

Predominance of *Trypanosoma cruzi* genotypes in two reservoirs infected by sylvatic *Triatoma infestans* of an endemic area of Chile

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We report results of *Trypanosoma cruzi* infection and parasite genotypes in the wild *Octodon degus* and synantropic reservoir *Rattus rattus* from an endemic area with sylvatic *Triatoma infestans* as the only detected vector. The infection status was determined by hemi-nested PCR directed to minicircles DNA and genotyping by hybridization tests with a panel of five specific probes, including two probes for TcI subgroups (clones 19 and 20). *O. degus* was found infected with 13.3% and mainly with sublineage TcIIId, and less with TcIIb and TcI. Meantime the synantropic *R. rattus* was found infected with 27.7% and mainly with TcI and much less with TcIIId, TcIIb and TcIIe. The results are discussed to explain the distribution of *T. cruzi* genotypes between these two reservoirs and the importance of sylvatic foci of *T. infestans* allowing the permanence of the wild and peridomestic cycle of Chagas disease.