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GENOME SEQUENCING

The Complete Genome Sequences of 12 Species of Enteromius (Cyprinidae, Cypriniformes, Actinopteri)

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Biodiversity Genomes

We present the complete genome sequences of 12 species of *Enteromius*. 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 publicly 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 using the Illumina TruSeq kit according to the manufacturer's instructions. The library was 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, O'Neill, and Pirro 2021).

Results and Data Availability

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

Enteromius afrohamiltoni SAIAB 203872 JAUYWG000000000

Enteromius anoplus SAIAB 200353 JAUMHG000000000

Enteromius argenteus SAIAB 84963 JAUCMR000000000

Enteromius fasciolatus SAIAB 187017 JAUMHR000000000

Enteromius mattozi SAIAB 78468 JAUMHE000000000

Enteromius paludinosus SAIAB 97062 JAUMHQ000000000

Enteromius radiatus SAIAB 190297 JAUCMS000000000

Enteromius thamalakanensis SAIAB 187035 JAUCMT000000000

Enteromius treurensis SAIAB 194790 JAUCMU000000000

Enteromius trimaculatus SAIAB 97060 JAUMHP000000000

Enteromius unitaeniatus SAIAB 203025 JAUMHI000000000

Enteromius viviparus SAIAB 235471 JAUCNO000000000

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