PROTEOMICS APPLIED TO CHAGAS DISEASE

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Chagas disease, which is caused by the protozoan *Trypanosoma cruzi,* is still a major cause of morbidity and mortality in Latin America. This disease is transmitted to vertebrate hosts by bloodsucking triatomine insects. We are currently applying proteomic tools to the study of *T. cruzi* life stages and triatomine salivas. Therefore, 2-DE maps of *T. cruzi* epimastigotes, trypomastigotes and amastigotes were constructed in acidic and alkaline regions using narrow pH gradients. Peptide mass fingerprinting permitted the identification of landmark 2-DE spots as well as stage-specific and differentially expressed proteins. *T. cruzi* sub-proteomes, i.e. membrane, nucleus and phosphoproteome are also being investigated. Proteomics was also applied to the study of salivas of several Chagas disease insect vectors from different Brazilian regions. A comprehensive proteome map of *Triatoma infestans* saliva was produced using 2-DE and nanoLC-MS/MS followed by a combination of stringent and sequence similarity database searches for protein identification. Most identified proteins presented blood-feeding associated functions. We also observed that proteins with anti-platelet aggregation functions belonging to lipocalin-like and apyrase families comprised most of the *T. infestans* saliva proteome.