Medical Research Institute
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Proteomic Analysis of Differentially Expressed Proteins in *Schistosoma mansoni* Infected Mice Pre and Post Treatment with Ivermectin and Praziquantel

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ABSTRACT

Schistosomiasis is a snail-transmitted helminthiasis and represents the third most important tropical disease with considerable morbidity and mortality rates, mainly in low and middle-income countries. Six species out of 24 documented schistosomes causes disease in humans, comprising *Schistosoma haematobium* the causative agent of urogenital schistosomiasis, *S. japonicum, S. mansoni, S. intercalatum, S. mekongi and S. guineensis* as agents of hepato-intestinal disease. In view of the economic and public health threats of schistosomiasis, this study was designed in order to examine the differentially expressed proteins in *S. mansoni* infected mice before and after treatment with ivermectin and praziquantal based on proteomic analysis.

Efficacy of ivermectin and praziquantel were assessed by parasitological studies. Histopathological study was performed using different stains (Hematoxylin Eosin and Massion Trichrome stains) on the dissected liver to detect pathological changes represented as granulomas. Tegumental alteration of adult worms were demonstrated by using scanning electron microscope. Proteins extracted from recovered adult worms using SDS-PAGE for proteomic analysis. Mass spectrometry were performed for identification and quantification of isolated proteins. Online databases was used to identify the proteins and their molecular weights and biological functions.

Parasitological studies revealed the presence of male, female and copula ia all studied groups. Also revealed the predominance of dead ova in both treated groups. Regarding histopathological studies fibro-cellular granuloma detected as a predominate type of granuloma found. Scanning electron microscope described the effect of both drugs (ivermectin and praziquantel) on tegument of adult worms and detected the presence of tegumental damage, erosin, focal swelling, focal lesion and loss of spines. Proteomic studies revealed the differential expression of seven proteins among control and treated groups.

These results can be used in the future to pursue drug efficacy on schistosomiasis. Moreover, it highlights the role of proteomic analysis on differential proteins identification. Such data could help in the application of efficient treatment for schistosomiasis.