Data Article

Dataset on evolution analysis of splenic transcriptome in bighead carp and silver carp

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Abstract
Bighead carp (Aristichthys nobilis) and silver carp (Hypophthalmichthys molitrix) are closely related species in the subfamily Xenocypridinae within Cyprinidae, and they are also two of the four most important pond–cultured fish species in China. The ability to resist some diseases often differs significantly in silver carp and bighead carp during fishery production. However, the evolutionary divergence of the immune defense functions in these two species is still not understood at the molecular level. The data presented in this article are related to the research article entitled “Comparative analysis of spleen transcriptome detects differences in evolutionary adaptation of immune defense functions in bighead carp and silver carp” (Li et al., 2018). Please refer to this data article for interpretation of the data. Data provided in this submission comprise the Ka/Ks ratios of orthologs as well as adaptive evolution genes, expression levels of orthologs, and TPM value of genes expressed only in spleen of bighead carp or silver carp. These data provide a better understanding of the differences in evolutionary adaptation of immune defense functions in bighead carp and silver carp.

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The spleen samples were collected from three-year-old bighead carp (A. nobilis) and silver carp (H. molitrix). The spleen tissues were collected from six healthy individuals per each species.

The experimental animals comprised bighead carp and silver carp collected from the Yellow River basin in Xingyang, Henan Province, China. The spleen tissues were collected from six healthy individuals per each species.
2.2. cDNA library construction and sequencing

The cDNA library was constructed by using Truseq™ RNA sample prep Kit (Illumina) and sequenced on an Illumina HiSeq. 4000 sequencing platform that generated paired-end reads of 151 nucleotides. The detailed description can be seen in Ref. [1].

2.3. Determination of orthologs

Orthologs among the bighead carp and silver carp were determined using OrthoMCL [3]. The detailed description can be seen in Ref. [1].

2.4. Substitution rate estimation for adaptive genes

The CodeML program in the PAML package was used to estimate the ratio (Ka/Ks values) of the number of non-synonymous substitutions per non-synonymous site (Ka) relative to the number of synonymous substitutions per synonymous site (Ks) [2].

2.5. Gene expression analysis

Gene expression levels were calculated using the transcripts per million (TPM) method. The detailed description can be seen in Ref. [1].

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Transparency document. Supporting information

Transparency document associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2019.01.003.

References

[1] G. Li, Y. Zhao, S. Guo, B. Liu, Y. Chen, X. Sun, J. Feng, Comparative analysis of spleen transcriptome detects differences in evolutionary adaptation of immune defense functions in bighead carp and silver carp, Fish Shellfish Immunol. 84 (2019) 148–157 (Epub 2018 Oct 01).
[2] Z. Yang, PAML 4: phylogenetic analysis by maximum likelihood, Mol. Biol. Evol. 24 (2007) 1586–1591.
[3] L. Li, C.J. Stoeckert Jr, D.S. Roos, OrthoMCL: identification of ortholog groups for eukaryotic genomes, Genome Res. 13 (2003) 2178–2189.