ABSTRACT

Trichomonas vaginalis is a human pathogen that affects annually approximately 258 million people worldwide. This parasite possesses organelles of mitochondrial origin called hydrogenosomes, which generate ATP under anaerobic conditions. The identification of the protein content at the subcellular level may provide new targets for antiparasitic drugs developments as well as it contributes for our understanding of the organelles function and evolution. The availability of protocols for organelles purification and the complete genome sequence allow the study of the organellar proteomes using mass spectrometry and bioinformatics, providing a powerful strategy that combine cell biology and proteomics. In our research, we used several approaches to identify the protein composition in hydrogenosomes and mitosomes. We performed transcriptomic and proteomic analysis to investigate the molecular responses of *Trichomonas vaginalis* upon iron availability. Furthermore, the changes in the proteome during the development of metronidazole resistance were also studied. The organelles separated by differential and Optiprep-sucrose gradient centrifugation were analyzed with nano-RP-HPLC/MALDI-TOF/TOF. We also used Triton X-114 phase partitioning to separate membrane proteins and iTRAQ technique to label the peptides of the samples used for comparative proteomic analyses. In order to confirm the mitochondrion localization of the proteins, the data was analyzed using 5 different bioinformatic tools such as PSORT II, TargetP, Euk-mPLoc 2.0, Yloc and Hunter. The present study makes a significant contribution to understanding the overall *organelles* network.