

عنوان مقاله:

A proteomics approach to identify metacyclogenesis regulated proteins in Iranian clinical isolates of *Leishmania tropica*

محل انتشار:

بیستمین کنگره ملی و هشتمین کنگره بین المللی زیست شناسی ایران (سال: 1397)

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خلاصه مقاله:

Leishmania as a protozoan parasite is the etiological agent of leishmaniasis, which is responsible for a spectrum of disease. *Leishmania* parasites including a dimorphic lifecycle are transmitted by the sand-fly vector. Promastigote forms in the alimentary tract of sand-fly are extracellularly flagellated. Metacyclogenesis defines as differentiation from procyclic to metacyclic promastigotes that correlates with high *Leishmania* infectivity. We compared the proteomes of procyclic and metacyclic promastigotes of *L. tropica* in Iranian isolates. Proteins of cell lysates were extracted and the protein concentration of stages determined by using BCA assay. After digestion of proteins with trypsin/LysC, Proteome profiling was done by LC-MS/MS. in the present study more than 100 proteins were identified in each understudy stages. Among these, 40S ribosomal protein SA, Proteasome endopeptidase complex, Putative serine peptidase and Mitochondrial RNA binding protein 1 were procyclic specific proteins. Tubulin beta chain and dynein light chain were detected in the metacyclic stage. This study has shown that a number of proteins differentially expressed in procyclic and metacyclic stages of *L. tropica* isolates. According to results, proteins associated with protein synthesis pathway were expressed in procyclic. Motion proteins were identified in a metacyclic stage in accordance with infectivity power of metacyclic form

کلمات کلیدی:

Leishmania tropica, Proteomics, LC-MS

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