



Identification of highly expressed host microRNAs that respond to white spot syndrome virus infection in the Pacific white shrimp *Litopenaeus vannamei* (Penaeidae)

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ABSTRACT. MicroRNAs (miRNAs) are known to play an important role in regulating both adaptive and innate immunity. Pacific white shrimp (*Litopenaeus vannamei*) is the most widely farmed crustacean species in the world. However, little is known about the role miRNAs play in shrimp immunity. To understand the impact of viral infection on miRNA expression in shrimp, we used high-throughput sequencing technology to sequence two small RNA libraries prepared from *L. vannamei* under normal and white spot syndrome virus (WSSV) challenged conditions. Approximately 19,312,189 and 39,763,551 raw reads corresponding to 17,414,787 and 28,633,379 high-quality mappable reads were obtained from the two libraries, respectively. Twelve conserved miRNAs and one novel miRNA that were highly expressed (>100 RPM) in *L. vannamei* were identified. Of the identified miRNAs, 8 were differentially expressed in response to the virus

infection, of which 1 was upregulated and 7 were downregulated. The prediction of miRNA targets showed that the target genes of the differentially expressed miRNAs were related to immunity, apoptosis, and development functions. Our study provides the first characterization of *L. vannamei* miRNAs in response to WSSV infection, which will help to reveal the roles of miRNAs in the antiviral mechanisms of shrimp.

Key words: MicroRNAs; *Litopenaeus vannamei*; White spot syndrome virus; High-throughput sequencing