

Comparative transcriptome analyses of silver carp and bighead carp

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Silver carp (*Hypophthalmichthys molitrix*) and bighead carp (*H. nobilis*) are two important aquaculture species in many Asian and eastern European countries due mainly to their fast growth rates and huge reproduction potential. On the contrary, in introduced countries such as the United States, both carps have been considered invasive species since they are giant planktivores: silver carp feeding predominantly on phytoplankton and bighead carp eating mostly zooplankton. To better understand molecular mechanisms of various biological processes (including feeding habits) in these two species, we conducted high throughput transcriptomic analyses of liver tissues of two silver carp and two bighead carp using the Illumina Solexa sequencing technology. A total of over 70 million raw reads were generated (about 18 million reads per sample), resulting in an average of 69,267 assembled transcripts per sample (76,419 transcripts for silver carp and 72,944 transcripts for bighead carp). The BLAST searches against zebra fish proteome resulted in 19,392-22,060 transcripts with more than one hit ($e < 1e-10$) in silver carp and 19,621-22,102 transcripts in bighead carp, matching to an average of 9960 zebrafish proteins (24% of the zebrafish proteome). Differential gene expression analyses of those transcripts with potential known functions showed 2322 genes significantly regulated between the two species with 1140 and 1182 highly expressed in bighead carp and silver carp, respectively. Gene Ontology and pathway analyses revealed a number of genes and networks that pertain to their growth and feeding habits. In this study, we characterized and compared transcriptomes of silver carp and bighead carp, which will be of significant importance not only in aquaculture practice (e.g., development of markers assisting breeding) but as well in basic research (e.g., deciphering adaptive feeding molecular mechanisms).