MECHANISMS CONTROLLING GENE EXPRESSION IN TRYPANOSOMA CRUZI.

Daniella C. Bartholomeu, Rosiane A. Silva, Patrícia R. Araújo, Wanderson D. DaRocha, Gustavo C. Cerqueira and Santuza M.R. Teixeira

Departamento de Bioquimica e Imunologia, Instituto de Ciências Biomédicas, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil.

Control of gene expression in trypanosomatids depends on several layers of regulation, with a predominance of regulatory pathways acting at a post-transcriptional level. This allows the rapid reprogramming of genetic expression required for the differentiation process associated with transmission between insect vector and mammalian host. We have studied post-transcription regulation in *Trypanosoma cruzi* by analyzing three gene families that are differentially expressed during the parasite life cycle: α– and β-tubulins, whose transcripts are found at higher levels in epimastigotes; amastins, which encodes surface glycoproteins with increased expression in amastigotes; and MASPs, which encode a large family of mucin-associated surface proteins expressed preferentially in trypomastigotes. In spite of the constitutive transcription, steady state levels of mRNAs from all these genes vary significantly when amastigotes, epimastigotes and trypomastigotes forms are compared. For the amastin and tubulin genes we found that these differences result from changes in mRNA half-life: the half-life of amastin mRNA is 7-fold longer in amastigotes than in epimastigotes whereas the half-life of tubulin transcripts is 2-fold longer in epimastigotes than in amastigotes. A 203-nt sequence present in the amastin 3'UTR, recognized by a protein more abundant in amastigotes than in epimastigotes and a 44-nt sequence resembling an AU-rich element (ARE) present in the α-tubulin 3´UTR were identified as important regulatory cis-elements. Further studies on tubulin gene expression indicated that this AU-rich element may be involved in an auto-regulatory mechanism that modulates the stability of tubulin transcripts in response to changes in the dynamics of *T. cruzi* microtubules.

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