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Abstract

Marine organisms are commonly under threat from various pathogens. *Edwardsiella tarda* is one of the fish pathogens that can infect both cultured and wild fish species. *E. tarda* can also infect other vertebrates, including amphibians, reptiles, and mammals. Bacteremia caused by *E. tarda* can be a fatal disease in humans. Blood acts as a pipeline for the fish immune system. Generating blood transcriptomic resources from fish challenged by *E. tarda* is crucial for understanding molecular mechanisms underlying blood immune response process. In this study, we performed transcriptome-wide gene expression profiling of Japanese flounder (*Paralichthys olivaceus*) challenged by 8 and 48 h *E. tarda* stress. An average of 37 million clean reads per library was obtained, and approximately 85.6% of these reads were successfully mapped to the reference genome. In addition, 808 and 1265 differential expression genes (DEGs) were found at 8 and 48 h post-injection, respectively. Gene Ontology (GO) functional enrichment and Kyoto Encyclopedia of Genes and