

GENOME SEQUENCING

The complete genome sequences of 12 species of Percopsiformes

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Biodiversity Genomes

We present complete genome sequences of 12 species of Percopsiformes.

Methods

Tissues from single, wild-collected individuals were used for this study. DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the standard process. Paired-end sequencing libraries were constructed 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 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O’Neill, and Pirro 2021).

Results and Data Availability

All genomes are available on Genbank:

Amblyopsis hoosieri	JAODUE000000000
Amblyopsis rosae	JAODTR000000000
Amblyopsis spelaea	JAODUF000000000
Aphredoderus sayanus	JAODUG000000000
Chologaster cornuta	JAODVN000000000
Forbesichthys agassizii	JAODLL000000000
Forbesichthys papilliferus	JAODOY000000000
Percopsis omiscomaycus	JAODLI000000000
Percopsis transmontana	JAOEHI000000000
Speoplatyrhinus poulsoni	JAOEGT000000000
Typhlichthys eigenmanni	JAODUK000000000
Typhlichthys subterraneus	JAODUH000000000

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