MOLECULAR AND BIOCHEMICAL CHARACTERIZATION OF PROTEASOME ß-SUBUNIT GENES FROM *TRYPANOSOMA CRUZI* STRAINS

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Proteasomes are proteolytic machineries implicated in many cellular functions, including protein turnover and immunosurveillance. The catalytic core consists of 28 subunits codified by 14 genes, 3 of which ß1, -2 and -5 are catalytically active and show caspase, trypsin and chymotrypsin-like activities, respectively. By using the completed genome sequences of Trypanosoma cruzi we identified 7 genes encoding proteasome beta subunits. Amino acid sequence homology for proteasome subunits within the *T. cruzi* family (23-38%) was lower than the corresponding orthologs from yeast (65%) and human (88%). In order to perform a comparative study of the expression profile of the ß genes, we used semi-quantitative RT-PCR from *T. cruzi* I (Colombian) and *T. cruzi* II (CL, CL-Brenner, Berenice-62, Berenice-78 and Y) strains. Our results showed similar levels of expression for all genes. Southern blot experiments revealed the presence of two copies for the ß1, ß2 and ß5 genes and their chromosomal localization showed no syntenic organization. Proteolytic activities were determined using fluorogenic substrates incubated with an enriched proteasome fraction. Our results indicated that proteasome activities markedly differ between *T.cruzi* I and II populations. Finally, the proteasome levels also correlated with the differences in proteolytic capabilities observed in this study.
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