MODULATION OF TRYPANOSOMA CRUZI TRANSCRIPTOME ASSAYED BY MICROARRAYS: INSIGHTS INTO THE REGULOME

Probst, C.[1]; Pavoni, D.P.[1]; Góes, V.M.[1]; Manhães, L.[1]; Dallagiovanna, B.M.[1]; Mortara, R.A.[2]; Romanha, A.J.[3], Schenkman, S.[2]; Buck, G.A.[4];Goldenberg, S.[1]; Krieger, M.A.[1]

[1]Instituto de Biologia Molecular do Paraná, Curitiba, Brasil; [2]Escola Paulista de Medicina, São Paulo, Brasil; [3]Instituto René Rachou, Belo Horizonte, Brasil; [4]Virginia Commonwealth University, Richmond, EUA

Trypanosoma cruzi, the causative agent of Chagas Disease, is a primitive eukaryote. Its gene expression regulation has several peculiarities, as polycistronic transcription, trans-splicing, post-transcriptional regulation and absence of a well-characterized RNA pol II promoter. Few microarray studies have evaluated the transcriptome of this parasite, identifying a small amount of differentially expressed genes (in general, 2-5%), and a systematic analysis of transcriptome regulation is missing. We have conducted a microarray analysis of *Trypanosoma cruzi* transcriptome, using a microarray containing aproximately 6,000 probes, on different processes as differentiation (metacyclogenesis), life cycle, drug resistance, cell cycle, stress response and protein overexpression. Taken together, these data provide a great opportunity to identify mRNA sets co-regulated in distinct situations, enabling to build the first representation of *T.cruzi* regulome, with co-regulation of genes involved in processes as replication, transcription, translation, among others; these groups are been analysed to identify cis-acting elements. This is the first study showing this kind of pattern in Trypanosomatidae. We are carrying an increase in the number of biological situations analysed, broadening our biological knowledge of *T.cruzi* gene expression regulation.

Acknowledgments: CNPq, FIOCRUZ, NIH

Key Words: *Trypanosoma cruzi*, microarray, gene expression, post-transcriptional regulation