Differential expression of olive flounder (*Paralichthys olivaceus*) transcriptome during viral hemorrhagic septicemia virus (VHSV) infection at warmer and colder temperature

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**Abstract**

The data presented here are related to the research article entitled "Temperature-dependent immune response of olive flounder (*Paralichthys olivaceus*) infected with viral hemorrhagic septicemia virus (VHSV)" [1]. In the cited article, we sequenced the whole transcriptome of the olive flounder using Illumina RNA-Seq. Differentially expressed genes (DEG) analysis of VHSV infected head kidney samples showed perturbations in gene expression. Herein we made a comparison of DEGs at early stage of VHSV infection of olive flounder (4 h post infection) in colder (13°C) and warmer (20°C) temperatures. The analysis of signaling pathways showed that several major immune pathways were altered. The gene ontology terms associated with the genes differentially expressed are also presented.

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How data was acquired | Illumina HiSeq. 2500
---|---
Data format | Raw data (FASTQ)
Experimental factors | Olive flounder were infected with VHSV at 13 and 20 °C. Samples of head kidney was collected at 4h post infection
Experimental features | DEGs of olive flounder at 13 and 20 °C post VHSV infection
Sample source location | National Institute of Fisheries Science, Busan, South Korea
Data accessibility | Data is available in the article and at: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA379500

**Value of the data**

- The information of unigenes expressed at colder and warmer temperature helps us to know how the response of host transcriptome varies with respect to surrounding environment.
- The comparison of modulated genes during VHSV infection at 13 and 20 °C helps for management measures in olive flounder aquaculture.
- The identification of affected signaling pathways in the head kidney of VHSV infected olive flounder sheds new light on the investigation of disease pathogenesis and for novel treatment targets.

1. Data

The data presented here are related to the research article entitled “Temperature-dependent immune response of olive flounder (Paralichthys olivaceus) infected with viral hemorrhagic septicemia virus (VHSV)” [1]. The olive flounder were challenged with VHSV at 13 °C and 20 °C, and DEG in the head kidney were analyzed. The whole transcriptome of olive flounder was sequenced using illumina RNA Seq. The quality of sequencing reads were assessed by contig length distribution of sequences and gene ontology functional analysis were conducted (Fig. 1, Supplementary table 1). Fig. 2 represents the number of unigenes which expressed during the infection period. All the unigenes were aligned to the eggNOG database and predicted the possible functions (Fig. 3). Table 1 describes the number of differentially expressed genes at 4 hours post infection of VHSV. The signaling pathways annotated in the transcriptome of olive flounder is shown in the Table 2 and Supplementary table. 2.

![Fig. 1. Analysis of sequencing reads assembly quality. Contig length distribution of Trinity assembly for olive flounder.](image)
Fig. 2. Unigenes expressed during VHSV infection in olive flounder at 13 °C and 20 °C. Three samples were screened at 4 hpi.

Fig. 3. EggNOG classification assigned to annotated unigenes.

Table 1
Analysis of differentially expressed genes during VHSV infection in olive flounder at 13 °C and 20 °C. Here upregulation is Group 2 > Group 1 and downregulation is Group 2 < Group 1 (p-value < 0.05).

| Group 1             | Group 2             | Up regulated genes | Down regulated genes |
|---------------------|---------------------|--------------------|----------------------|
| 13 °C (4 h post infection) | 20 °C (4 h post infection) | 569                | 797                  |
### Table 2
Immune signalling pathways annotated in the olive flounder head kidney transcriptome.

