USE OF QconCAT TO DEFINE THE ABUNDANCE OF SCHISTOSOME SURFACE PROTEINS

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Schistosomes, the causative agents of schistosomiasis, are helminth parasites for which significant proteomic data have been generated. As a result, we know a great deal about the protein composition of the adult worm tegument. However, we know little about the stoichiometry of the various components especially in the surface membranes which represent the parasite-host interface. Here we present a novel proteomic strategy to define the relative and absolute levels of tegumental proteins from *Schistosoma mansoni*. Multiplex protein quantification was achieved by designing a gene to create and express an artificial protein (SmQconCAT) comprising a concatenation of 33 tryptic signature peptides. These represented transmembrane, membrane-associated and host proteins identified in our previous proteomic studies. Isotopic labelling during heterologous expression of the construct provides the basis for the approach by introducing a 6 Da difference between the target peptide and its respective "heavy" ion after trypsin digestion, followed by LC-MALDI-ToF analysis. Among the investigated targets aquaporin, three phosphohydrolases and dysferlin were abundant at the parasite surface. These data provided insights into the principal biochemical processes occurring at the tegument surface and a more rational way to select vaccine candidates.

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