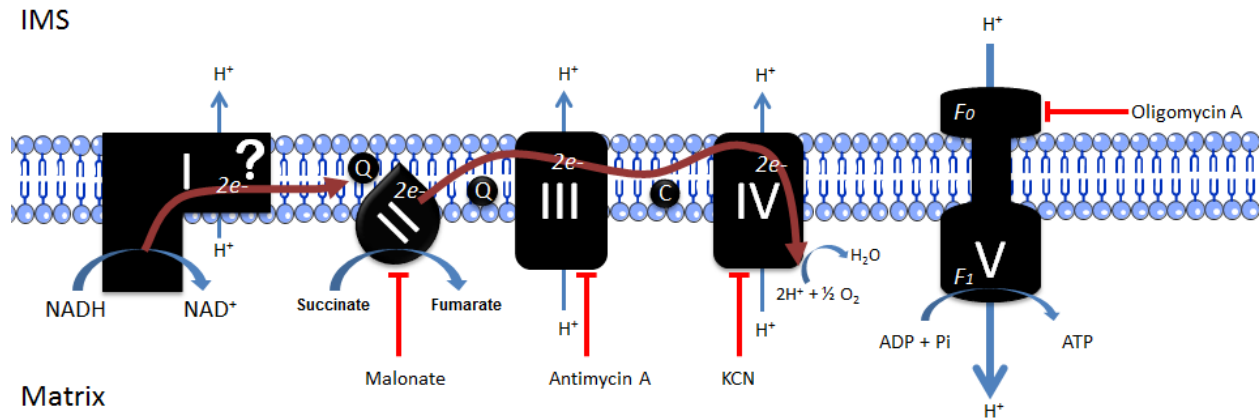


Figure 3 Schematic representation of the electron transport chain in *T. cruzi*. The major complexes of the electron transport system are present in the inner mitochondrial membrane, and some enzymes/intermediates are generated in the inter membrane space (IMS) or mitochondrial matrix. Q: ubiquinone; C: cytochrome c. The F_0 - F_1 ATP synthase is responsible for ADP phosphorylation resulting from the proton-motive force generated through an electrochemical gradient.

1.2.2 *T. cruzi* life cycle

This protist affront a myriad of environmental conditions during its complex life cycle, which occurs inside the entire digestive tube of triatomine insect vectors, the blood of more than 100 species of mammals, and the cytoplasm of (potentially) every mammalian nucleated cell in every tissue and organ (31). Inside the insects, parasites proliferate in the gut as non-infective forms, named epimastigotes, and later develop into infective non-replicating metacyclic trypomastigotes (32). During the insect bloodmeal, the metacyclic forms are expelled together with the insect feces and potentially being in contact with the skin of the mammalian host. The metacyclic forms eventually enter into the host through mucous or the abrasion caused by the host when scratching after being bitted (33). Once inside the host, the metacyclic trypomastigotes must invade the host-cells, differentiate into intracellular amastigotes and reach the cytoplasm to initiate the cell proliferation (34). After several rounds of binary divisions, amastigotes, differentiate to trypomastigotes forms passing through a transient replicative form

called intracellular epimastigotes (35, 36). Trypomastigotes lyse the infected cells and burst into the extracellular environment. Trypomastigote forms can infect neighboring cells or eventually reach the bloodstream, from where they can infect cells in remote tissues or infect an uninfected Triatomine bug during its bloodmeal (Figure 4) (37-39). As a consequence of its complex life cycle, *T. cruzi* faces different environments with markedly different biochemical characteristics and availability of nutrients.

