# The first appraisal of miRNA pathways in *Schistosoma mansoni*: computational analysis and developmental gene expression

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RNA silencing refers to a series of nuclear and cytoplasmatic processes involved in the post-transcriptional regulation of gene expression or post-transcriptional gene silencing (PTGS), either by sequence-specific mRNA degradation or by translational arrest. The mechanism is conserved in animals and includes at least three distinct pathways with several overlapping points, involved on silencing of endogenous or exogenous sequences. The best characterized small RNA is microRNAs (miRNAs), which predominantly makes genes silencing through post-transcriptional mechanisms. In this work we used bioinformatics approach to identity gene products in parasitic trematode *S. mansoni* with sharing similarities with enzymes involved in the post-transcriptional gene silencing mediated by miRNA pathway. We searched the *S. mansoni* genome and transcriptome databases, respectively, with the amino acid sequences of well-known proteins related to the miRNA pathway. We identified the total of 13 putative proteins involved in miRNA pathway in the parasite. Next, the levels *of SmDicer1* and *SmAgo 2, 3* and *4* were identified by qRT-PCR using cercariae, adult worms, eggs and schistosomula with the following times of in vitro cultivation 3,5; 8,5; 18,5; 24; 48 and 72 hours. This results shown that, the two genes are differentially expressed through cercariae-schistosomula differenciation, and have similar levels in eggs, and adult worms. In cercariae *SmDicer1* is down-regulated. These results suggest that this pathway is an important mechanism for the regulation of gene expression in this parasite. Future experiments are needed to prove this hypothesis.

Keywords: miRNAs, *Schistosoma mansoni*, qRT-PCR, gene expression;
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