

Molecular epidemiology of Chagas disease in the wild transmission cycle: The evaluation in the sylvatic vector *Mepraia spinolai* from an endemic area of Chile

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The sylvatic transmission cycle of Chagas disease in Chile is composed of wild mammals and insects of the genus *Mepraia*. We determined infection rates and *Trypanosoma cruzi* genotypes in *Mepraia spinolai*. We collected 227 insects from two ecologically contrasting areas to assess *T. cruzi* infection. Polymerase chain reaction (PCR)-amplified minicircle DNAs were characterized by Southern blot and hybridization tests with genotype-specific probes. Infection in insects from the more fertile area was almost 2-fold higher than in the poorer area. The genotype TCI was the most prevalent and other genotypes such as TCIIb, TCIIId, and TCIIe were found at lower rates. The areas differed in their genotype distribution but not in their genotype diversity. We suggest that the difference in abundance and richness of mammals between the areas may be producing the detected infection levels in vectors. Our results are compared with those reported for mammals from the same area. Copyright © 2009 by The Am