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PRIMARY STRUCTURE OF TRYPANOSOMA CRUZI SMALL SUBUNIT RIBOSOMAL RNA CODING REGION

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Trypanosoma cruzi rRNA, trypanosomatids, rDNA sequencing, rRNA molecular evolution

Trypanosoma cruzi small subunit ribosomal RNA molecules (SSU rRNA) exhibit a slower electrophoretic mobility than their homologous from vertebrates. T. cruzi SSU rRNA gene was sequenced from genomic recombinant plasmid clones. The assigned coding region was 2319 bp which represent to our knowledge the longest SSU rRNA gene described to date. On the basis of sequence comparisons with published sequences from other kinetoplastids, we conclude that the extra nucleotides in T. cruzi gene occur in highly variable regions of the rRNA genes. T. cruzi gene substitutions analysed in a secondary structure rRNA model, indicate a strong conservation in the so called universal core. A phylogenetic analysis of this family of organisms indicate that the actual branching order of Trypanosoma species can not be unequivocally determined.

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Parallel evolution between kDNA and nuclear markers in Leishmania genus

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Key words : kDNA, taxonomy, DNA polymorphism, Leishmania.

Quantified kDNA RFLP analysis of diversified sample of Old World Leishmania previously characterized using 15 isoenzyme loci show highly significant correlation between these two sets of genetical markers. Moreover, the data involving maxicircle as well as minicircle variabilities are correlated together too. These results clearly show that kinetoplastic and nuclear genomes do not evolve independently in Old world Leishmania, and that, if some recombination occurs in the kinetoplast, it is not sufficient to break the general pattern of linked evolution between the two genomes on the evolutionary scale. This fact has important consequences for stock typing and strain specific kDNA probe designing.