

Differential protein expression in distinct *Trypanosoma cruzi* life-cycle stages

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Chagas disease, caused by *Trypanosoma cruzi*, is a parasitic infection that affects millions of people worldwide. *T. cruzi* is classified into six different DTUs (discrete typing units), TcI-TcVI, according to specific genetic markers. There is some correlation between the DTU and the epidemiological and clinical manifestations, but the reasons for that remain unclear. The aim of this study is to compare the whole proteome of noninfective (epimastigote) and infective (metacyclic trypomastigote) life-cycle stages of nine different strains or clones, belonging to TcI, TcII, and TcVI, which are the major DTUs causing Chagas disease in Latin America. We conducted in-solution digestion of each sample, followed by LC-MS/MS analysis using a high-resolution Q-Exactive Orbitrap mass spectrometer. The MS/MS spectra were analyzed using Proteome Discoverer and the *T. cruzi* database available at UniProt. We have identified over 2,000 unique proteins. Some of the identified proteins are exclusively expressed in TcI, TcII, or TcVI. Moreover, we have found clear proteomic differences between the two life-cycle stages. Our comparative proteomic analysis of the three DTUs could eventually explain some epidemiological and clinical manifestations differences observed in *T. cruzi* infection. Finally, our results indicate the existence of potential markers specific for each DTU and novel targets for new drug and vaccine development.

Key words: *Trypanosoma cruzi*, proteomics, protein expression.