MINING FOR CONSERVED MOTIFS AND SIGNIFICANT FUNCTIONS IN S. MANSONI CERCARIAL SECRETIONS

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Abstract:

ABSTRACT Amy L. Schmidbauer MINING FOR CONSERVED MOTIFS AND SIGNIFICANT FUNCTIONS IN S. MANSONI CERCARIAL SECRETIONS Schistosomiasis is a disease caused by a parasitic flatworm of the genus Schistosoma. It infects an estimated 200 million people and 165 million head of livestock worldwide. There is medical interest in characterizing the parasitic proteins that interact with the human host for either the development of vaccines or the identification of drug targets. The cercarial secretome and adult tegument sub-proteome of S. mansoni have both been recently published (Knudsen, Medzihradszky et al. 2005) (van Balkom, van Gestel et al. 2005). As secretome proteins are secreted extracellularly, and tegument sub-proteome proteins are anchored in the cellular membrane, we hypothesize that both sets of proteins employ similar secretion machinery and mechanisms. Motivated by the discovery in the malarian parasite, Plasmodium falciparum, of conserved sequence motifs that are required for export downstream of N-terminal signal sequences (Hiller, Bhattacharjee et al. 2004), S. mansoni secretory and tegumental proteins were analyzed for conserved motifs using recursive iterations of MEME and MAST. To compliment the conserved motif analysis, an automated workflow to process InterProScan functional domain and GO annotation data, that employs statistical methods for determining significant functions, was developed. A conserved motif, enriched in the mechanically-induced vesicle secretion proteins, was elucidated and insight was gained into both the functions of proteins found to contain the motif, as well as the effects of different cercarial secretion induction methods. A hypothesis of the secretion model empoloyed by the invading parasite was generated.

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