

Transmission dynamics of *Trypanosoma cruzi* determined by low-stringency single primer polymerase chain reaction and southern blot analyses in four indigenous communities of the Sierra Nevada de Santa Marta, Colombia

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This study attempted to evaluate the transmission dynamics of *Trypanosoma cruzi* in four indigenous communities of Sierra Nevada de Santa Marta (SNSM), Colombia. Low-stringency single primer-polymerase chain reaction (LSSP-PCR) of the minicircles and Southern blot analyses were used to characterize samples from patients, vectors, and reservoirs in these communities. The LSSP-PCR profiles revealed a high genetic variability but with similarities among the parasites present in the samples of vectors, patients, and reservoirs of the same and different communities. Cluster and analysis of molecular variance (AMOVA) analyses of data derived from LSSP-PCR and Southern blot suggest a gene flux among populations of *T. cruzi* circulating in patients, vectors, and reservoirs. The results support the idea that the domestic and wild transmission cycles overlap in the SNSM, with *Rhodnius prolixus* as the main vector and *Triatoma dimidiata* playing an important role in the transmission of Chagas disease