Chagas disease is a vector-borne zoonosis caused by the protozoan Trypanosoma cruzi. This taxon had been described as composed of two lineages (TCI and TCII) and five subgroups (I–V). After a short acute or primary infection, the mammal host sustains subclinical infections, which are microscopically undetectable in peripheral blood during the undetermined and chronic phases. Conversely, parasitemia in those phases is detected only by polymerase chain reaction (PCR). The classic parasitologic diagnostic method for Chagas disease xenodiagnosis, which can amplify T. cruzi after feeding on infected hosts. Although xenodiagnosis is specific, it lacks sensitivity and is limited to high levels of parasitemia. The epidemiology of Chagas disease and clinical symptoms are associated with the infective T. cruzi genotypes. Therefore, would be useful to know the dynamics of these genotypes.

In the present study, we assess the occurrence of temporal fluctuations of T. cruzi DTUs in peripheral blood of two naturally infected wild reservoir specimens of O. degus by using a combination of two diagnosis methods: 1) xenodiagnosis with domestic and sylvatic vectors (Triatoma infestans and Mepraia spinolai), respectively, and 2) PCR DNA-based detection specific for minicircles and hybridization analyses with T. cruzi genotype-specific probes.

Ten nymphs (stages II and III) of each vector species were allowed to feed simultaneously on anesthetized O. degus for 30 minutes or until engorgement on the rodent (mean ± SD weight of ingested blood = 0.2 ± 0.05 mg). After 30 days, feces and intestinal contents of the triatomines were observed under a light microscope. The minimal theoretical parasitemia detected under these conditions is approximately 5 parasites/mL (1 parasite/0.2 mL). However, because several but not all insects (2–5) were parasite positive by visual examination, the estimated parasitemia would be > 10–25 parasites/mL.

After microscopic inspection, the intestinal contents of each vector species pool was collected and PCR was performed as reported. Amplicons were subjected to electrophoresis on an agarose gel and transferred to nylon membranes. Copies of these membranes were hybridized separately with each probe under high stringency conditions. Construction of genotype-specific probes was performed as described. Different T. cruzi clones were used as templates to generate DNA probes to determine parasite genotypes. The probes were P10-labeled.

A total of 35 O. degus were captured at the field and analyzed. Overall, only two O. degus showed infection with both vector species and six were positive only for M. spinolai. The two O. degus samples positive for both vector species were subjected to serial xenodiagnosis to determine the genotype of the T. cruzi population circulating at different times: time 0, one year, two years, and two and a half years. Results obtained with O. degus sample 5, which was infected with a one genotype (TCI), are shown in Figure 1. This result was confirmed with both vector species at different times. Results obtained with O. degus sample 8 showed mixed infection with DTUs TCI, TCII, and TCVI at time zero for M. spinolai, but only TCII for T. infestans. However, one year later, both vectors showed mixed infections with lineages TCI and TCV. After two years, both vectors contained only genotype TCII. After two and a half years, vectors were still infected with TCII.

Trypanosoma cruzi colonizes several tissues and evades the immune response by a concomitant low parasitemia level not detectable by several diagnosis methods. Parasites circulate as mixed infections. This finding is common for T. cruzi because several mammals and vectors are infected with more than one T. cruzi genotype, which results in recombination and hybrid genotypes.

We report that infection of rodents can show temporal fluctuations of different T. cruzi genotypes, which is probably the result of fluctuation of relative proportions of parasite loads of different genotypes in peripheral blood. We detected infections in this O. degus with at least three of the four T. cruzi genotypes during the complete follow-up (xenodiagnosis at time 0). Two genotypes (TCII and TCVI) disappeared, and another one (TCV) appeared one year later. During the second year, only one genotype (TCII) was detected and maintained. A different scenario was detected for O. degus sample 5, which showed infection with only TCI during the entire sampling period.

In this study, we preferentially detected genotype TCI in both vector species. This genotype was likely circulating at high parasitemia levels in O. degus sample 18 because experimental infections in T. infestans with different T. cruzi DTUs indicated that genotype TCI is transmitted at a low rate; genotype TCI...
is transmitted at a high rate. Our results for *T. cruzi* genotypes in these two animals are consistent with local prevalence in the study area. Recent studies of *T. cruzi* genotypes circulating in the wild vector in this disease-endemic area showed that TCI and TCIi are the most prevalent genotypes.

We suggest that both rodent species showed moderate or high levels of parasitemia. We used xenodiagnosis with two sylvatic rodent species because insect vectors amplify high levels of parasitemia. We used xenodiagnosis with two infected sylvatic rodent.

The temporal fluctuation of the four *T. cruzi* genotypes could be explained by at least two hypotheses that are not mutually exclusive. First, colonization of different tissues with *T. cruzi* described in patients and experimentally infected animals with organ damage releases *T. cruzi* into the vascular system; these parasites then colonize other tissues. Second, infection is controlled by the immune system. Both processes might reach an equilibrium and explain the low parasitemia levels observed in immunocompetent patients in the chronic phase of Chagas disease. Future parasitologic studies of molecular pathogenesis may be necessary to understand the mechanisms underlying infection control in naturally infected hosts.

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