**Title (Times New Roman, 14 pt, Bold, Center)**

Author(s) name (Times New Roman, 12 pt, center)
Underline the presenting author and asterisk the Corresponding author.

*Affiliation(s) (Times New Roman, 12 pt, italic, align left)*

Indicate the superscript number in front of the affiliations

E-mail address of presenting and corresponding authors (Times New Roman, 12 pt, align left)

**ABSTRACT (not exceed 250 words, justify, divided into 5 sections)**

**Backgrounds**: ……………………..…………………….………………...…………………….....

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**Objective(s)**: ………………..…..…………………….………………...……………………….....

**Methods**: ……………………..…………………….………………...……………….…………....

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**Results**: ……………………..…………………….………………...………………………..….....

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**Conclusion**: ……………………..…………………….………………...……………………….....

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**Keywords**: 3-5 keywords use commas to separate each word

Please see an example of the abstract below.

**Comprehensive Analysis of MiRNA Profiling in *Schistosoma mekongi***

**Across Life Cycle Stages**

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**ABSTRACT**

**Backgrounds**: *Schistosoma mekongi*, a significant schistosome parasite, has various life stages, including egg, cercaria, female, and male, that play crucial roles in the complex life cycle.

**Objectives**: This study aimed to explore the microRNA (miRNA) profiles across these developmental stages to understand their potential functions and evolutionary significance.

**Methods**: MicroRNAs were extracted from egg, cercaria, female, and male stages. The library preparation was performed using a TruSeq Small RNA Library Prep Kit for Illumina and then sequenced on the NovaSeq 6000 platform. Pre-processed sequencing reads of small RNA were obtained, and annotations were performed against the *S. japonicum* reference miRNA database.

**Results**: The result indicated variations in miRNA profiles across different life stages, with notable similarities observed between female and male *S. mekongi*. Principal Coordinate Analysis (PCoA) and unsupervised clustering revealed distinct miRNA signatures for each stage. Gene ontology (GO) analysis unveiled the potential roles of these miRNAs in various biological processes. The differential expression of specific miRNAs was prominent across stages, suggesting their involvement in crucial developmental processes. Furthermore, orthologous miRNA analysis against various worm species revealed distinct presence-absence patterns, providing insights into the evolutionary relationships of these miRNAs.

**Conclusion**: This comprehensive investigation into the miRNA profiles of *S. mekongi* offers valuable insights into the functional and evolutionary aspects of miRNAs in schistosome biology.

**Keywords**: microRNA, profiling, *Schistosoma mekongi*