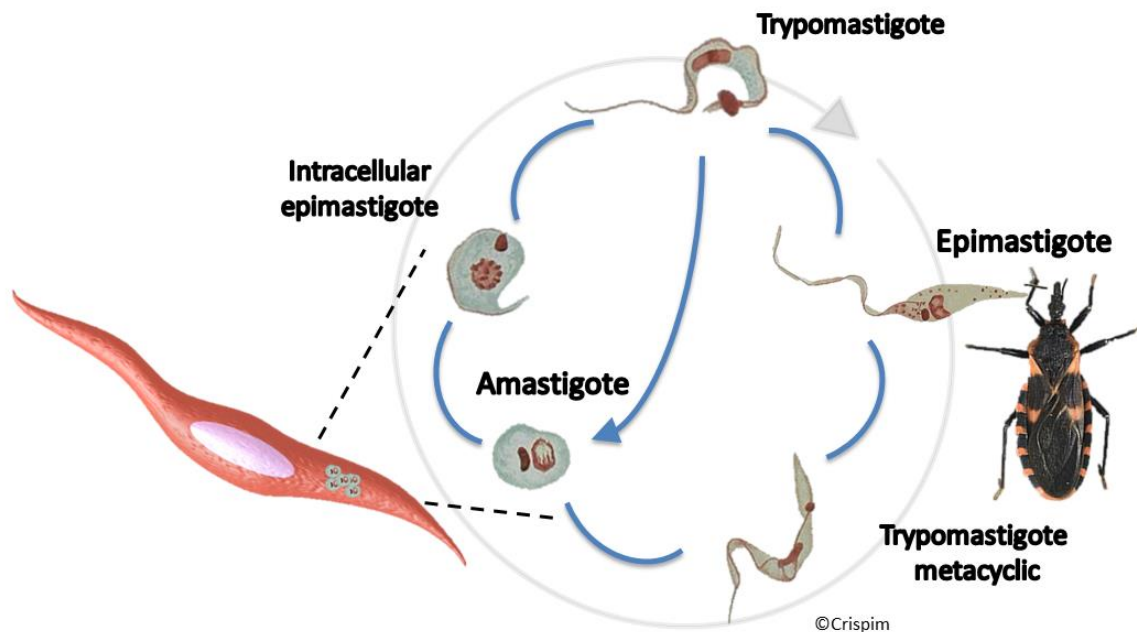


Figure 4 Schematic representation of the *Trypanosoma cruzi* life cycle. Replicative, non-infective epimastigotes forms, differentiate to the non-replicative, infective metacyclic trypomastigotes inside the insect gut. Metacyclic forms invade the mammalian host cells and differentiate into replicative amastigote forms to establish the infection. These forms give rise to a transient stage called intracellular epimastigotes, which differentiate into trypomastigotes. After cells lysis, trypomastigotes can disseminate in the mammalian host through the bloodstream. The ingested trypomastigotes, by uninfected insect vector during its bloodmeal, differentiate again into epimastigotes, which can colonize the insect digestive tract.

1.2.3 The journey of *T. cruzi* inside the insect vector

T. cruzi infection occurs essentially in the intestinal tract of the vector insect. The insect digestive system is composed by the anterior midgut (stomach, AM), the posterior midgut (PM) and the rectum. Classically, the blood is hemolysed in the AM, then the nutrients are digested in the PM, finally the rectum stores the remains of the digestion process. Bloodstream trypomastigotes enter first in the AM where they face to inhospitable environment where parasite population decreases dramatically (40). The remaining trypomastigotes quickly reach the PM to differentiate in epimastigote and sustain the infection. *T. cruzi* preferentially growth in the insect rectum (41, 42), however it also can be found in the other intestinal region depending of the infection process. Nevertheless, parasites, through the digestive system, have to rapidly adapt to tremendous stress in theses environments such as temperature and pH variation, osmotic pressure, nutritional deprivation, and sudden interaction with insect immune defence and microbiota system. Temperature variation has been shown to affect the parasites infection *in vitro* as well *in vivo* (43, 44) because the temperature modifies several biochemical processes such as molecular transport, enzyme activity but also the vector feeding pattern (33). During the triatominae feeding process the excreta pH exhibits change of almost 3 fold from an acidic to an alkaline pH, associated with an increase in osmolality in the same proportion (45). *T. cruzi* has to endure striking period of starvation as its vector, the triatominae, can affront fasting periods up to one years (45). Throughout the insect vector starvation process, the parasites show an astonishing resilience to the insect nutritional deprivation condition (42, 45, 46). Indeed, the *T. cruzi* colonization pattern remains unaltered up to four month and living parasites can be find 200days after the last blood meal in triatominae rectum (41). Furthermore, *T. cruzi* must confront to the insect immune system which produces several molecules such as lysozymes (47),

defensins or nitric oxide (32). Additionally, an increase number of studies indicate an intimate interplay between *T. cruzi* and the triatomine microbiota (48). The gut microbiota can have an impact in the parasite development and growth (32, 40, 44). For example, *Serratia marcescens* can impair the *T. cruzi* infection (49). On the other hand, *T. cruzi* successful infection also affects microbiota composition, with an increase of it diversity (48) while other failed to show a clear correlation between triatomine, *T. cruzi* and microbiota (44, 50). The complex interactions and fitness mechanisms among the parasites, the insect and it microbiota remains largely unsolved as this interplay appears to be specific to parasites strains and invertebrates species and/or population (50, 51). Taken together, *T. cruzi* have to exhibit outstanding adaptation mechanisms to establish a successful infection along it journey inside the insect.

