Proteomic analyses of crude extracts of *S. venezuelensis* and *S. stercoralis* filariform larvae L3 and of excretory/secretory products of *S. venezuelensis* larvae

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The proteomic analysis of crude extract of S. stercoralis and S. venezuelensis larvae and excreted/secreted larvae products of S. venezuelensis were performed using the shotgun platform (LC-MS / MS) for separation and identification of tryptic peptides. There were identified 272 proteins: 158 in S. stercoralis (CSS) and 62 in S. venezuelensis (CSV) crude extracts. Analysis of secretory/excretory products of S. venezuelensis (ESPSV) revealed 52 proteins. Twenty-nine proteins were shared among the three helminth products analyzed. From the 108 proteins found exclusively in CSS, seven showed homology among species of the Strongyloides genus: of those, three have homology with S. stercoralis (allergen polyprotein homolog, metalloproteinase precursor and L3NIEAG.01); two with (macrophage migration inhibitory factor and 14-3-3 zeta); one with S. papillosus (glyceraldehyde 3 phosphate dehydrogenase) and one (Beta-tubulin) identified has homology with the three Strongyloides species (S. stercoralis, S. ratti, S. papillosus). A total of thirteen proteins were identified in both CSV and CSS, however only two proteins (HSP 60 and TPA_inf: eukaryotic translation elongation factor) has homology with S. stercoralis and S. ratti respectively. The ubiquitin protein was the most representative of the secreted/excreted products of S. venezuelensis (ESPSV); however, it showed no signal peptide. In contrast, three proteins of CSS (eosinophil peroxidase and metalloproteinase precursors and Vtype ATPase subunit B) and two of the CSV (70 kDa and 70 kDa heat shock putative) showed signal peptides, suggesting that multiple pathways can be used by Strongyloides molecules secretion. This study described herein, corroborates that immunogenic proteins of Strongyloides can be identified in proteomics analysis, which can be used as candidates for vaccination strategies and diagnosis approaches.

Keywords: *Strongyloides stercoralis.* Crude extract Secretory/excretory products. Proteomics

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