Chromosome-level genome assembly of the Chinese Longsnout catfish *Leiocassis longirostris*

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Abstract

The Chinese Longsnout catfish *Leiocassis longirostris* (*L. longirostris*) is one of the most economically important freshwater catfish in China. It is a valuable model for studies on sexual dimorphism, comparative and conservation biology since its wild resources have declined sharply. However, there is lack of high-quality chromosome-level genome information for comparative genomic analysis and genome evolutionary studies. Therefore, we constructed the first high-quality chromosome-level reference genome for *L. longirostris* using a combined strategy of BGI-SEQ500, Nanopore, and Hi-C technologies. The assembled genome of *L. longirostris* contained a total length of 703.19 Mb with 389 contigs, and an N50 size of 4.29 Mb. Using the Hi-C data, we finally successfully generated 82 chromosome-level scaffolds anchored onto 26 chromosomes with a total length of 685.53 Mb (97.44% of the total genome sequences), ranging in size from 17.36 Mb to 43.97 Mb. A total of 23,708 protein-coding genes were identified in the *L. longirostris* genome, and up to 97.73% of *L. longirostris* genes were functionally annotated. In addition, the genome contained 239.11 Mb (33.99% in the total genome) repetitive sequences and 6,303 non-coding RNAs. The phylogenetic analysis indicated that the divergence time between *L. longirostris* and their closest relative species *Pelteobagrus fulvidraco* was approximately 26.6 million years. Collinearity analyses showed 26 chromosomes of *L. longirostris* displayed high homology with the corresponding scaffold ([?]3M) of *P. fulvidraco* and the corresponding chromosomes of the *Ictalurus punctatus*. The high-quality reference genome of *L. longirostris* was assembled for the first time and will pave a way for genome-scale selective breeding, genome comparisons and evolution investigations.

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