1.3 *T. cruzi* metabolism

1.3.1 Carbohydrate metabolism in *T. cruzi*

The ATP synthesis in *T. cruzi* can occur at substrate level phosphorylation through the glycolytic pathway and through oxidative phosphorylation. Trypanosomatids have a high rate of glucose incorporation and consumption which is associated with the production and excretion of reduced compounds from glucose catabolism instead of its complete oxidation. This metabolic particularity occurs even under aerobic conditions and is called “aerobic fermentation of glucose” (52). In the case of *T. cruzi*, the major products of aerobic glucose catabolism by epimastigotes are the alanine (Ala) and to a lesser extent succinate (53-55). Ala production might be linked to reoxidation of glycolytically produced NADH, even under aerobic conditions (55-57). Furthermore, trypanosomatids did not present Pasteur effect (a considerable decrease in

glucose consumption in aerobiosis) which is related to the lack of major controls on the glycolysis as described above.

1.3.2 Amino acids (AA) metabolism

Beyond the carbohydrates consumption, early works showed that several AA are metabolized by *T. cruzi* (58). Classically AA should be oxidized through their conversion to glutamate or aspartate, and then be processed via the Krebs cycle into the mitochondrion. Since, various studies appoint that AA transport and metabolism are relevant processes to supply the derived metabolites to many biological processes in *T. cruzi* (11, 12, 14, 59). These AA could be produced by proteolysis of proteins, biosynthesized from metabolic precursors or to be taken up from the extracellular medium (14).

1.3.2.1 AA Uptake

The metabolite incorporation is the first essential step for various metabolic routes, as it allows the entry of essential nutrients into the cell and regulate its intracellular concentrations. In the case of the AA, their availability and metabolism results from an equilibrium among protein degradation, their uptake and their biosynthesis. Since AA participate in a broad variety of metabolic pathways, they are important for *T. cruzi* survival (14). As AA are available in most of environments that *T. cruzi* encounters throughout its life cycle, the uptake of various AA has been biochemically characterized. Briefly, two systems for Arg and for Pro (59-62), one for Glu (63), one for Lys (64, 65), one for Cys (66), one for Asp (67), one for the branched-chain AAs (BCAA) Val Ile and Leu (68), one for His (69), one for Gln (70) and one for GABA (71) has been already biochemically characterized (Table 6). Most of these processes has been associated to members of the AAAP (AA/Auxin Permease), a family of transporters grouping H⁺/AAs and

auxin permeases (72-75). Some transport system has been associated to specific transport functions in *T. cruzi* (76-79). The gene TcAAP7 was identified, through heterologous expression and overexpression in epimastigotes, to encode for the Lys transport in *T. cruzi* (64, 65). Furthermore, the Arg high-affinity as well as the non stereospecific Pro transport system has also been associated to the genes encoding for TcAAAP411/TcAAP3 and TcAAP24 respectively (76-79).

1.3.2.2 AA as energy source

First evidence of AA consumption was reported by Chang et al who observed an increase of pH at the end of epimastigotes exponential growth. The alkalization of the culture medium was due to the excretion of significant amounts of NH_4^+ , a hallmark of AA degradation. This fact was confirmed by other authors, whose studies showed that asparagine, glutamine, aspartate, glutamate, leucine, isoleucine, and proline can be metabolized by *T. cruzi* (11, 12, 25, 58, 69, 80-84). More recently, Pro degradative pathway has been characterized in detail and it was shown that it is able to sustain energetically the *T. cruzi* growth and host cells infection process (82, 83). His can be completely oxidized by *T. cruzi* powering ATP production through the oxidative phosphorylation (69). It has been shown that His is relevant in the epimastigote bioenergetics and persistence within the invertebrate host (69). Arg has been proposed to be involved in the management of the energetic metabolism through an arginine kinase (ArgK) (EC 2.7.3.3). The phosphorylation of Arg to phospho-Arg (P-Arg) using ATP would act as an “energetic reservoir”, similar to phosphocreatine in mammalian, restoring ATP levels when it is needed (61).

