GENE STRUCTURE AND REGULATION OF MOLECULAR CHAPERONE ClpA/HSP100 OF *TRYPANOSOMA CRUZI*

Campos, R.A.[1], Silva, R.[1], Rondinelli, E.[1], Urmenyi, T.P.[1]

Instituto de Biofísica Carlos Chagas Filho, Lab. Metabolismo Macromolecular Firmino Torres de Castro, Universidade Federal do Rio de Janeiro, Brasil

Members of the HSP100/Clp family of chaperones promote disaggregations of proteins complexes and protein degradation. Being a heat-inducible protein, HSP100 is a good model for studying gene regulation. We aim to study the ClpA/HSP100 gene structure, expression and regulation in *Trypanosoma cruzi*. The predicted amino acid sequence of HSP100 of *Trypanosoma brucei* was used to search for orthologous sequences in the draft genome of *T. cruzi* clone CL Brener. A coding region of 1810pb was identified, and an internal segment was selected for PCR-based amplification and used as a probe in genomic southern blots. The hybridization pattern is compatible with HSP100 genes being present in low copy number in the genome. Protein similarity analysis and inspection of the relevant region of the draft genomic sequence showed that the coding region obtained is incomplete due to a gap at the 3' end. Experiments are being performed to obtain the missing sequence. We are also performing northern blot analysis to determine HSP100 mRNA levels and half-life in normal and elevated temperatures. The complete coding region will be cloned into expression vectors and the recombinant protein used to generate HSP100-specific antibodies in order to characterize the subcellular localization of the protein.

Key-words: gene expression; HSP100; *Trypanosoma cruzi*

Supported by CNPq; FAPERJ