

Comparative transcriptome analysis of zebrafish (*Danio rerio*) brain and spleen infected with Spring Viremia of Carp Virus (Abstract)

Xueqin liu

College of Fisheries, Huazhong Agricultural University, Wuhan, China

Corresponding author: xueqinliu@mail.hzau.edu.cn

ABSTRACT

SVCV is the pathogen of spring viremia of carp (SVC) and often causes acute hemorrhagic symptoms in various kinds of cyprinids and induces serious environmental and economic losses. However, the molecular mechanisms of infection remain poorly understood, especially at the individual level. In this study, zebrafish was employed as the infection model to explore the pathogenesis of SVCV. 4 groups of zebrafish tissues were set and RNA sequencing (RNA-Seq) technology was employed to analyze the differentially expressed genes (DEGs) after SVCV-infection. A total of 360,971,498 clean reads were obtained from 12 samples, 382 DEGs in the brain and 926 DEGs in the spleen were identified. These DEGs were annotated into three ontologies after gene ontology (GO) enrichment analysis. The Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis showed that these DEGs were primarily related to Influenza A pathway and Herpes simplex infection pathway in brain and Tuberculosis and Toxoplasmosis pathways in spleen, and all of these pathways may be involved in response to pathogen invasion. At the same time, 3' and 5' alternative splicing (AS) events were significantly up-regulated in the spleen. The transcriptome analysis results demonstrated changes and tissue-specific influences caused by SVCV in vivo, which provided us with more information to understand the complex relationships between SVCV and its host.

Keywords: Molecular mechanisms, infection, zebrafish, SAVCV-infection, Herpes infection.

