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Data Article

Transcriptome data of *Epinephelus fuscoguttatus* infected by *Vibrio vulnificus*



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ABSTRACT

Vibriosis disease by *Vibrio* spp. greatly reduced productivity of aquaculture, such as brown-marbled grouper (*Epinephelus fuscoguttatus*), which is an economically important fish species in Malaysia. Preventive measures and immediate treatment are critical to reduce the mortality of *E. fuscoguttatus* from vibriosis. To investigate the molecular mechanisms associated with immune response and host-bacteria interaction, a transcriptomic analysis was performed to compare between healthy and *Vibrio*-infected groupers. This permits the discovery of immune-related genes, specifically the resistance genes upon infection. Herein, we provide the raw transcriptome data from Illumina HiSeq. 4000 that have been deposited into NCBI SRA database with the BioProject accession number PRJNA396437. A total of 493,403,076 raw sequences of 74.5 Gb were obtained. Trimming of the raw data produced 437,186,232 clean reads of ~58 Gb. These datasets will be useful to elucidate the defence mechanisms of *E. fuscoguttatus* against *Vibrio vulnificus* infection for future development of effective prevention and treatment of vibriosis.

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Specifications Table

Subject area	Biology
More specific subject area	Transcriptomics
Type of data	Transcriptome sequences
How data was acquired	Illumina HiSeq. 4000
Data format	Raw data (FASTQ)
Experimental factors	Survival of groupers on day 31 post infection
Experimental features	Datasets for gill and whole-body tissues
Sample source location	Universiti Malaysia Terengganu (UMT), Terengganu, Malaysia (5°24'26.6"N 103°05'17.1"E)
Data accessibility	http://www.ncbi.nlm.nih.gov/bioproject/396437

Value of the data

- This dataset provides the transcriptome sequences from gill and whole-body tissues of control (healthy) and *Vibrio*-infected *E. fuscoguttatus*.
- Downstream analysis will allow the identification of genes involved in the mechanism of host immune response against *Vibrio* infection.
- This study will provide a better understanding on the molecular mechanisms associated with immune defense and host-pathogen interaction.
- The data can be a reference transcriptome for grouper and useful for comparative analysis with other fish diseases.

1. Data

This article reports the transcriptome data from gill and whole-body tissues of control (healthy) and *V. vulnificus*-infected *E. fuscoguttatus* at day 31 post infection. The raw data were deposited in the NCBI SRA database as detailed in [Table 1](#).

2. Experimental design, materials and methods

2.1. Fish sampling and infection experiment

Brown-marbled grouper (*Epinephelus fuscoguttatus*) fingerlings were obtained from Fisheries Research Institute (FRI) Tanjung Demong, Besut in Terengganu, Malaysia (5°46'09.0"N 102°33'02.6"E). Fingerlings with length of ~5 cm were acclimatised in aerated seawater (25 °C, salinity ~35 parts per thousand (PPT), pH 7.9) for one week. For experimental infection, healthy fingerlings were randomly selected and immersed in 20 L seawater containing 1×10^7 CFU mL⁻¹ of *Vibrio vulnificus* for 30 min, whereas the controls were immersed in clean seawater. Both control and infected fingerlings were then transferred independently into new aquarium containing fresh seawater, and observed daily for 30 days. At day 31-post-infection, fingerlings that survived from the experimental infection and the controls were collected and flash frozen in liquid nitrogen respectively. Samples were then kept at -80 °C prior to RNA extraction.

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