

***Trypanosoma cruzi* Alkaline 2-DE: Comparative Proteome Analysis of Human Life Stages**

1-

Magalhães, A.D.¹; Charneau, S.^{1,3}; Guércio, R. A.P.¹; Queiroz, R. M. L.¹; Santana, J. M.²; Sousa, M.V.¹; and Ricart, C.A.O.¹

- 1- Laboratory of Biochemistry and Protein Chemistry, Department of Cell Biology, University of Brasília, Brazil. E-mail: ricart@unb.br
- 2- Laboratory of Parasite-host Interaction, Department of Cell Biology and Faculty of Medicine, University of Brasília, Brazil.
- 3- Ceilândia Campus, University of Brasília, Brazil

Trypanosoma cruzi, a flagellate protozoan, is the etiological agent of Chagas disease, a chronic illness that causes irreversible damage to heart and digestive tract in humans. During its life cycle, it differentiates into different life stages in insect vector (epimastigote and metacyclic trypomastigote) and mammalian host (bloodstream trypomastigote and amastigote) 2-DE bloodstream trypomastigote and amastigote samples was performed using anodic “paper bridge” sample loading supplemented by increased concentration of DTT and Triton X-100 on Multiphor II (GE Healthcare) equipment with an electrode pad embedded in DTT-containing solution near the cathode (Magalhães, *et al.*, *Proteome Science* 2008, 6: 24). We performed a comparative image analysis of the 2-DE gels using the Image Master Platinum 6.0 software (GE Healthcare). Therefore, we detected 700 spots in amastigote and 784 in trypomastigote 2-DE gels. Statistical analysis permitted the determination of differentially expressed spots among the *T. cruzi* life forms. 45 spots were more expressed by the amastigote form and, 26 by the trypomastigote. 103 spots were exclusively expressed by the trypomastigote and 34 by the amastigote form. 208 spots presented differential expression levels in each life form. 44 of these spots were selected and submitted to peptide mass fingerprinting and MS/MS analysis resulting in the identification of 28 proteins.

Support: CNPq , FAPDF

Keywords: Chagas Disease, *T. cruzi*, basic pH range, proteomics