ID 282

Revealing new perspectives on the regulation of gene expression by the trans-splicing mechanism in Shistosoma mansoni

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Schistosomiasis is the second most prevalent neglected tropical disease caused by a Trematode flatworm from the genus Schistosoma. Schistosomes possess a complex life cycle requiring numerous and intricate mechanisms to rule transcriptional and post-transcriptional gene regulation. Thus, it is believed that spliced leader (SL) trans-splicing could play an important role in the parasite biology. The purpose of this study was is to shed light on the function of the trans-splicing mechanism in S. mansoni by searching gene categories that could be target of this process and attempting to silence transcripts harboring the SL sequence. Here, we analyze different life stages cDNA libraries enriched on SL-transcripts of S. mansoni. Our results show that, contrary to previous hypothesis, trans-spliced transcripts are associated to specific gene categories, such as carbohydrate metabolic process, RNA metabolism and DNA repair. Several trans-spliced transcripts were verified in at least two different stages of the S. mansoni life cycle. The marjority of the SL-transcripts are shared among males, females and mixed-sex adults, being followed by SL-transcripts shared by all adults and schistosomula. Among the analyzed life stages, the one presenting the lower number of shared genes is the egg. The results also reveal a set of SL-transcripts that are observed only in one stage of the life cycle and could represent transcripts that undergo stage-specific trans-splicing. Finally, we demonstrated that trans-splicing knockdown in sprocysts caused a reduction on the levels of all tested trans-spliced transcripts, but surprisingly the only phenotypic effect observed was a diminished larvae size. Financial support: CNPq, FAPEMIG