



## Data Article

The first transcriptome sequencing and data analysis of the Javan mahseer (*Tor tambra*)

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## ABSTRACT

The Javan mahseer (*Tor tambra*) is one of the most valuable freshwater fish found in *Tor* species. To date, other than mitogenomic data (BioProject: PRJNA422829), genomic and transcriptomic resources for this species are still lacking which is crucial to understand the molecular mechanisms associated with important traits such as growth, immune response, reproduction and sex determination. For the first time, we sequenced the transcriptome from a whole juvenile fish using Illumina NovaSeq6000 generating raw paired-end reads. *De novo* transcriptome assembly generated a draft transcriptome (BUSCO5 completeness of 91.2% [Actinopterygii\_odb10 database]) consisting of 259,403 putative transcripts with a total and N50 length of 333,881,215 bp and 2283 bp, respectively. A total count of 77,503 non-redundant protein coding sequences were predicted from the transcripts and used for functional annotation. We mapped the predicted proteins to 304 known KEGG pathways with signal transduction cluster having the highest representation followed by immune system and endocrine system. In addition, transcripts exhibiting significant similarity to previously published growth-and immune-related genes were identified which will facilitate future molecular breeding of *Tor tambra*.

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