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## RNA-seq analysis of *Macrobrachium rosenbergii* hepatopancreas in response to *Vibrio parahaemolyticus* infection

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The Malaysian giant freshwater prawn *Macrobrachium rosenbergii*, an economically important crustacean worldwide are being affected by Vibriosis, a disease caused by *Vibrio* strains such as *Vibrio parahaemolyticus*. *M. rosenbergii* possesses an innate immune system which provides defense against pathogenic agents. The information regarding the regulation of innate immune system in this species is lacking thus it is necessary in providing solutions to control and minimize the loss of production due to this bacterial disease. In this study, we performed a transcriptome profiling of *M. rosenbergii* hepatopancreas infected with *V. parahaemolyticus* using the Next Generation™ sequencing method (Illumina HiSeq™2000). A total of 54,295,342 and 54,708,014 high-quality reads obtained from *Vibrio*infected and control *M. rosenbergii* DNA libraries. The overall *de novo* assembly and clustering of both reads generated 64,411 uni-genes with an average length of 698 bp. Based onBLASTX search (E-value <10<sup>-5</sup>) against NR, Swissprot, GO, COG and KEGG databases, 22,455 uni-genes (34.86% of all unigenes) were annotated with gene descriptions, gene ontology terms and metabolic pathways. The unigene differential expression analysis revealed 14,569 unigenes were differentially expressed in the infected shrimp compared to the controls. Several differentially expressed genes are involved in various animal immune functions. The large number of transcripts obtained in this study would provide valuable resources for further genomic research into freshwater prawns.

### Biography

Ramarao Seriramalu is a PhD student under supervision of Associate Prof Dr Subha Bhassu who is an academican in Institute of Biological Sciences, Faculty of Science at University Malaya.

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