

Transcriptome analysis of the hepatopancreas in *Macrobrachium rosenbergii* under copper stress

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Introduction

- Cu is a widespread environmental contaminant in aquatic ecosystems.
- *Macrobrachium rosenbergii* is one of the important freshwater cultured prawns in the world.
- There is still a lack of systematic research on the molecular response of the hepatopancreas of *M. rosenbergii* under Cu stress.

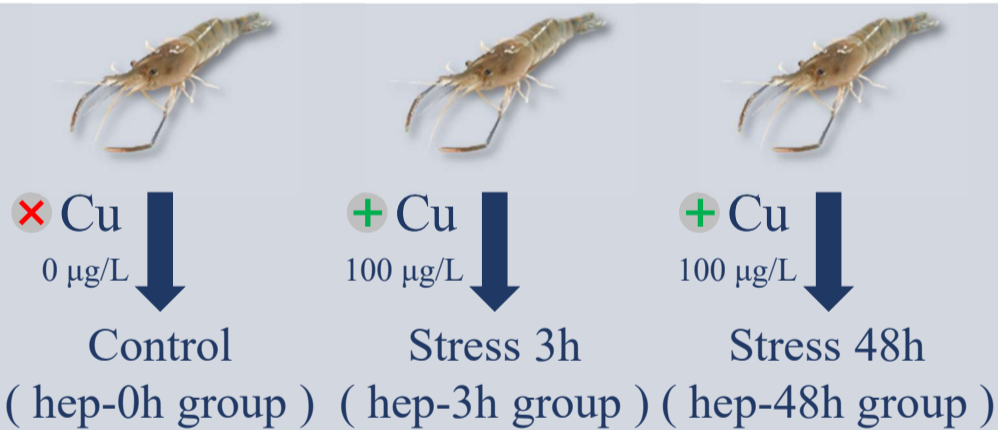
Objectives

- The RNA-seq technology was used to identify potential genes and pathways related to stress response induced by Cu stress in the hepatopancreas of *M. rosenbergii*.
- To explore the molecular mechanism of *M. rosenbergii* against Cu toxicity

Materials and Methods

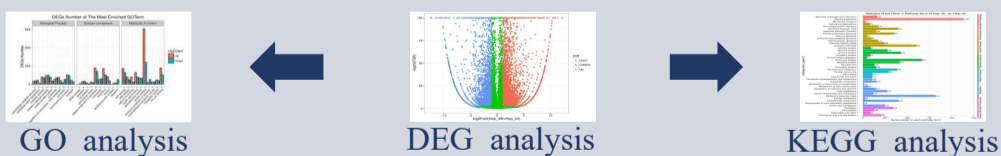
Macrobrachium rosenbergii

(10.89 ± 1.42g)



Hepatopancreas

transcriptome analysis



Results

Table 1 Statistics of the sequencing and assembly data.

Summary	0 h	3 h	48 h	Total
Total Raw Reads	65,384,862	58,978,912	55,185,928	179,549,702
Total Clean Reads	65,117,218	58,693,126	54,982,780	178,793,124
Total Clean Reads Ratio (%)	99.59	99.52	99.63	99.58
Number of unigenes	88,579	99,729	102,062	85,984
Mean Length of unigenes (bp)	697.92	735.61	693.59	1077.23
N50 length of unigenes (bp)	1704	1954	1782	2559
N90 length of unigenes (bp)	232	237	226	351

