

A draft genome assembly of spotted scat (*Scatophagus argus*): the first reference genome for Scatophagidae fish.

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Abstract

Spotted scat (*Scatophagus argus*) is an economically important marine cultured fish species in Asia, especially in Southeast China. As an XY sex-determining type fish species, spotted scat can be used as a model for understanding the mechanism of novel sex determination system evolution in vertebrates. However, genomic resources of spotted scat are lacking, and no highly contiguous reference genome has been released. In this study, the first chromosome-level genome of spotted scat was constructed using PacBio's single-molecule real-time (SMRT) sequencing and high-throughput chromosome conformation capture (Hi-C) sequencing technologies. The genome comprised 572.42 Mb, with the contig N50 of 19.60 Mb. A total of 24,256 protein-coding genes were predicted in the genome, and 96.30% of the predicted genes were functionally annotated. Evolutionary analysis showed that spotted scat diverged from the common ancestor of Japanese puffer (*Takifugu rubripes*) approximately 114.8 million years ago. In addition, doublesex and mab-3 related transcription factor 1 (*dmrt1*), a gene associated with sex determination process, was not found in the high-quality female genome, while it existed in the re-sequencing data of three XY genotype male fish. The conserved *dmrt1* locus of vertebrates was substituted by its truncated homologue (*dmrt1b*), which derives from *dmrt1* via allelic diversification and mutations. The genomic resources offer a strong foundation for further research on the sex determination of spotted scat and facilitate the understanding of the evolution of sex chromosomes in teleost species.

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