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Abstract

Summer mortality syndrome is one of the most serious issue for *Marsupenaeus japonicus* aquaculture in China. Since it causes massive economic loss and threatens sustainability of *M. japonicus* aquaculture industry, thus, there is an urgent desire to reveal the heat stress-host interactions mechanisms that lead to mass mortalities of *M. japonicus* in hot summer months. MicroRNAs (miRNAs) are small noncoding RNAs that involved in regulation of diverse biological processes, including stress and immune response, and might serve as potential regulators in the heat stress-host interactions. In the present study, miRNAs with heat stress responsive and immune properties were identified and characterized in *M. japonicus* by small RNA sequencing and bioinformatics analysis. In total, 79 host miRNAs were identified, among which 15 miRNAs were differentially expressed in response to heat stress. Target genes prediction and function annotation revealed that a variety of host cellular processes, such as signal transduction, transcription, anti-stress response, ribosomal