

Identification of androgenic gland microRNA and their target genes to discover sex-related microRNA in the oriental river prawn, Macrobrachium nipponense

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ABSTRACT. The oriental river prawn, *Macrobrachium nipponense*, is an important aquaculture species in China. The androgenic gland produces hormones that play crucial roles in the differentiation of crustaceans to the male sex. MicroRNA (miRNA) post-transcriptionally regulates many protein-coding genes, influencing important biological and metabolic processes. However, currently, there is no published data identifying miRNA in *M. nipponense*. In this study, we identified novel miRNA in the androgenic gland of *M. nipponense*. Using the high-throughput Illumina Solexa system, 1077 miRNA were identified from small RNA libraries by aligning with the *de novo* androgenic gland transcriptome of *M. nipponense* (obtained from RNA-Seq) and the sequences in the miRBase21 database. A total of 8,248, 76,011, and 78,307 target genes were predicted in the EST and SRA sequences provided in the NCBI database, and the androgenic gland transcriptome of *M. nipponense*, respectively. Some potential sex-

related miRNA were identified based on the function of the predicted target genes. The results of our study provide new information regarding the miRNA expression in *M. nipponense*, which could be the basis for further genetic studies on decapod crustaceans.

Key words: *Macrobrachium nipponense;* Androgenic gland; microRNA; Targeted genes; Sex-determination