Involvement of a NO-dependent modification in the control of *Trypanosoma cruzi* gene transcription

Magalhães, R. D. M.[1]; Mattos, E. C. [2]; Rozanski, A. [1];Galante, P. A. F. [1]; Camargo, A.A.[1]; Alves, M.J.M.[2]

1- Sírio-Libanes Hospital, São Paulo, Brazil
2- Instituto de Química, Universidade de São Paulo, São Paulo, Brazil

Introduction: *The Trypanosoma cruzi* gene expression is thought regulated mainly at post-transcriptional level because parasite has polycistronic genome, however little is known about transcriptional control in the parasite. The involvement of NO-dependent modifications with transcriptional regulation in animal cells is well established, and increasing evidence is accumulating regarding this kind of regulation in plant cells. This control mechanism can be performed directly, by modifying transcription factors, or indirectly, through secondary core protein linked or not to the epigenetic control. The NO-dependent modifications are also involved in the modulation of proteins responsible for *T. cruzi* response after contact with host elements, such as the extracellular matrix. Nitration of tyrosine residues of histones H2A and H4 was found in trypomastigotes. The ChIP-seq technique is an innovative method that uses the next generation sequencing to identify genome regions bound to interest proteins, generating maps protein-DNA interaction. **Objective:** This study aims to identify the effect of nitration of proteins associated with chromatin to control gene expression of *T. cruzi* trypomastigote form during the adhesion to ECM using the ChIP-seq technique. **Materials and Methods:** The library construction and sequencing of the samples proceded in Sírio-Libanes Hospital and a pipeline was implemented to *in silico* analysis using BWA, MACS, MAnorm and intermediated home developed scripts. **Results and Discussion:** In this study were identified 1290 genome regions prevalent in samples of parasite incubate with ECM and 969 in samples of parasite without ECM, using peak calling parameters to search narrow regions. Using broad parameters setup, it was discovery 19 regions in samples incubate with ECM and 22 regions in samples not incubate. Eight of this regions were validate using qPCR technique. **Conclusions:** This work shows, for the first time the involvement of nitration in *T.cruzi* transcription process after its contact with extracellular matrix of vertebrate host.

Key-words: *Trypanosoma cruzi*, transcription, CHIP-seq, extracellular matrix, nitration
Acknowledgment: FAPESP