1.3.2.3 Alanine metabolism in *T. cruzi*

As described above, Ala (together with succinate), is one of the main end-products from glucose degradation by epimastigote (55). It has been proposed that Ala production could be necessary to reoxidate the NADH glycolytically produced, even under aerobic conditions (55-57). Ala is at the same time the main intracellular and secreted AA which appears to be produced separately and kept compartmentalized (54). Ala possesses a central role in the AA catabolism, through its participation in the Glu conversion into α -KG. This reaction can be considered as the main gate to entry the TCA cycle for several AA that are converted into Glu to be fully oxidized, such as His, Gln, Pro, degradation via the Krebs cycle (Figure 5). Indeed, the Glu dehydrogenase can convert Glu into α -KG producing NH_4^+ or alternatively, the $-\text{NH}_2$ group from Glu can be transferred to pyruvate by aminotransferase, such as Ala (ALAT) or a Tyr aminotransferase (TAT), producing Ala (Figure 5). The significant amounts of NH_4^+ produced (25, 53, 80), from the AA catabolism (11, 12, 25, 58, 69, 80-84) needs to be detoxified. A main detoxifying pathway for this excretion product is the urea cycle. However, *T. cruzi* lacks it (85, 86). In this sense, the parasite requires a specific metabolic network to address NH_4^+ accumulation. Recent works showed that NH_4^+ storage in acidic compartments (reserosome and lysosomes) by intracellular NH_4^+ transporter (87) as well as its condensation with Glu by the glutamine synthetase (88) are essential for NH_4^+ detoxification and participate in various *T. cruzi* biological functions. The deficiency of the intracellular NH_4^+ transporter leads to alterations in the replication, differentiation and response to starvation and osmotic stress (87). The glutamine synthetase inhibition impairs the epimastigote replication under excess of ammonium and the establishment of the host-cell infection (88). In this context, it is important to underline that as α -KG-Glu interconversion is reversible, the concerted action of a NAD-linked Glu dehydrogenase, and aminotransferases should contribute as well with the detoxification of the excess of NH_4^+

produced by the AA consumption. Taken together, the robust transamination system, yielding to accumulation of Ala instead of NH_4^+ (55), indicates the central role of Ala in the nitrogen detoxification. Furthermore, early studies suggested that, despite of being an end-product of the metabolism, Ala could be metabolized by *T. cruzi* since it was able to trigger O_2 consumption (58). Indeed, depending on the relative quantity of substrates and products, Ala could be reconverted into pyruvate by the same aminotransferases or Ala dehydrogenases that produce it (57, 89). In addition, the influx and efflux of Ala has been shown to participate in the response to osmotic stress (90-92). The osmoregulation process is present in all *T. cruzi* stages and is complete about 5 min (92). The AA efflux, where Ala is the principal AA, responsible for approximately 50% of the regulatory volume response.

