

ANALYSIS OF SOLUBLE PROTEIN EXPRESSION OF DIFFERENT *TRYPANOSOMA CRUZI* PHYLOGENETIC GROUPS

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Trypanosoma cruzi strains represent subspecies based on their genetic and biological characteristics as well as on the host-parasite relationship. According to these, the strains are classified into two major groups: *T. cruzi* I and II. The morpho-biological diversity of parasite may suggest different patterns of protein expression that could play important roles in infectivity and survival of the parasite. In this work, 2D electrophoresis was used to analyze soluble proteins expression by epimastigote forms of *T. cruzi* I (Dm 28c and D7) and II (CL Brener and GLT) strains. Parasites were submitted to four cycles of alternating freezing-thawing in presence of PBS and protease inhibitors. Soluble proteins were precipitated by TCA and then solubilized in CHAPS, Urea, DTT and ampholytes. Experiments carried out in pH 4-7, range with an increased number of spots resolvable, showed a considerable diversity in protein expression. Variation in intensity of several spots not only between strains of the same but between both groups studied was also observed. Identified proteins by mass spectrometry could be grouped into functional categories like metabolism, structural proteins, protein destination, protein synthesis. These preliminary data could be the starting point to elucidate the preferential association of *T. cruzi* strains to distinct hosts and to unravel the pathways of Chagas disease.

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