

IDENTIFICATION OF IMMUNOGENIC PROTEINS OF *ANGIOSTRONGYLUS COSTARICENSIS* BY PROTEOMIC METHODOLOGIES

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Angiostrongylus costaricensis is a Metastrongylidae worm that causes an intestinal acute inflammatory process named abdominal angiostrongyliasis. Humans are accidental hosts and do not eliminate L1 in feces, what difficults the diagnosis. This study aimed to determine the proteomic profile of immunogenic proteins of this helminth. Cellular extracts of female or male adult worms were fractionated using IPG strips (pH 3-10 L and 4-7) as the first step and 15% T SDS-PAGE in the second dimension. Some gels were stained with colloidal Coomassie and others were directly blotted onto a PVDF membrane probed with antiserum from mice experimentally infected with *A. costaricensis*. 34 spots were recognized by mice serum and identified by MALDI-TOF/TOF MS after N-terminal chemical derivatization with 4-sulphophenyl isothiocyanate (SPITC) combined with either Mascot software or manual sequencing followed by BLAST algorithm for database searching. Samples without derivatization were also directly analyzed using Mascot. Immunogenic spots included heat shock proteins, beta tubulin, protein disulfide isomerase, calreticulin, actin and galectin, among others. These results suggest that immunoproteomics can improve the search for candidate proteins for diagnostic assays and vaccine/drug design and may also help to better understand parasite biology and pathogenesis.

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