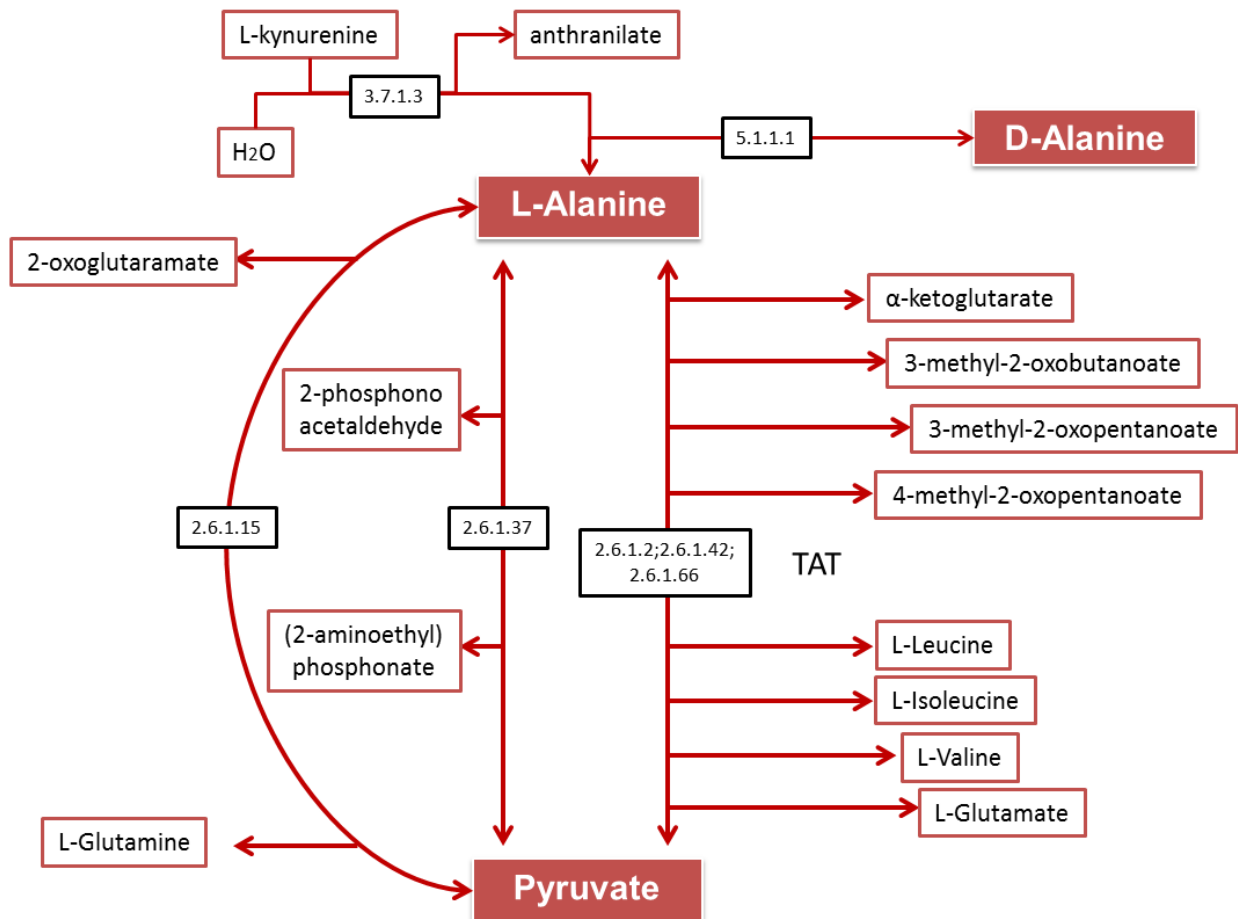


Figure 5 Schematic representation of the Alanine metabolism.. ECs numbers correspond to: 3.7.1.3: kynureninase, 5.1.1.1: alanine racemase, 2.6.1.15: glutamine-pyruvate transaminase, 2.6.1.37: 2-aminoethylphosphonate-pyruvate transaminase, 2.6.1.2: alanine transaminase and tyrosine transaminase (TAT), 2.6.1.42/2.6.1.66: TAT.

1.3.2.4 D-AA metabolism

D-AAs (D-AA) functions remains little studied. The AA α -carbon which is connected to an amine group (-NH₂), a carboxyl group (-COOH), a hydrogen (75) and a side chain (-R) is a stereocenter. Effectively, depending on the spatial arrangement of these four different groups, it exist two stereoisomers: the levorotatory (L) and the dextrorotatory (D) which are not superimposable mirror images. Living organisms principally employ L-AA as proteins building block. Several hypotheses have addressed the asymmetry origin of the biomolecules. The abiotic hypothesis suggests that the molecular symmetry may have been broken, through physical induction, before the appearance of life. On the other hand, biotic origin hypothesis suggest biomolecules symmetric selection based on some biological advantage (93). Ultimately, the asymmetric origin of life remains open. Nevertheless, D-AAs are key constituents of the bacterial peptidoglycan (PG) (94). Indeed, D-AAs presence within PG confer resistance to proteolysis, additionally it presence has been associated to resistance to antimicrobial agents (95, 96). D-AA also possess critical roles in various other bacterial physiological processes, such as biofilm formation, peptidoglycan remodeling, energy catabolism, small peptides production and sporulation (97-101). D-AA has been considered biologically irrelevant in higher eukaryote for a long time. However, recent studies elucidated the presence of various D-AAs, such as D-Ser, D-Asp or D-Ala and appoint a tightly regulated D-AA metabolism in the nervous system but also in the mammalian endocrine system (102, 103). For example, D-Ser and D-Asp and it respective

racemases were shown to have a central role in mammalian brain neurotransmitters system (104, 105).

