

Transcriptome analysis reveals mechanisms of organismal response in *Exopalaemon carinicauda* with "Zombie Disease"

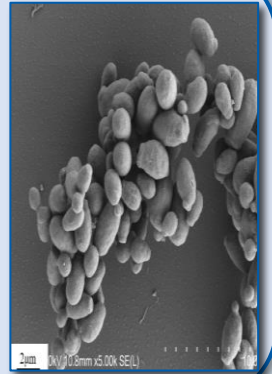


Ran Zhao, Wenjun Shi, Jianqiang Zhu, Libao Wang, Hui Li, Qi Jiang, Xihe Wan*
 (1. Shanghai Ocean University, Pudong 200120, China;
 2. Institute of Oceanology & Marine Fisheries, Jiangsu, Nantong 226007, China)



The ridgetail white prawn, *Exopalaemon carinicauda*, one of the important commercial shrimp species naturally distributed in the coasts of the Yellow Sea and the Bohai Sea, China.

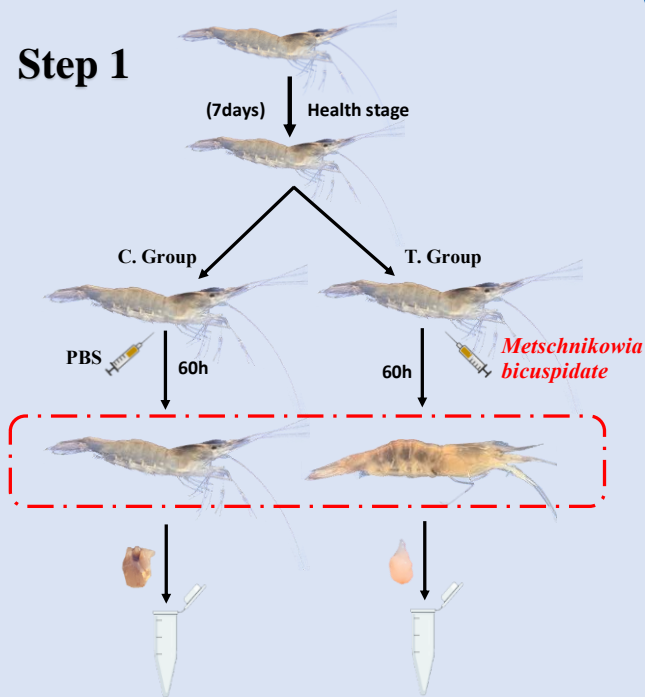
In recent years, an epidemic disease called "Zombie Disease" by local farmers has appeared in the *E. carinicauda* breeding area of Jiangsu Province, and the pathogen was found to be *Metschnikowia bicuspidata* after isolation and identification. However, the organismal response mechanism of *E. carinicauda* after infection has not been reported.



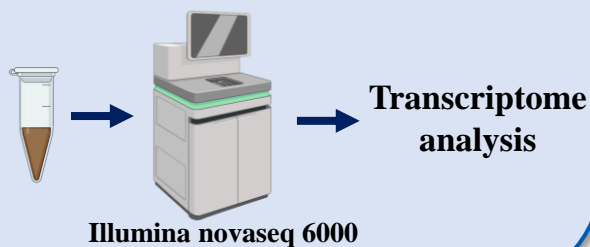
1. Introduction

2. Materials and methods

Step 1



Step 2



3. Results

Tab. 1 Quality control of the RNA-seq data obtained from different samples.

| Sample | Raw Reads | Clean Reads | Clean Bases | Q30(%) | GC Content (%) |
|--------|-----------|-------------|-------------|--------|----------------|
| C-1 | 73264638 | 72853978 | 10875846060 | 93.11% | 43.69% |
| C-2 | 69762456 | 69449584 | 10367317033 | 93.63% | 43.91% |
| C-3 | 72742586 | 72387824 | 10804261763 | 93.90% | 43.42% |
| T-1 | 69891130 | 69590130 | 10380228574 | 93.75% | 43.70% |
| T-2 | 65801936 | 65524978 | 9779274278 | 93.57% | 43.93% |
| T-3 | 68803894 | 68501780 | 10219018610 | 93.34% | 43.90% |

