

# Real-time PCR strategy for the identification of *Trypanosoma cruzi* discrete typing units directly in chronically infected human blood

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© 2017 Elsevier B.V. The protozoan *Trypanosoma cruzi* is the causative agent of Chagas disease, a major public health problem in Latin America. This parasite has a complex population structure comprised by six or seven major evolutionary lineages (discrete typing units or DTUs) TcI-TcVI and TcBat, some of which have apparently resulted from ancient hybridization events. Because of the existence of significant biological differences between these lineages, strain characterization methods have been essential to study *T. cruzi* in its different vectors and hosts. However, available methods can be laborious and costly, limited in resolution or sensitivity. In this study, a new genotyping strategy by real-time PCR to identify each of the six DTUs in clinical blood samples have been developed and evaluated. Two nuclear (SL-IR and 18S rDNA) and two mitochondrial genes (COII and ND1) were selected to develop original primers. The method was evaluated with eight genomic DNA of *T. cruzi* population