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MicroRNA repertoire and comparative analysis of *Andrias davidianus* infected with *ranavirus* using deep sequencing

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Abstract

Andrias davidianus is a large and economically important amphibian in China. Ranavirus infection causes serious losses in *A. davidianus* farming industry. MicroRNA mediated host-pathogen interactions are important in antiviral defense. In this study, five small-RNA libraries from ranavirus infected and non-infected *A. davidianus* spleens were sequenced using high throughput sequencing. The miRNA expression pattern, potential functions, and target genes were investigated. In total, 1356 known and 431 novel miRNAs were discovered. GO and KEGG analysis revealed that certain miRNA target genes are associated with apoptotic, signal pathway, and immune response categories. Analysis identified 82 downregulated and 9 upregulated differentially expressed miRNAs, whose putative target genes are involved in pattern-recognition receptor signaling pathways and immune response. These findings suggested miRNAs play key roles in *A. davidianus*'s response to ranavirus and could provide a reference for further miRNA functional identification, leading to novel approaches to improve *A. davidianus* ranavirus resistance.

Keywords: Andrias davidianus; microRNA; ranavirus; deep sequencing

1. Introduction