It is believed that D-AAs are principally originated in nature from L-AA racemization by AA racemases (106). A large broad of racemases and epimerases has been cataloged and characterized in the bacteria and fungi kingdom. Briefly, some racemases classically use, with some exceptions, the pyridoxal phosphate (PLP) as cofactor such as the serine racemase (107), alanine racemase (AR), and aspartate racemase (AsR), while glutamate racemase (GR) and proline racemase (PR) are generally PLP-independent. Regardless of the type of racemase, the AA α -proton is removed then reprotonated on the same or the opposite side of the C α (108). This reaction is reversible and works in both directions: L to D and D to L. PR is, until now, the first and only biochemically characterized racemase in *T. cruzi* (109, 110). Two PR isoforms are present in all life cycle stages, and are involved in parasites differentiation and infections as well as acting as a B-cell mitogen (110, 111). The Ala racemase (AR) (EC 5.1.1.1) catalyzes the interconversion of L-Ala and D-Ala, the bacterial AR is classically a PLP dependent enzymes (Figure 5) (108). AR is a key enzyme in bacteria to generate D-Ala for the biosynthesis of PG. Indeed, the AR absence could be lethal in absence of exogenous D-Ala in bacteria (97, 112, 113). Other studies appoint that prokaryotic ARs are also implicated in regulating spore germination regulation (101, 114) and D-Ala catabolism (115, 116). AR has been also found in some eukaryotic microorganisms associated with the formation nonribosomal peptide such as cyclosporin A (117) or HC-toxin (118) or as well D-Ala catabolism (119). Furthermore, AR was also found in aquatic animals (120-124). Various eukaryotic ARs from aquatic invertebrate were characterized (120, 124-126) and it has been hypothesized that AR is involved in the osmotic regulation (127). Regarding kinetoplastids, AR activity was only reported in *Leishmania*

amazonensis associated with D-Ala release and a possible role in response to hypotonic stress (128). Interestingly, significant amount of free D-AA and as well D-AA-bearing peptides were found in the *T. cruzi* insect forms (129). These evidences stress the existence and the relevance of D-AA metabolism in *T. cruzi*. Putative AR have been found in *T. cruzi* genome, appointing the relevance of the D-AAs metabolism (11, 14).

5. Conclusions

- Beyond being a main end-product of the metabolism of glucose and AAs, L-Ala can:

- ✓ Be taken up by the cells through a low specificity non-stereoselective active transport system with a main driving force being a transmembrane H^+ gradient, most likely created by a plasma membrane located proton-pumping ATPase
- ✓ Be oxidized with production of CO_2 , triggering O_2 consumption, contributing to the maintenance of the inner mitochondrial membrane potential and powering ATP production through the oxidative phosphorylation.

- Here we describe, for the first time, that the putative TcAR_A genes in *T. cruzi* encode at least a functional recombinant enzyme (rTcAR_A):

- ✓ rTcAR_A biochemical parameters were determined, being the enzyme able to perform its activity across in a large spectrum of pH and temperature. Furthermore, TcAR_A also racemize Ser with similar kinetic parameters when compared to Ala racemization.
- ✓ AR activity was detected through all the parasites life cycle stages and TcAR_A is localized in the cytoplasm.

-D-Ala :

- ✓ Is likely transported by the same transport system of L-Ala.
- ✓ Can be catabolized, through its conversion to L-Ala by TcAR_A, producing CO_2 and used for ATP production by OxPhos to feed the energy metabolism

- Thiadiazolidinones compounds a new class of AR inhibitors:

- ✓ Inhibited TcAR_A activity.

- ✓ Presented promising anti-parasitic activity, inducing the PCD features in *T. cruzi* and *T. brucei*.

