

Haplotype distribution of five nuclear genes based on network genealogies and Bayesian inference indicates that *Trypanosoma cruzi* hybrid strains are polyphyletic

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ABSTRACT. Chagas disease is still a major public health problem in Latin America. Its causative agent, *Trypanosoma cruzi*, can be typed into three major groups, *T. cruzi* I, *T. cruzi* II and hybrids. These groups each have specific genetic characteristics and epidemiological distributions. Several highly virulent strains are found in the hybrid group; their origin is still a matter of debate. The null hypothesis is that the hybrids are of polyphyletic origin, evolving independently from various hybridization events. The alternative hypothesis is that all extant hybrid strains originated from a single hybridization event. We sequenced both alleles of genes encoding EF-1 α , actin and SSU rDNA of 26 *T. cruzi* strains and DHFR-TS and TR of 12 strains. This information was used for network genealogy analysis and Bayesian phylogenies. We found *T. cruzi* I and *T. cruzi* II to be monophyletic and that all hybrids had different combinations of *T. cruzi* I and *T. cruzi* II haplotypes plus hybrid-specif-

ic haplotypes. Bootstrap values (networks) and posterior probabilities (Bayesian phylogenies) of clades supporting the monophyly of hybrids were far below the 95% confidence interval, indicating that the hybrid group is polyphyletic. We hypothesize that *T. cruzi* I and *T. cruzi* II are two different species and that the hybrids are extant representatives of independent events of genome hybridization, which sporadically have sufficient fitness to impact on the epidemiology of Chagas disease.

Key words: *Trypanosoma cruzi*; Chagas disease; Molecular evolution; Phylogeny; Small subunit rDNA