Schistosoma mansoni Functional Genomics; Applied to the Development of Vaccines

Leonardo P. Farias[1], Cibele A. Tararam[1], Bogar Omar Araújo Montoya[1], Henrique Krambeck Roffato[1], Patrícia A. Miyasato[2], Kátia Oliveira[3], Vanderlei Rodrigues[4], Toshie Kawano[2], Sergio Verjovski-Almeida[3], Luciana C.C. Leite[1].

[1]Centro de Biotecnologia; [2] Laboratório de Parasitologia - Instituto Butantan; [3]Instituto de Química and [4]Fac. Medicina Ribeirão Preto - Universidade de São Paulo

Schistosoma mansoni is the parasite responsible for schistosomiasis, affecting more than 200 million individuals worldwide. The treatment of the disease is based on chemotherapy with praziquantel, but chemotherapy does not prevent re-infection, and the development of a vaccine is considered to be the more effective approach. With sequencing of the parasite's Transcriptome, screening of the database allows functional genomic approaches for searching novel genes/proteins as vaccine candidates. We here report on several strategies used to mine the database to select 30 genes which were initially evaluated as vaccine antigens by the DNA vaccine technology. A few displayed protective potential and were cloned, expressed as recombinant proteins, further characterized as to their expression in the different stages by Real time RT-PCR and Western blot, and their immunolocalization in the parasite was investigated by confocal microscopy. Proteins that showed increased expression in the schistosomula stage and surface localization were considered to be more promising. The recombinant proteins were used to evaluate the immune response induced against these proteins in infected individuals as compared to individuals which are exposed but not infected (considered to be resistant). Some of the proteins were shown to have a higher titer in resistant individuals indicating a correlation with protection. Finally the proteins were also evaluated as vaccine antigens in challenge experiments and some confirmed their protective potential. Our results reinforce the importance of reversed vaccinology in the development of vaccines.

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