

# Chromosomal-level genome assembly of silver sillago (*Sillago sihama*)

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## Abstract

Silver sillago, *Sillago sihama* is a member of the family Sillaginidae and found in all Chinese inshore waters. It is an emerging commercial marine aquaculture species in China. In this study, high-quality chromosome-level reference genome of *S. sihama* was first constructed using PacBio Sequel sequencing and high-throughput chromosome conformation capture (Hi-C) technique. A total of 66.16 Gb clean reads were generated by PacBio sequencing platforms. The genome-scale was 521.63 Mb with 556 contigs, and 13.54 Mb of contig N50 length. Additionally, Hi-C scaffolding of the genome resulted in 24 chromosomes containing 96.93 % of the total assembled sequences. A total of 23,959 protein-coding genes were predicted in the genome, and 96.51 % of the genes were functionally annotated in public databases. A total of 71.86 Mb repetitive elements were detected, accounting for 13.78% of the genome. The phylogenetic relationships of silver sillago with other teleosts showed that silver sillago was separated from the common ancestor of *S. sinica* about 7.92 million years ago. Comparative genomic analysis of silver sillago with other teleosts showed that 45 unique and 100 expansion gene families were identified in silver sillago. Expansion gene families were involved in immune and olfactory receptors. In this study, the genomic resources provide valuable reference genomes for functional genomics research of silver sillago.

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