

GENOME SEQUENCING

The complete genome sequence of the Acestrorhamphid *Psalidodon fasciatus*

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Biodiversity Genomes

We present the first genome assembly of *Psalidodon fasciatus*, a rheophilic fish recently classified within Acestrorhamphidae and distributed across major South American river basins. Known for its karyotypic diversity and cryptic speciation potential, *P. fasciatus* was sequenced using Illumina Hi-Seq and assembled with SPAdes and Zanfona, resulting in 471,706 scaffolds at 60× coverage. The assembled genome is available in GenBank (Assembly ID: ASM5207532v1) and provides a valuable resource for evolutionary and taxonomic studies in Brazilian ichthyofauna.

Introduction

Psalidodon fasciatus (Cuvier, 1819) is a rheophilic species recently placed within the family Acestrorhamphidae (Terán, Benitez, and Mirande 2020; Melo et al. 2024) with a distribution spanning the Paraná, Paraguay, and Uruguay river basins, as well as the northeastern region of the São Francisco River basin (Melo et al. 2024) ([Figure 1](#)). As with this genus and others such as *Astyanax*, the taxonomic classification of its individuals has proven challenging (Pazza et al. 2008), leading to several phylogenetic reclassifications (Castro et al. 2014; Rossini et al. 2016; Terán, Benitez, and Mirande 2020; Goes et al. 2022; Garduño-Sánchez et al. 2023).

An important area of research involving *P. fasciatus* concerns speciation and population dynamics (Peres et al. 2009; Ferreira-Neto et al. 2012; Matoso et al. 2013; Penteado, Kavalco, and Pazza 2013; Kavalco et al. 2016). The presence of populations with distinct chromosomal and morphological patterns across different hydrographic basins suggests that the species may represent a complex of cryptic species still undergoing differentiation (Artoni et al. 2006).

In genetics, *P. fasciatus* has been used in studies focusing on karyotypic and chromosomal variation. Several studies indicate that this species exhibits significant genetic polymorphisms, with variations in chromosome number and structure among populations, suggesting a high evolutionary potential (Pazza and Kavalco 2007; Panonato-Alves et al. 2013; Goes et al. 2022). Here, we present the first genome assembly of *Psalidodon fasciatus*, highlighting its potential as a new model organism for research on Brazilian ichthyofauna.



Figure 1. Specimen of *Psalidodon fasciatus*. Scale bar: 1cm (Photo: Kerniske et al. 2021)

Methods

We collected the sample tissue from an individual collected in the sinkhole 2 of the State Park of Vila Velha, Ponta Grossa, Brazil ($-25^{\circ}13'28.002''\text{S}$, $-50^{\circ}2'27.6072''\text{W}$) under authorization by Chico Mendes for Biodiversity and Conservation (ICMBIO—SISBIO—license number 15115-1), and the experimental procedures were approved by the Ethics Committee on the use of the Animals for Research at (CEUA Process number 0769342/2021). The use of the genetic data in this study was authorized by the National System for the Management of Genetic Heritage and Associated Traditional Knowledge (SISGEN number A6F96AE).

DNA extraction was performed with the Qiagen DNAeasy Genomic Extraction Kit using a standard process. 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 a paired-end, $2 \times 150\text{bp}$ format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions using Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled using SPAdes v2.5 (Bankevich et al. 2012) followed by a final step using Zanfona (Kieras, O'Neill, and Pirro 2021). Genome assembly completeness was evaluated with BUSCO v6 (Manni et al. 2021; Tegenfeldt et al. 2025).

Results and availability

The genome assembly resulted in 471,706 scaffolds with a coverage depth of 60X (Table 1). All raw sequencing data and the assembled genome of *Psalidodon fasciatus* are available in the GenBank database (Assembly ID: ASM5207532v1).

Table 1. Genome assembly statistics

Voucher number	JSSB7SIPGJ-Furna
Raw Data	SRR33069403
Assembled Genome	ASM5207532v1
No. of scaffolds	471,706
No. of base pairs	1,316,875,484
N50	23 kbp
L50	23,730
GC content (%)	38
Average genome coverage	60x
BUSCO scores	Actinopterygii C:45.7% [S:45.2%, D:0.4%], F:21.7%, M:32.7%, n:3640, E:15.3%

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