



Trypanosoma cruzi infection in wild mammals of the National Park 'Serra da Capivara' and its surroundings (Piauí, Brazil), an area endemic for Chagas disease

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Summary We studied the prevalence of *Trypanosoma cruzi* infection among eight species of wild small mammals ($n=289$) in an area where human cases of infection/disease have occurred. Dogs ($n=52$) and goats ($n=56$) were also surveyed. The study was carried out inside a biological reserve, the National Park 'Serra da Capivara' and its surroundings in Piauí State, Brazil. The marsupial *Didelphis albiventris* and the caviomorph rodent *Trichomys apereoides* were found to be the most important reservoirs in the study area. *Trichomys apereoides* was the most abundant species (80%) and *D. albiventris* the most frequently infected (61%). Both *T. cruzi* I and *T. cruzi* II genotypes were isolated from these species. One specimen of *Tr. apereoides* displayed a mixed *T. cruzi* I/zymodeme 3 infection. Serum prevalence among dogs suggests that they may be involved in the maintenance of the parasite in the peridomestic environment, in contrast to goats, which are not apparently of any epidemiological importance. The distinct distribution and patterns of infection observed in the study areas suggest that even in the same biome, epidemiological

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studies or determination of control measures must take into account ecological peculiarities.

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1. Introduction

Trypanosoma cruzi (Kinetoplastida: Trypanosomatidae), the agent of Chagas disease, is a widely distributed trypanosomatid. It has been detected in more than 100 mammalian species, belonging to eight orders, which are spread through all phyto-geographic regions of the Neotropics (Barretto, 1979).

Trypanosoma cruzi displays extreme genetic diversity. The geographic distribution of its genetic variants and their association with particular hosts remain unclear. The earliest studies, based on the analysis of six isozymes, recognized three main subpopulation assemblages or zymodemes: zymodemes 1(Z1), 2(Z2) and 3(Z3) which, in Brazil, were associated mainly with human infection (Z2) and to the enzootic transmission cycle (Z1 and Z3). Subpopulation Z3 is prevalent mainly in Amazonas and is associated with acute or indeterminate human cases. Infrequent cases of human infection by this zymodeme were also reported in Bahía and Pará states. In the wild, Z3 is associated with terrestrial and burrowing animals, mainly armadillos (Miles, 1983).

Recent molecular studies (analysis of rRNA genes, minixon genes and microsatellites) recognized two main subpopulations of *T. cruzi*: *T. cruzi* I (TcI, corresponding to Z1) found in wild mammals, particularly opossums of the genus *Didelphis*, and *T. cruzi* II (TcII, corresponding to Z2), associated with areas of Brazil endemic for Chagas disease and recently linked to placental mammals (Devera et al., 2003). It has been suggested that TcI originated from *Didelphis marsupialis* and TcII from primates and/or caviomorph rodents (Briones et al., 1999; Miles, 1983). The phylogenetic relatedness of Z3 subpopulation to TcI or TcII is still controversial (Araujo et al., 2002).

Domestic and sylvatic transmission cycles of *T. cruzi* may be isolated or connected (Miles et al., 1977). Nevertheless, the so-called sylvatic transmission cycle is far more complex than was formerly understood, since distinct transmission cycles may occur simultaneously in the same forest fragment independently of the forest strata or behavior pattern of the hosts (Fernandes et al., 1999; Jansen et al., 2000; Lisboa et al., 2000). Brazil is considered to be free from vectorial transmission of Chagas

disease. Nevertheless detailed studies of still unknown aspects of the biology and ecology of *T. cruzi*, including the variables that modulate the transmission cycles among its reservoir hosts, are of pivotal importance in a former endemic area, if definitive control of the disease is proposed.

In the National Park 'Serra da Capivara' (PARNA) the signs of very ancient human colonization in South America, attested by paintings on the walls of caves and rock shelters (Guidon and Arnaud, 1991) suggest that an ancient interaction between *T. cruzi* and primates, including humans, may have occurred in this ecosystem.

This paper presents the results of a study on the infection of wild small mammals and domestic mammals by *T. cruzi* inside the PARNA and in two neighboring districts.

2. Materials and methods

2.1. Study area

The region studied, located in the southwest of the state of Piauí, is one of the poorest and most underdeveloped regions in Brazil. The climate is semi-arid and the region is known as 'caatinga' (white scrub) due to the whitish color of the leafless vegetation during the dry season. The mammalian fauna in the caatinga is actually a subset of the fauna of Atlantic rainforest and 'Cerrado', a central region of Brazil (FUNDMHAM, 1998). The wild small mammalian fauna consists mainly of marsupials and rodents; they prefer the more humid microhabitats among the rocks, but can also be found close to human dwellings.

The PARNA is located between latitude 08°26'50" and 08°54'23" S and longitude 42°19'47" and 42°45'51" W in Piauí; there has been no human influence, besides protection measures, in this area for the last 20–30 years. We studied three areas inside the PARNA, Zabelé (Z), Sitio dos Oitenta (S80) and Pedra Solta (PS) and two surrounding administrative districts, João Costa (JC) and Coronel Jose Dias (CJD). They are 40 km away from each other. Both districts are subjected to much human activity and the vegetation is highly degraded by deforestation, burning and pressure from raising goats (Figure 1). In JC, both the cardiac and digestive forms of the

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