Differentiation of Trypanosoma cruzi I subgroups through characterization of cytochrome b gene sequences

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To identify and characterize chilean samples of Trypanosoma cruzi and their association with hosts, the first 516 bp of the mitochondrial cytochrome b gene were sequenced from eight biological samples, and phylogenetically compared with other known 20 American sequences. The molecular characterization of these 28 sequences in a maximum likelihood phylogram (-ln L = 1255.12, tree length = 180, consistency index = 0.79) allowed the robust identification (bootstrap % >99) of three previously known discrete typing units (DTU): DTU IIb, IIa, and I. An apparently undescribed new sequence found in four new chilean samples was detected and designated as DTU Ib; they were separated by 24.7 differences, but robustly related (bootstrap % = 97 in 500 replicates) to those of DTU I by sharing 12 substitutions, among which four were nonsynonymous ones. Such new DTU Ib was also robust (bootstrap % = 100), and characterized by 10 unambiguous substitutions, with a single nonsynonymous G to T change at s