

Genotyping of *Trypanosoma cruzi* in a hyper-endemic area of Colombia reveals an overlap among domestic and sylvatic cycles of Chagas disease

Mejía-Jaramillo, Ana María

Agudelo-Uribe, Luz Adriana

Dib, Juan Carlos

Ortiz, Sylvia

Solari, Aldo

Triana-Chávez, Omar

Background: Chagas disease is a neglected illness caused by the *Trypanosoma cruzi* parasite, which widely affects American communities. This study attempted to identify *T. cruzi* genotypes circulating in four indigenous communities of the Sierra Nevada of Santa Marta, Colombia, to investigate parasite transmission dynamics in these communities. In addition, some epidemiological variables to determine the risk factors for infection with this parasite, such as the prevalence of *T. cruzi* infection, the triatomine species, and the domestic and sylvatic mammals that act as vectors and reservoirs of the parasite in the domestic, peridomestic and sylvatic cycles, were examined.

Methods. We developed a prospective study to identify the main risk factors associated with *T. cruzi* infection in the region. The *T. cruzi* prevalence was determined by ELISA, IFA and PCR.

Triatomines species and both domestic and sylvatic mammals from all communities were captured and sampled. To analyze parasite transmi