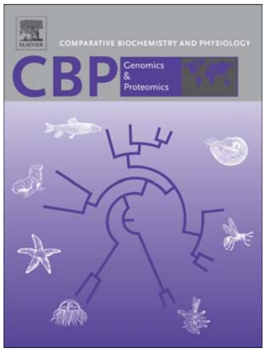

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PII: S1744-117X(17)30042-4
DOI: doi:10.1016/j.cbd.2017.05.003
Reference: CBD 458

To appear in: *Comparative Biochemistry and Physiology - Part D: Genomics and Proteomics*

Received date: 9 December 2016
Revised date: 7 March 2017
Accepted date: 27 May 2017

Please cite this article as: Jiang, Jie-Lan, Mao, Ming-Guang, Lü, Hui-Qian, Wen, Shi-Hui, Sun, Meng-Lei, Liu, Rui-ting, Jiang, Zhi-Qiang, Digital gene expression analysis of *Takifugu rubripes* brain after acute hypoxia exposure using next-generation sequencing, *Comparative Biochemistry and Physiology - Part D: Genomics and Proteomics* (2017), doi:10.1016/j.cbd.2017.05.003

Digital gene expression analysis of *Takifugu rubripes* brain after acute hypoxia exposure using next-generation sequencing

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Running title: DGE analysis of *Takifugu rubripes* brain after hypoxia exposure

ms. has 17 pages, 3 figures, 4 tables

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Abstract

The adverse effects of hypoxia are confined to biochemical, physiological, developmental and behavioral processes, especially injury of the brain. In this study, a subset of genes in the brain of *Takifugu rubripes* were analyzed using digital gene expression (DGE) profiles and next-generation sequencing after acute hypoxia. Among 32 differentially expressed genes, 29 were up-regulated and 3 were down-regulated following hypoxia exposure. Using Gene Ontology analysis, it was found that transcription and translation, metabolism, and the stress response were affected by exposure to hypoxia. KEGG analysis revealed that the neuroactive ligand-receptor interaction pathway was significantly enriched in hypoxia-exposed *T. rubripes*. To further confirm the differential expression of genes, quantitative real-time PCR was performed to test six candidate genes, with the following five genes exhibiting the same expression patterns as the sequencing results: Proto-oncogene c-fos, Kruppel-like factor 2, immediate early response 2, proopiomelanocortin A and rhodopsin. This work is the first to identify and annotate genes in *T. rubripes* affected by hypoxia stress. This investigation provides data for understanding the molecular mechanism of fish adaptation to hypoxia and provides a reference for rationally setting dissolved oxygen levels in aquaculture.

Key words: hypoxia; brain; *Takifugu rubripes*; digital gene expression profiles

1. Introduction

Takifugu rubripes is an economically important fish in China. Since wild resources have recently declined, artificial breeding is increasing and has become a prosperous industry. In