

GENOME SEQUENCING

The Complete Genome Sequences of 3 Species of *Malacoctenus* Fishes (Labrisomidae, Blenniiformes)

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Biodiversity Genomes

We present the complete genome sequences of *Malacoctenus gilli*, *Malacoctenus tetranemus*, *Malacoctenus triangulates*. Illumina sequencing was performed on genetic material from museum specimens. The reads were assembled using a de novo method followed by a finishing step. The raw and assembled data are available via Genbank.

Methods

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. A paired-end sequencing library was constructed for each specimen using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, 2021).

Results and Data Availability

All data, including raw reads and assembled genome sequence, is available via Genbank.

Malacoctenus gilli	JASSRZ000000000
Malacoctenus tetranemus	JAUESF000000000
Malacoctenus triangulatus	JAUESE000000000

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