Mapping of Some Genes on the Chromosomes of *Schistosoma mansoni* by *In Situ* Hybridization

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ABSTRACT

This study aimed to localize some genes on the chromosomes of Schistosoma mansoni by in situ hybridization. Chromosome preparation of S. mansoni from intramolluscan stages was hybrdized to biotin labeled DNA probes. The probes were prepared from cDNA clones identified by sequencing the 5'region of the inserted cDNA known as Expressed Sequence Tags (EST). Ten of these cDNAs code for specific proteins have been localized on S. mansoni chromosomes. Results have revealed that: gene code for fatty acid binding protein is located on q arm of chromosome number 2, phosphoinositide - specific phospholipase gene on q arm of chromosome number 3, gene similar to human phosphodiesterase on q arm of chromosome number 1, glyceraldehyde - 3 - phosphate dehydrogenase gene on q arm of chromosome number 1, Y-box binding protein gene on p arm of chromosome number 2, female specific polypeptide gene on q arm of chromosome number 5, LGG on q arm of chromosome number 4, calcium binding protein on p arm of chromosome number 3, gene similar to chicken cytochrome gene is located on q arm of chromosome number 2 and homosapiens mRNA for S. mansoni protein located on q arm of chromosome number 4..

Key words: ***Mapping genes, S.mansoni, in situ hybridization.***

INTRODUCTION

Schistosomes are the causative agents of the disease schistosomiasis. Over 200 million people in 74 countries and territories in the world are affected and 500-600 million are at risk (Kojima, 1998). In fact, schistosomiasis has been estimated to be the second most important tropical disease , after malaria , in term of socioeconomic impact and effect on health (Cook 1990).

Control projects for parasitic diseases have been hampered by lack of enough genetic information (Maizels, ***et al.,* 1993**) and until recently, there have been few studies directed at understanding genome structure and organization in these parasites (McManus and Hope, 1993). A complete physical map, consisting of overlapping recombinant DNA clones spanning an entire genome, is a primary guide for exploring the arrangement of an organism's genetic material and the information it encodes (Weissenbach, *et al.*, 1992).