

Gene Expression Profile among the Life Cycle Stages of Parasite
Schistosoma mansoni Using cDNA Microarrays

Katia C. Oliveira, Ricardo DeMarco, Thiago M. Venancio,
Sergio Verjovski-Almeida,

Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo

Schistosoma mansoni is the most widespread agent of schistosomiasis around the world. This parasite has a complex biological cycle divided into six different stages: egg, miracidium, germ ball, cercaria, schistosomulum and adult. To determine which genes participate in the development of the parasite throughout the life cycle, custom cDNA microarrays were used. The platform contains 4608 unique probes which represent different gene categories such as metabolism, signal transduction, cellular cycle among others. Total RNA from the five stages was isolated, and linearly amplified. Hybridization was performed by combining one stage with the next in the biological cycle (egg x miracidium, cercaria x schistosomulum, schistosomulum x adult). Data was normalized with the Lowess algorithm and analyzed with Significance Analysis of Microarrays (SAM) to select differentially expressed genes. A preliminary analysis (False discovery rate < 0.02%) shows that 4 genes were identified as more expressed in egg than miracidium and 232 genes had the opposite pattern. The next comparison revealed 155 genes more expressed in cercaria than in schistosomulum and 140 genes with an opposite pattern. Finally, the comparison between schistosomulum and adult shows only 2 genes with elevated expression in schistosomulum and 367 genes in adult. Among them, there are novel transcripts with unknown function and further characterization is warranted.

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