

China Completes Draft Genome of Grass Carp

The grass carp (*Ctenopharyngodon idellus*) is an important farmed fish, accounting for about 16% of global freshwater aquaculture and possesses a vegetarian diet. However, the lack of a complete genome sequence has made it difficult to conduct in-depth investigation on grass carp biology and breeding for better quality fish. As the first step, researchers from the CAS Institute of Hydrobiology, the CAS National Center for Gene Research, Sun Yat-Sen University and other institutions have reported a draft genome sequence and transcriptomic analysis of grass carp, adding this important species to the other sequenced teleosts: cod, fugu, medaka, tetraodon, stickleback and zebrafish. This study provides genomic insights into the evolutionary history of the grass carp and its unique vegetarian diet adaptation.

Adopting a whole-genome shotgun sequencing strategy and a modified *de novo* Phusion-meta assembly pipeline, researchers constructed the final assemblies of a gynogenetic female adult grass carp (0.90 Gb) and a wild, water-captured male adult (1.07 Gb) genomes. Based on 27 Gb of RNA-seq data and homologous gene information from zebrafish, a total of 27,263 protein-coding genes were annotated in the female genome. In addition, 114 scaffolds were anchored on 24 linkage groups, covering 573 Mb (64%) of the female assembly with 17,456 (64%) annotated genes localized.

Compared with 12 other vertebrate genomes, grass carp has the closest relationship to zebrafish. They share 7,227 families, and many immune-associated function domains in grass carp have undergone significant expansion. The estimated divergence time between zebrafish and grass carp was around 49 to 54 million years ago. The gene collinearity and FISH analysis demonstrated that zebrafish chromosomes 10 and 22 correspond to a single chromosome, LG 24, in grass carp, suggesting a

chromosome fusion in grass carp genome during evolution.

By comparison of the assemblies between the male and female grass carp, scientists identified a total length of 2.38 Mb which was male-specific and mainly localized on LG24. LG24 has the largest physical size but the smallest genetic distance, indicating a significantly lower exchange rate in the process of meiosis. As above, the fusion of LG24 in grass carp may be related to sex chromosome differentiation.

Grass carp are typically herbivorous. How grass carp effectively absorb nutrients from plants to support their rapid growth is an unanswered research question. Analysis of the genes predicted from the assemblies of these non-host reads did not find cellulose-digesting enzymes in gut, implicating that the grass carp intestine might not digest and absorb cellulose.

The analyses of transcriptome data revealed the genes with differential expression levels are significantly enriched in the pathways associated with the circadian rhythm in gut, steroid biosynthesis, terpenoid backbone biosynthesis and glycerophospholipid metabolism pathways in liver. Grass carp may maintain a continuous feeding rhythm in order for them to get enough nutrients from their food.

As a member of the Cyprinidae family and the only species of the genus *Ctenopharyngodon*, the analysis of grass carp genome sequence will not only provide key technical support for exploring important economic trait-related genes and genetic improvement of farmed species, but also lay a solid foundation for theoretical studies related to fish genome evolution, sex determination and differentiation mechanisms.

Their study was published in *Nature Genetics* with the title “The draft genome of the grass carp (*Ctenopharyngodon idellus*) provides insights into its evolution and vegetarian adaptation”.

