GENOME SEQUENCING

The Complete Genome Sequences of 7 Hypoplectrus species (Serranidae, Perciformes)

Arturo Acero¹, Stacy Pirro², Ricardo Betancur³

¹ Universidad Nacional de Colombia, ² Iridian Genomes, ³ Department of Biology, University of Oklahoma https://doi.org/10.56179/001c.117765

Biodiversity Genomes

Species in the genus *Hypoplectrus* are found primarily in coral reefs in the Caribbean Sea and the Gulf of Mexico, particularly around Florida and the Bahamas. They are a popular choice for hobbyist saltwater aquariums. Members of this genus are simultaneous hermaphrodites, as they have both male and female sexual organs at the same time as an adult. We present the genome sequences of 7 species of *Hypoplectrus*. Raw read data and assembled genomes are available in Genbank.

Methods

Tissue from single, wild-collected individuals were used for this study. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the 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 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 v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All raw read data and assembled genomes are available on Genbank:

Species	Raw Read	Assembled Genome	
Hypoplectrus aberrans	SRR19070321	JAOYMT000000000	
Hypoplectrus chlorurus	SRR18184334	JAOXJR00000000	
Hypoplectrus guttavarius	SRR18184176	JAOXOB000000000	
Hypoplectrus indigo	SRR19070349	JAOXJS00000000	
Hypoplectrus nigricans	SRR18272038	JAOWBK00000000	
Hypoplectrus providencianus	SRR17839752	JAOWBC00000000	
Hypoplectrus randallorum	SRR17839729	JAOXNY000000000	

_

Funding

Funding was provided by Iridian Genomes, grant# IRGEN_RG_2021-1345 Genomic Studies of Eukaryotic Taxa.

Submitted: May 19, 2024 EDT, Accepted: May 23, 2024 EDT

Biodiversity Genomes 2

REFERENCES

Bankevich, Anton, Sergey Nurk, Dmitry Antipov, Alexey A. Gurevich, Mikhail Dvorkin, Alexander S. Kulikov, Valery M. Lesin, et al. 2012. "SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing." *Journal of Computational Biology* 19 (5): 455–77. https://doi.org/10.1089/cmb.2012.0021.

Bolger, Anthony M., Marc Lohse, and Bjoern Usadel. 2014. "Trimmomatic: A Flexible Trimmer for Illumina Sequence Data." *Bioinformatics* 30 (15): 2114–20. https://doi.org/10.1093/bioinformatics/btu170.

Kieras, M, K O'Neill, and S Pirro. 2021. "Zanfona, a Genome Assembly Finishing Tool for Paired-End Illumina Reads." 2021. https://github.com/zanfona734/zanfona.

Biodiversity Genomes 3