

GRAPHICAL ABSTRACT

Transcriptome Profile and Gene Expression during Different Ovarian Maturation Stages of *Macrobrachium rosenbergii* (De Man, 1879)

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INTRODUCTION

M. rosenbergii, or giant river prawn, is the most economically crucial cultured freshwater crustacean. Ovary is the primary tissue for studying gene and protein expressions involved in crustacean growth and reproduction. Despite significant interest in M. rosenbergii, its gene discovery has been at a relatively small scale compared to other genus. In this study, comprehensive transcriptomic sequencing data for different maturation stages of the ovary of M. rosenbergii were observed.

OBJECTIVES

The aim was to identify candidate genes associated with reproduction and ovarian development in M. rosenbergii.

METHODOLOGY

- 20 female M. rosenbergii samples were categorised into four maturation stages: 1,2,3,4.
- The BLASTX unigene search against NCBI, NR, NT, KO, Swiss-Prot, Protein Family (PFAM), gene ontology (GO), and KOG databases.
- The differentially expressed genes (DEG) analysis was conducted.

RESULTS

- The results revealed that contrasting stages 3 and 1 exhibited the highest total differentially expressed genes than other stage comparisons.
- Identification of cyclin B, insulin receptor (IR), estrogen sulfotransferase (ESULT), and vitellogenin (Vg), which are critical in ovarian maturation.
- First time identified in this study: SUMO-activating enzyme subunit 1, E3 ubiquitin-protein ligase RNF25, and neuroparsin.

DISCUSSION

During each reproductive cycle, female crustacean gonads undergo a sequence of morphological transformations. Consequently, each maturation phase would have different genes expressed. The transcriptome data procured in this study were conserved and annotatable from databases.

CONCLUSION

The data obtained in the present study considerably contributes to the knowledge of gene expression and genome structure in M. rosenbergii ovaries throughout its developmental stage.