| KEGG ID   | KEGG Description                                                                 | Number of Unigenes |
|-----------|----------------------------------------------------------------------------------|--------------------|
| Ko04151   | PI3K-Akt signaling pathway [PATH:ko04151]                                        | 296                |
| Ko04010   | MAPK signaling pathway [PATH:ko04010]                                            | 200                |
| Ko04014   | Ras signaling pathway [PATH:ko04014]                                             | 193                |
| Ko04140   | Autophagy - animal [PATH:ko04140]                                               | 175                |
| Ko04024   | cAMP signaling pathway [PATH:ko04024]                                            | 166                |
| Ko04062   | Chemokine signaling pathway [PATH:ko04062]                                       | 164                |
| Ko04144   | Endocytosis [PATH:ko04144]                                                       | 160                |
| Ko04152   | AMPK signaling pathway [PATH:ko04152]                                            | 146                |
| Ko04210   | Apoptosis [PATH:ko04210]                                                         | 125                |
| Ko04668   | TNF signaling pathway [PATH:ko04668]                                             | 120                |
| Ko04150   | mTOR signaling pathway [PATH:ko04150]                                            | 116                |
| Ko04310   | Wnt signaling pathway [PATH:ko04310]                                             | 107                |
| Ko04625   | C-type lectin receptor signaling pathway [PATH:ko04625]                          | 105                |
| Ko04620   | Toll-like receptor signaling pathway [PATH:ko04620]                              | 100                |
| Ko04120   | Ubiquitin mediated proteolysis [PATH:ko04120]                                    | 99                 |
| Ko04660   | T cell receptor signaling pathway [PATH:ko04660]                                  | 99                 |
| Ko04064   | NF-kappa B signaling pathway [PATH:ko04064]                                      | 77                 |
| Ko04060   | Cytokine-cytokine receptor interaction [PATH:ko04060]                            | 76                 |
| Ko04630   | Jak-STAT signaling pathway [PATH:ko04630]                                        | 69                 |
| Ko04657   | IL-17 signaling pathway [PATH:ko04657]                                           | 68                 |
| Ko04662   | B cell receptor signaling pathway [PATH:ko04662]                                 | 67                 |
| Ko04624   | Toll and Imd signaling pathway [PATH:ko04624]                                   | 40                 |
| Ko04610   | Complement and coagulation cascades [PATH:ko04610]                              | 21                 |
| Ko04217   | TNF signaling pathway [PATH:ko04668]                                             | 13                 |
| Ko05220   | Wnt signaling pathway [PATH:ko04310]                                             | 13                 |
| Ko04060   | Chemokine signaling pathway [PATH:ko04062]                                       | 10                 |
| Ko04510   | PI3K-Akt signaling pathway [PATH:ko04151]                                        | 9                  |
| Ko00970   | Aminoacyl-tRNA biosynthesis [PATH:ko04062]                                       | 9                  |
| Ko05203   | MAPK signaling pathway [PATH:ko04010]                                            | 8                  |
| Ko00051   | AMPK signaling pathway [PATH:ko04152]                                            | 8                  |
| Ko04068   | Chemokine signaling pathway [PATH:ko04062]                                       | 8                  |
| Ko04150   | AMPK signaling pathway [PATH:ko04152]                                            | 8                  |
| Ko04270   | MAPK signaling pathway [PATH:ko04010]                                            | 8                  |
| Ko04380   | NF-kappa B signaling pathway [PATH:ko04064]                                      | 8                  |
| Ko04150   | PI3K-Akt signaling pathway [PATH:ko04151]                                        | 8                  |
| Ko04150   | MAPK signaling pathway [PATH:ko04010]                                            | 6                  |
| Ko04013   | Toll and Imd signaling pathway [PATH:ko04624]                                   | 6                  |
| Ko04727   | AMPK signaling pathway [PATH:ko04152]                                            | 6                  |
| Ko05152   | C-type lectin receptor signaling pathway [PATH:ko04625]                          | 5                  |
| Ko00563   | NOD-like receptor signaling pathway [PATH:ko04621]                               | 5                  |
| Ko05012   | Ubiquitin mediated proteolysis [PATH:ko04120]                                   | 5                  |
| Ko04010   | Ras signaling pathway [PATH:ko04014]                                            | 5                  |
| Ko04666   | Endocytosis [PATH:ko04144]                                                       | 5                  |
| Ko04611   | Complement and coagulation cascades [PATH:ko04610]                              | 5                  |
| Ko04010   | PI3K-Akt signaling pathway [PATH:ko04151]                                        | 4                  |
| Ko04370   | MAPK signaling pathway [PATH:ko04010]                                            | 4                  |
| Ko04510   | Chemokine signaling pathway [PATH:ko04062]                                       | 4                  |
| Ko04144   | Ubiquitin mediated proteolysis [PATH:ko04120]                                   | 4                  |
| Ko04510   | MAPK signaling pathway [PATH:ko04010]                                            | 4                  |
| Ko05133   | Complement and coagulation cascades [PATH:ko04610]                              | 4                  |
2. Experimental design, materials and methods

2.1. Experimental animals

Olive flounder of average weight 39.7 g were purchased from a commercial fish farm (Geoje Island) without any history of VHSV. Animals were maintained at 11–13 °C, and acclimated for one week.

2.2. Viral challenge, preparation of mRNA library and RNA seq

The fish of each groups were intraperitoneally injected (Isolate: FDC-VHS2014-5) with a VHSV dose of $1 \times 10^4$ TCID$_{50}$ per fish or control media in 0.1 ml and acclimatized at 13 and 20 °C, separately. Total RNA was isolated from the head kidney of three individual VHSV-infected olive flounder cultured on 13 and 20 °C. At 4 h post infection, three individuals were randomly collected from each group and head kidneys were excised for gene expression analysis. Kidney tissue samples were stored at −80 °C until RNA isolation. Total RNA was isolated using a standard Trizol extraction protocol (Invitrogen, Germany) according to the manufacturer’s instructions. The concentration and integrity of the RNA were assessed with a Thermo Scientific NanoDrop 8000 Spectrophotometer and Agilent 2100 Bioanalyzer, respectively. RNA with an OD$_{260/280}$ ≥ 1.8 and an RNA integrity number ≥ 7.0 was used in subsequent experiments. Equal amounts of high quality RNA from each sample were then used separately for cDNA synthesis and sequencing. The cDNA library was prepared with ~1.0 μg of total RNA following manufacturer’s recommendations of TrueSeq RNA library Preparation Kit (Illumina, USA). The library was then amplified, and the final library yielded ~ 500 ng of cDNA with an average fragment size of ~ 350 bp. The resulting cDNA libraries were then paired-end sequenced (2 × 100 bp) with HiSeq. 2500 platform (Illumina, USA). All sequencing reads were deposited in the NCBI Sequence Read Archive (SRA) under the accession number SRP102673.

2.3. Transcriptome de novo assembly, annotation and differential expression

The raw reads of fastq format were undergone pre-processing and high quality sequences were subject to de novo assembly using Trinity software [2]. The assembled unigenes were BLASTX mapped against NCBI non redundant protein and swiss-prot databases. Gene ontology (GO) terms were assigned to each unigene based on the GO terms annotated to its corresponding homologs. The differential expression of unigenes were analyzed by aligning individual sample reads with reference transcriptome using Bowtie2 [3]. Moreover, unigenes were assigned to biochemical pathways according to the Kyoto Encyclopedia of Genes and Genomes (KEGG) database using BLASTX, followed by retrieving KEGG Orthology (KO) information. Additionally, the Clusters of Orthologous Groups (COG) screening was performed using the eggNOG database [4].

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.06.085.
Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.06.085.

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