

Proteomic Analysis of Excretory Secretory Antigen (ESA) from *Entamoeba histolytica* HM1: IMSS

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Abstract : Amoebiasis is caused by the *Entamoeba histolytica* and still endemic in many parts of the tropical region, worldwide. Currently, there is no available vaccine against amoebiasis. Hence, there is an urgent need to develop a vaccine. The excretory secretory antigen (ESA) of *E. histolytica* is a suitable biomarker for the vaccine candidate since it can modulate the host immune response. Hence, the objective of this study is to identify the proteome of the ESA towards finding suitable biomarker for the vaccine candidate. The non-gel based and gel-based proteomics analyses were performed to identify proteins. Two kinds of mass spectrometry with different ionization systems were utilized i.e. LC-MS/MS (ESI) and MALDI-TOF/TOF. Then, the functional proteins classification analysis was performed using PANTHER software. Combination of the LC-MS/MS for the non-gel based and MALDI-TOF/TOF for the gel-based approaches identified a total of 273 proteins from the ESA. Both systems identified 29 similar proteins whereby 239 and 5 more proteins were identified by LC-MS/MS and MALDI-TOF/TOF, respectively. Functional classification analysis showed the majority of proteins involved in the metabolic process (24%), primary metabolic process (19%) and protein metabolic process (10%). Thus, this study has revealed the proteome the *E. histolytica* ESA and the identified proteins merit further investigations as a vaccine candidate.

Keywords : *E. histolytica*, ESA, proteomics, biomarker

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