Identification of conserved microRNAs and their target genes in Nile tilapia (*Oreochromis niloticus*) by bioinformatic analysis

X.H. Li, J.S. Wu, L.H. Tang and D. Hu

School of Geography and Biological Information, Nanjing University of Posts and Telecommunications, Nanjing, Jiangsu, China

Corresponding author: X.H. Li
E-mail: lixh@njupt.edu.cn

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ABSTRACT. MicroRNAs (miRNAs) are a class of non-coding RNAs that play important roles in posttranscriptional regulation of target genes. miRNAs are involved in multiple biological processes by degrading targeted mRNAs or repressing mRNA translation in various organisms. Their conserved nature in various organisms makes them a good source of new miRNA discovery using comparative genomic approaches. In the present study, conserved Nile tilapia (*Oreochromis niloticus*) miRNAs were identified using a bioinformatic strategy based on expressed sequence tag and genome survey sequence databases. A total of 21 new miRNAs were detected and were found to belong to 17 families. Using mature miRNA sequences as queries, potential targets for tilapia miRNAs were predicted using a local BLAST program and the miRanda software. Target proteins identified using miRanda and BLAST analyses included transcription factors and molecules important in metabolism, transportation, immunity, stress-related activity, growth, and development. These miRNAs and their targets in tilapia may increase the understanding of the role of...
miRNAs in regulating the growth and development of tilapia.

**Key words:** Bioinformatic analysis; *Oreochromis niloticus*; MicroRNAs; Target genes