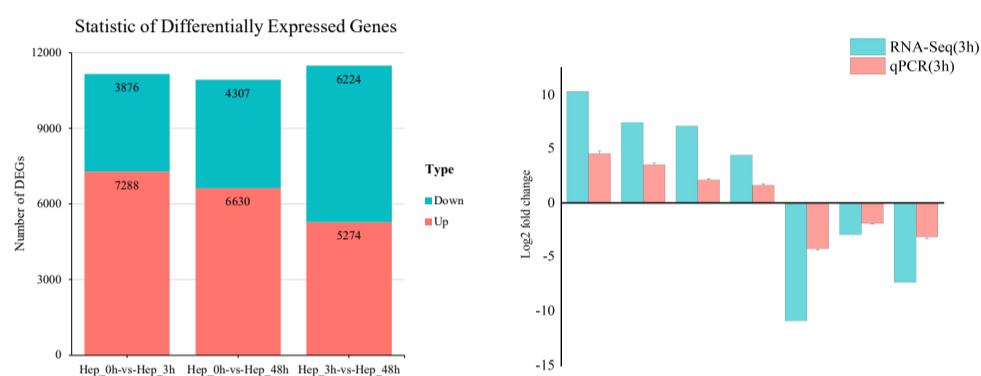


Fig.1. Numbers of DEGs in each comparison

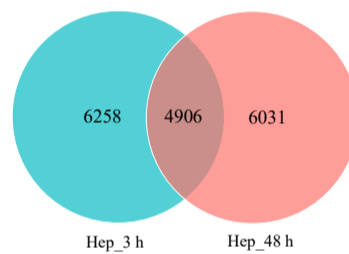


Fig.2. Venn diagrams showing the DEGs between Hep_3 h and Hep_48 h

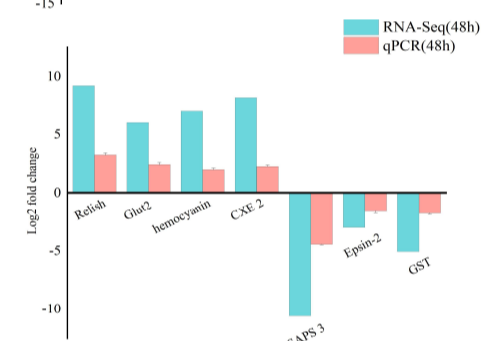


Fig.5. Comparison of gene expression data between RNA-Seq and qRT-PCR

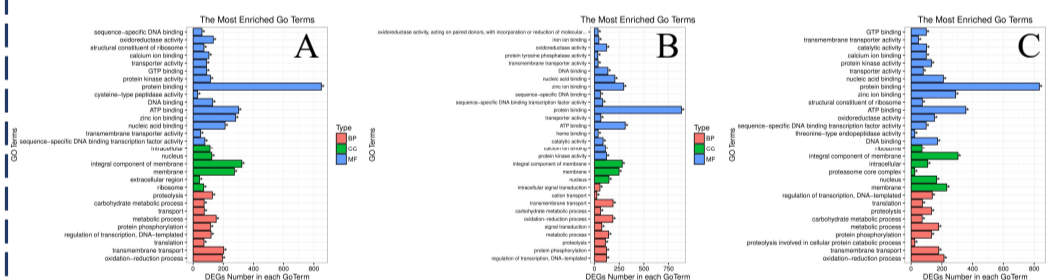


Fig. 3. Gene ontology assignments of DEGs between (A) Hep_0h and Hep_3h sample. (B) Hep_0h and Hep_48h sample and (C) Hep_3h and Hep_48h sample. * Means correct P-value ≤ 0.05.

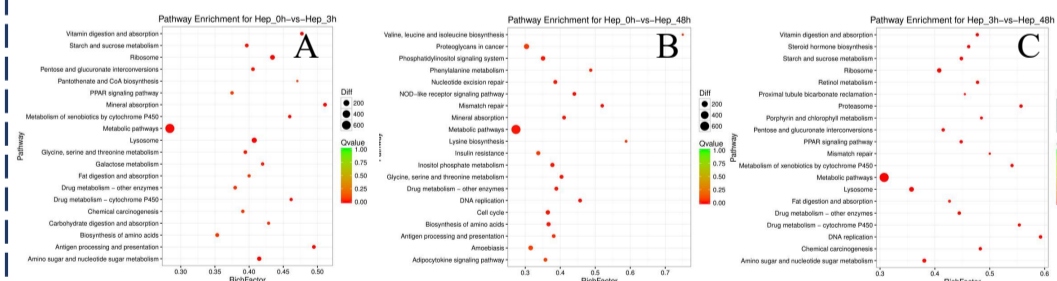


Fig. 4. Comparative KEGG pathways analysis between (A) Hep_0h and Hep_3h (B) Hep_0h and Hep_48h and (C) Hep_3h and Hep_48h.

Conclusion

In this work, multiple key genes in the cell cycle, mismatch repair, and nucleotide excision repair pathways were inhibited, indicating that Cu may disrupt the genomic stability of the hepatopancreas by interfering with the DNA damage repair pathway. However, the organism attempted to reduce the damage caused by Cu by regulating metabolism, copper ion homeostasis, detoxification, immunity, and apoptosis processes. In summary, our research provides basic data and theoretical basis for revealing the molecular response mechanism of *M. rosenbergii* to Cu stress in aquatic environments.