Computational Prediction and Expression Patterns of Intronic MicroRNAs and Their Targets in Schistosoma Mansoni

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Abstract

MicroRNAs are noncoding RNAs of ~22 nucleotides in length that suppress the translation of target genes by binding to their target mRNAs and, thus, have a central role in gene regulation. To date, 362 putative Schistosoma mansoni microRNAs have been identified by sequencing and computational approaches. In this study, an approach combining bioinformatic prediction and qRT-PCR analysis was used to investigate the hypothesis that there are miRNAs belong to intronic regions of known protein-coding genes in the S. mansoni genome. Our analysis revealed 19 novel S. mansoni intronic microRNAs. Furthermore, the profile of miRNA expression during parasite development suggested a differential expression and an up-regulation of sma-new-miR_i17-5p. We observed a positive correlation between the intronic miRNAs sma-new-miR_i15-5p and sma-new-miR_i18-3p and putative RNA polymerase II associated factor 1 and helicase host genes, respectively. The target prediction showed that genes related to the ubiquitin-proteasome pathway, post-translation modification and signal transduction might be modulated by the identified intronic miRNAs. These findings suggested potentially relevant functional roles of intronic microRNAs in S. mansoni and might help to clarify several questions regarding parasite biology.

Keywords: Schistosoma mansoni, intronic miRNAs, miRNA expression, target prediction.

Supported by: CAPES, CNPq e UFOP.