

GENOME SEQUENCING

The Complete Genome Sequences of 20 Species of African Tetras and Relatives of Families Alestidae, Hepsetidae, and Lepidarchidae (Teleostei: Characiformes)

Bruno F. Melo¹, Stacy Pirro², Melanie L. J. Stiassny¹

¹ Department of Ichthyology, American Museum of Natural History, ² Iridian Genomes

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Biodiversity Genomes

We present the complete genome sequences of 20 species of African tetras, robbers, and tigerfishes in the families Alestidae, Hepsetidae, and Lepidarchidae. Illumina sequencing was performed on genetic material from wild-caught and aquarium 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.

Introduction

African characiform fishes are represented by 128 species distributed in the clade Alestoidea with the families Alestidae, Hepsetidae, and Lepidarchidae (Melo and Stiassny 2024). Although much of the recent research is centered on their phylogenetics and phenotypic evolution (Melo and Stiassny 2022; Stiassny et al. 2023), only one *Hepsetus* genome is available (Yang et al. 2023). Here we release 20 new assembled genomes of African characiforms that will provide a foundation for further comparative genomic studies.

Methods

Single wild-collected and aquarium individuals were sampled for this study. Tissues were obtained from the Department of Ichthyology of the American Museum of Natural History, New York. DNA extraction was performed using the Qiagen DNeasy Blood and Tissue 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, is available via GenBank.

taxname	specimen_voucher	genome_accession
<i>Alestes dentex</i>	AMNH 264421	JBBIGA000000000

taxname	specimen_voucher	genome_accession
<i>Alestopetersius hilgendorfi</i>	AMNH 269853	JBBIGB000000000
<i>Arnoldichthys spilopterus</i>	AMNH 278245	JBBPDA000000000
<i>Bathyaethiops greeni</i>	AMNH 257179	JBBPDD000000000
<i>Brachyalestes nurse</i>	AMNH 257766	JBBPCY000000000
<i>Brachypetersius altus</i>	AMNH 276859	JBBPDB000000000
<i>Brachypetersius gabonensis</i>	AMNH 271746	JBBJLR000000000
<i>Brycinus macrolepidotus</i>	AMNH 276727	JBBPCZ000000000
<i>Bryconaethiops microstoma</i>	AMNH 276883	JBBJLS000000000
<i>Clupeocharax schoutedeni</i>	AMNH 269862	JBBPDH000000000
<i>Hemigrammopetersius urotaenia</i>	AMNH 271744	JBBPDC000000000
<i>Hepsetus odoe</i>	AMNH 263267	JBBJLQ000000000
<i>Hydrocynus forskahlii</i>	AMNH 249806	JBBPCX000000000
<i>Ladigesia roloffi</i>	AMNH 261335	JBBKCR000000000
<i>Lepidarchus adonis</i>	AMNH 261317	JBBIGC000000000
<i>Micralestes humilis</i>	AMNH 263289	JBBPDG000000000
<i>Nannopetersius ansorgii</i>	AMNH 275931	JBBPDE000000000
<i>Phenacogrammus interruptus</i>	AMNH 274784	JBBPCW000000000
<i>Rhabdalestes septentrionalis</i>	AMNH 278672	JBBMFX000000000
<i>Tricuspidaletes caeruleus</i>	AMNH 252193	JBBPFO000000000

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