Mature microRNAs (miRNAs) are small, non-coding RNAs which can elicit post-transcriptional repression of target genes. Mature miRNAs are single-stranded RNA molecules (~22 nt) processed from a precursor molecules (pre-miRNAs). To regulate protein-coding genes the mature miRNAs bind with imperfect complementarity to sites in the 3′ UTR leading to mRNA degradation or inhibition of translation. Several strategies have been used to identify and characterize miRNAs and their targets in a range of organisms. In this study, we used an integrated computational approach to identify and characterize Protostome and Mollusca-specific miRNAs in the genome of Biomphalaria glabrata available in Vectorbase (https://www.vectorbase.org/). The B. glabrata genome was screened using the einverted EMBOSS and BLASTn to identify hairpin-like sequences. The secondary structure of the hairpin candidates was predicted using RNAfold and sequences retained which had MFE < -20 kcal / mol. The retained sequences were then filtered for GC content (retaining 30 to 65% CG content) and used for BLASTN against mature miRNAs of Protostome and Mollusca species. In the next steps, hairpin candidate sequences were discarded which displayed similarity with protein-coding genes, non-coding RNA (ncRNAs), and repetitive elements. Finally, a machine-learning approach, miPred, was used to classify the putative precursor miRNA sequences based on features of miRNAs, and retained precursor miRNAs that were most likely to be real. We identified 37 Protostome-specific miRNAs and 5 Mollusca-specific miRNAs in the genome including clustered miRNAs such as miR-745b/745a. Most of bgl-miRNAs showed highly conservation in phylogenetic analysis and in primary and secondary structures compared to their orthologs. Several miRNAs showed 100% of identity compared to Protostome and Mollusca miRNAs deposited in miRBase version 21.0. Given the important roles of miRNAs in animals, the identification and characterisation of Protostome and Mollusca-specific miRNAs in B. glabrata will facilitate approaches towards prevention and treatment of Schistosomiasis.

**Keywords:** Biomphalaria glabrata, microRNAs, Bioinformatics.

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