

Phylogenetic analysis of microsatellite markers further supports the two hybridization events hypothesis as the origin of the *Trypanosoma cruzi* lineages

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To better understand the evolution of the etiologic agent of Chagas disease, we cloned and sequenced 25 alleles from five *Trypanosoma cruzi* microsatellite markers. The study of the sequences showed highly conserved alleles present in *T. cruzi* clones belonging to TCI, TCIIc, and TCIIe. This result was also confirmed by the phylogenetic analysis of MCLE01 allele sequences. The examination by capillary electrophoresis of six microsatellite markers from 19 *T. cruzi* clones showed a high proportion of the alleles found both in the TCI and TCII sublineages. The phylogenetic reconstruction of these 19 clones produced a tree with two major clusters with bootstrap support of 100% and 95%. The first cluster includes *T. cruzi* clones belonging to the TCI and TCIIa lineages. The second cluster is composed of TCI, TCIIc, TCIIId, and TCIIe *T. cruzi* clones. The analysis of five microsatellite markers in the CLBrenner genome showed that almost all the microsatellite markers are synteny; non-Esmeraldo and