

PROTEOME MAP OF *TRYPANOSOMA CRUZI* EPIMASTIGOTES IN ALKALINE PH RANGE

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Trypanosoma cruzi is the etiological agent of Chagas disease. During its life cycle, the parasite differentiates into diverse life stages. The correlation between biological features of *T. cruzi* developmental stage and gene expression can be assessed by 2-DE based proteomic strategies. Here, we present a 2-DE proteome map of *T. cruzi* epimastigotes in the 6-11 pH range. The final 2-DE protocol consisted of addition of 10% isopropanol to the IPG gel strip rehydration buffer, sample loading using the "paper bridge" method, use of paper strip embedded in DTT solution near the cathode and isoelectric focusing using the Multiphor II apparatus (GE). 697 spots were detected in the resulting gel. Landmark spots were subjected to trypsin digestion followed by peptide mass fingerprinting. Most of the identified spots corresponded to metabolic enzymes, specially those related to amino acid metabolism. A small G-protein, a cyclophilin A and a heat shock protein were also identified. There was a good correlation between theoretical and experimental values of Mr and pI for the spots analyzed. 2-DE maps of trypomastigotes and amastigotes are now being constructed in order to find stage specific proteins. Support: TDR/OMS, FAPDF.