

Investigation of the DNA content of *Trypanosoma cruzi* and *Trypanosoma rangeli*

Lucila Langoni Naves¹, Marcos Vinícius da Silva², Virmondes Rodrigues Jr.², Eliane Lages-Silva², Luis Eduardo Ramirez², Emanuella Francisco Fajardo¹, André Luiz Pedrosa^{1*}

¹ Departamento de Bioquímica, Farmacologia e Fisiologia, Instituto de Ciências Biológicas e Naturais, Universidade Federal do Triângulo Mineiro, Uberaba, Brasil

² Departamento de Imunologia, Microbiologia e Parasitologia, Instituto de Ciências Biológicas e Naturais, Universidade Federal do Triângulo Mineiro, Uberaba, Brasil

Trypanosoma cruzi is a human protozoan parasite and it is the causative agent of Chagas' disease. Currently the specie is divided into six highly polymorphic taxonomic groups. The genome of CL Brener clone was estimated at 106.4-110.7Mb and DNA content analyses revealed that it is a diploid hybrid clone. *Trypanosoma rangeli* is a hemoflagellate that share the same reservoirs and vectors as *T. cruzi*, but differently of *T. cruzi*, it is not pathogenic to vertebrate hosts but it is pathogenic for the invertebrate vector. The genome of *T. rangeli* was previously estimated at 24Mb and parasite strains can be divided in KP1(+) and KP1(-) according to the presence or absence of the kDNA minicircles. Previous sequencing of two loci of *T. rangeli* suggested that some of its strains could be heterozygous, since we have observed sequence polymorphisms between the alleles investigated. The objective of this study was to investigate the DNA content in different strains of both parasites. The KP1(+) strains of *T. rangeli* used were P07 and P19 and KP1(-) SO29 and *T. cruzi* strains used were Alv, RN1, JG and CL Brener. The epimastigote forms were cultured in LIT medium at 28°C and subsequently fixed in 70% ethanol and labeled with propidium iodide for flow cytometry analysis. The DNA content of *T. cruzi* strains were estimated in 69Mb, 77.8Mb and 106.4Mb for Alv, RN1 and JG strains, respectively. In the KP1(+) strains of *T. rangeli*, DNA content were estimated at 75.4Mb, 71.5Mb, for strains P07 and P19, respectively. In KP1(-) lineages DNA content of SO29 strain was estimated in 66.2Mb. From these results we conclude that there was a greater variation in the DNA content of *T. cruzi* strains. Differences in DNA content of *T. rangeli* strains were not associated with genotype/line of the parasite. From the comparison with sequence data of two loci, the P07 strain seems to correspond to a diploid hybrid of *T. rangeli*.

Keywords: *Trypanosoma cruzi*. *Trypanosoma rangeli*. DNA content, Flow cytometry, Hybrid lineages.