

REAL TIME RT-PCR VALIDATION OF DIFFERENTIALLY EXPRESSED GENES OF *SCHISTOSOMA MANSONI* FOR INVESTIGATION AS VACCINE CANDIDATES

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Introduction: *S. mansoni* is the predominant parasite responsible for schistosomiasis, which affects 200 million individuals in tropical regions of the world, being endemic in 74 countries, including Brazil. The anti-parasite drug is effective, but has little effect on reinfection, requiring repetitive treatment. The development of a vaccine would be the most efficient measure to control this disease. With the outcomes of the *S. mansoni* ESTs Genome Project it was possible to select *in silico* genes preferentially expressed in lung schistosomulum/adult stages and hypothetical genes with exportation signals. The majority of them do not possess similarities with proteins from other organisms, indicating that these could be genes exclusive of the parasite, possibly associated with its intra-host survival. **Objective:** Comparison of the expression of the differentially expressed genes among intra-hosp stages of the parasite by Real Time RT-PCR for validation of the genes and investigation as possible vaccine candidates. **Results and conclusions:** The real-time PCR studies identified many preferentially expressed genes in adult worms and schistosomulum and some genes only expressed in adult worms. There was partial correlation with the genes selected *in silico* for increased expression in schistosomulum. **Acknowledgements:** PAPESP for financial support.