Computational analysis of the *Schistosoma mansoni* genome for the identification of vaccine candidates

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**Introduction**

It is widely recognized that new approaches towards the development of vaccine candidates for schistosomiasis are needed. The genome sequence, transcriptomic and proteomic data opens possibilities for vaccine development with the use of computational methods for antigen prediction. We will use these data to predict cell localization and epitopes to identify candidate antigens. The information will be mined via a relational database. Selected candidates will be tested for immunoreactivity with sera from infection resistant humans and in vaccination challenge tests using animals.

**Methods**

A total of 13,273 genes models were obtained from SchistoDB to Predict cellular localization of the proteins. We performed the SignalP and THMM analysis to determine proteins that may be in exposed to the host.

T cell epitopes are pathogen derived antigenic peptide fragments that, if bound to an MHC molecule of an antigen presenting cell, interacts with the T cell receptor triggering an adaptative immune response to the pathogen. Several immunoinformatics tools have been developed to identify epitopes. We tested the most of these methods. And by the capability of combine several methods in a unique analysis, the FRED framework was chosen to task of prediction of epitopes in the *Schistosoma mansoni* proteome to determine the peptides and proteins candidates.

Recombinant proteins and peptides will then be tested in a dot blot, western blot or array format against sera from normal endemic, infected and control individuals. This experiment will allow us to identify which candidate antigens are immunogenic and also which peptides are capable of stimulating an immune response.

**Results**

Currently we have identified and stored in SchistoDB a total of 13,273 genes models, among them 2,616 code for proteins which could possibly be exposed to the host immune system according this approach. The FRED Framework analysis has shown that approximately 70% of the exposed proteins have an average of 3 epitopes. Currently we have integrated other information to reduce the number of selected antigens (such as EST and microarray data).

**Conclusion**

We expect that by the end of the proposed work we will have selected at least 50 different antigens that were tested up to the in vitro reactivity assays and 10 that were tested in challenge assays. We also expect to have identified which peptides are antigenic on the selected proteins. The results will create the basis of following experiments to develop vaccines for further testing initially in animal models, including primates.

**Acknowledgements**

This work was supported by WHO/TDR (ID No. A70310), FAPEMIG and CNPQ

**References**