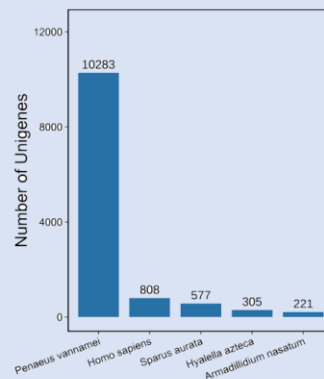


Fig. 1 Annotation of unigenes to Nr database

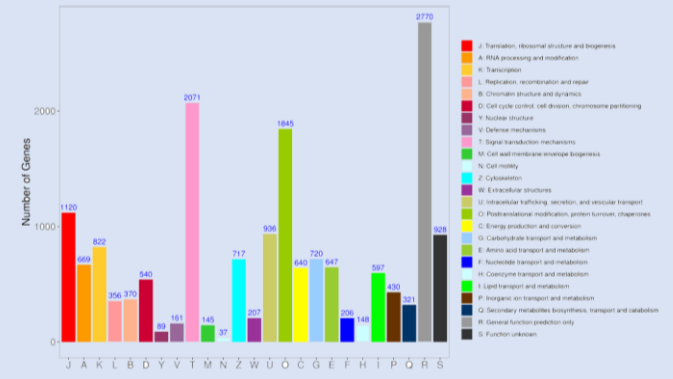


Fig. 2 Annotation of unigenes to COG/KOG database

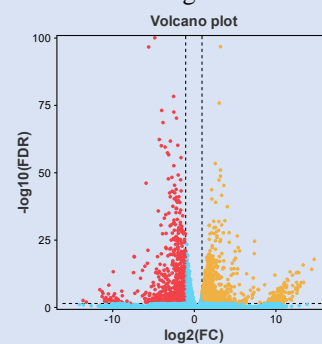


Fig. 3 Volcano maps of differentially expressed genes in C-Group vs T-Group

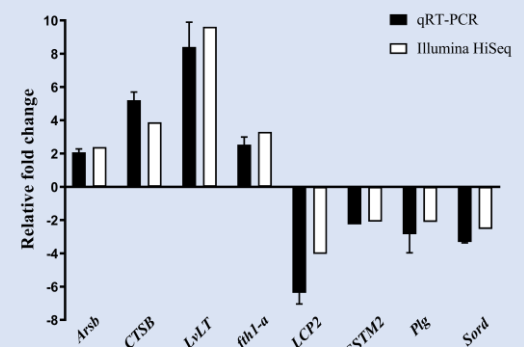


Fig. 4 Validation of 8 DEGs with qRT-PCR.

4. Conclusion

◆ *E. carinicauda* infected with *M.bicuspidata* upregulated *CTL* to enhance pathogen recognition and activate the immune system, and upregulated *CTSB*, *Arsb* to promote lysosome degrade pathogens.

◆ In addition, the expression of *GST*, *LPSAT*, *Plg* and other genes was suppressed after infection, disrupting the antioxidant system, glycerophospholipid metabolism and protein digestion and absorption pathways in *E. carinicauda*.

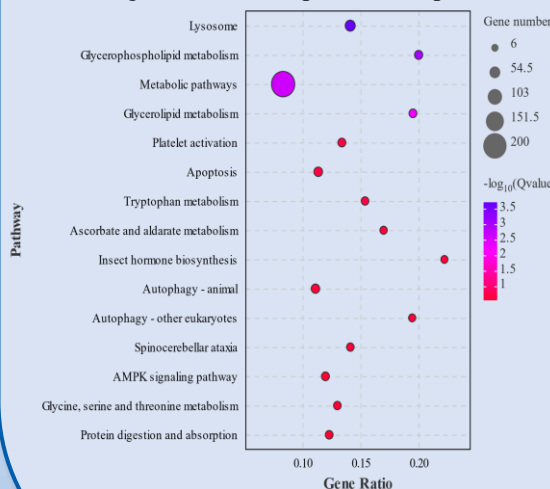


Fig. 5 KEGG pathway enrichment analysis of DEGs.

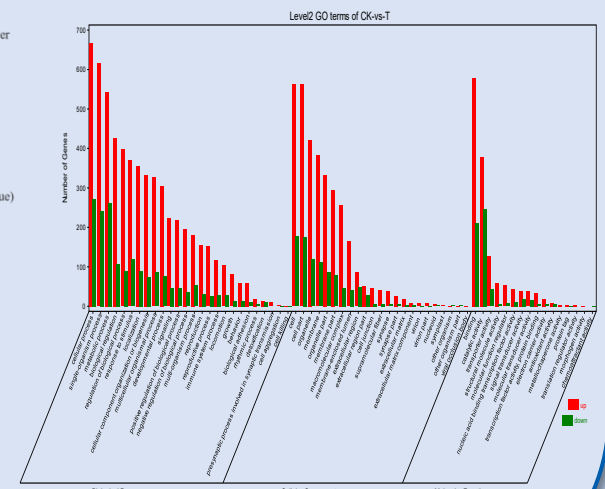


Fig. 6 GO enrichment terms of DEGs