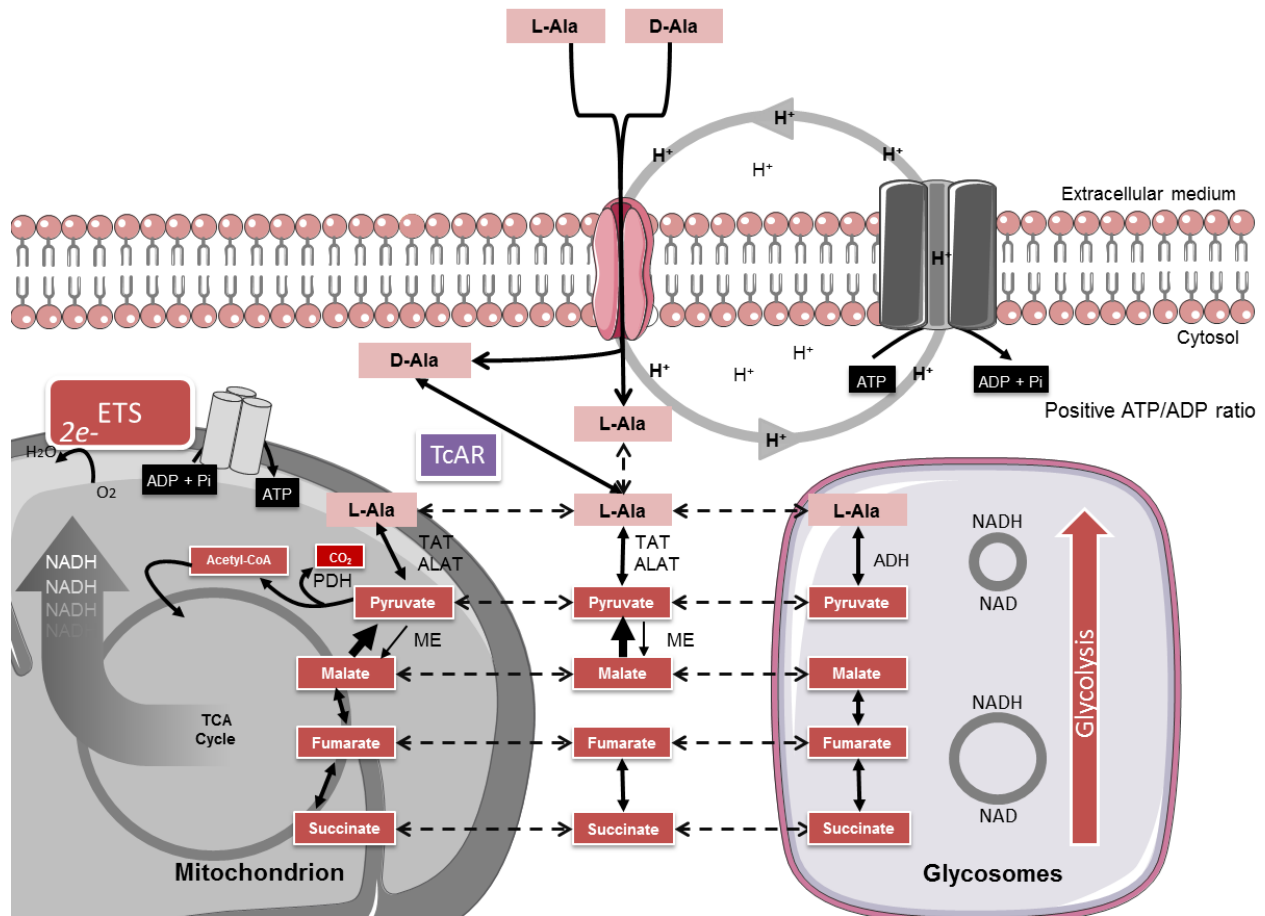


Figure 38 Schematic proposal for the uptake and catabolism of L-Ala and D-Ala in *T. cruzi*. The glycosomal and mitochondrial compartments and the TCA cycle are indicated. The metabolic flux at each enzymatic step is represented by arrows of different thicknesses. Dashed arrows indicate the intracellular shuttle of the molecules between different compartments. ETC: Electron Transport Chain; TAT: tyrosine aminotransferase; ALAT: Ala aminotransferase; ADH: Ala dehydrogenase; ME: malic enzyme; PDH: pyruvate dehydrogenase; TcAR_A Alanine racemase.

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