

## GENOME SEQUENCING

# First genome of a deep-sea notacanthid fish, *Notacanthus arronte* (Notacanthiformes; Notacanthidae)

David Barros-García<sup>1</sup>, André M. Machado<sup>1,2</sup>, Juan Carlos Arronte<sup>3</sup>, André Gomes-dos-Santos<sup>1</sup>, L. Filipe C. Castro<sup>1,4</sup>, Elsa Froufe<sup>1,5</sup>

<sup>1</sup> CIIMAR/CIMAR LA, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, 4450-208 Matosinhos, Portugal., <sup>2</sup> FCUP - Department of Biology, Faculty of Sciences, University of Porto (U. Porto), Rua do Campo Alegre, Porto, Portugal., <sup>3</sup> Spanish Institute of Oceanography, Santander Oceanographic Centre (COST-IEO), CSIC, Severiano Ballesteros 16, 39004 Santander, Spain., <sup>4</sup> Department of Biology, Faculty of Sciences, University of Porto, 4169-007 Porto, Portugal., <sup>5</sup> ICBAS - School of Medicine and Biomedical Sciences, University of Porto, Laboratory of Cytogenetics

<https://doi.org/10.56179/001c.144906>

---

## Biodiversity Genomes

---

We present the first genome assembly of the recently described deep-sea spiny eel, *Notacanthus arronte* (Notacanthiformes: Notacanthidae). The whole genome was assembled using Illumina short-read sequencing approaches. The raw data and assembled genome are publicly available under the NCBI Accession Number JBQVWD000000000 under BioProject Accession PRJNA1294845.

## Introduction

*Notacanthus arronte* (Bañón et al. 2024) is a recently described species of deep-sea spiny eel belonging to the order Notacanthiformes (family Notacanthidae). Notacanthiformes, together with the sister lineage Anguilliformes (true eels) and others, comprise the superorder Elopomorpha. This superorder represents one of the earliest-diverging lineages within teleosts, in the aftermath of the whole genome duplication event (3R) (Chen, Samadi, and Chen 2015).

Notacanthids are globally distributed deep-sea benthopelagic or benthic fish (Nelson, Grande, and Wilson 2016). They inhabit depths ranging from 125 to 4,900 metres, from the continental slope to the abyssal plain (Nelson, Grande, and Wilson 2016). Ecologically, they are highly specialised, feeding on sessile/low mobile invertebrates (e.g., polyps, ophiuroids), and are among the most common species in their ecosystems (Carrasón and Matallanas 2002; Coggan, Gordon, and Merret 1998). Notacanthids are also characterised by a slow growth rate and late reproductive maturity, making them extremely sensitive to human activity, with some populations declining nearly 97% over 20 years (Devine, Baker, and Haedrich 2006; Vedishcheva, Orlov, Orlova, et al. 2016).

Despite their key position in the vertebrate Tree of Life and their ecological importance, no genome assembly representative of this family has been produced to date, and the first transcriptomic information has only been obtained recently (Gomes-dos-Santos et al. 2025). Therefore, here we present the genome assembly of *Notacanthus arronte*, the first genome resource belonging to a notacanthid species.

## Methods

An adult specimen of *N. arronte* was captured in the Cantabrian Sea (North of the Iberian Peninsula) at a depth of 528 metres, as part of the DEMERSALES19 campaign carried out by the Spanish Institute of Oceanography (IEO-CSIC). DNA extraction was performed using the Qiagen MagAttract HMW DNA extraction kit (Dobra) at CIIMAR.

Two distinct whole genome sequencing approaches were applied, Illumina Paired-end reads (PE) and Illumina long insert size Mate-pair reads (MP), at Macrogen Inc., Korea. Briefly, the Illumina PE library was obtained using a Truseq Nano DNA Illumina library preparation kit, followed by paired-end ( $2 \times 150$  bp) sequencing in a NovaSeq6000 machine, and the Illumina MP library (10 kb insert size) was obtained using a Nextera Mate Pair Library ( $2 \times 150$  bp), followed by paired-end ( $2 \times 150$  bp) sequencing in a NovaSeq6000 machine.

The raw sequencing reads from both libraries were trimmed and quality filtered using Trimmomatic v.0.38 (Bolger, Lohse, and Usadel 2014). Genome assembly was produced using SOAPdenovo2 (Luo et al. 2012), specifying the k-mer length (k=23).

## Results and Data Availability

The genome assembly yielded a total size of 1.36 Gbp, with 54,118 scaffolds, and a scaffold N50 length of 196,238 kb.

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession JBQVWD000000000. The version described in this paper is version JBQVWD010000000.

## Funding

This research was funded by national funds through FCT – Fundação para a Ciência e a Tecnologia within the scope of the Strategic Funding UIDB/04423/2020 (<https://doi.org/10.54499/UIDB/04423/2020>), UIDP/04423/2020 (<https://doi.org/10.54499/UIDP/04423/2020>), and LA/P/0101/2020 (<https://doi.org/10.54499/LA/P/0101/2020>). Foundation for Science and Technology also funded through the project PerSeave (10.54499/2022.04750.PTDC) and DOI identifier <https://doi.org/10.54499/2022.04750.PTDC>, FCT also funded DBG under contract (10.54499/2020.04364.CEECIND/CT0008), AGS (2023.07625.CEECIND/CP2848/CT0010 and DOI identifier <https://doi.org/10.54499/2023.07625.CEECIND/CP2848/CT0010>), EF (CEECINST/00027/2021/CP2789/CT0003 and DOI identifier <https://doi.org/10.54499/CEECINST/00027/2021/CP2789/CT0003>) and LFCC (CEECINST/00133/2018/CP1510/CT0004 and DOI identifier ).

### ***Author contributions***

DBG, LFC and EF conceptualized, supervised and administrated the study. JCA provided the tissue samples required and DBG performed the DNA extraction. AMM and AGS carried out the assembly analysis. DBG and AGS wrote the original manuscript. All authors reviewed and edited the manuscript.

### ***Acknowledgements***

The authors would like to thank the staff involved in the research survey Demersales19 (ERDEM project) carried out by the Spanish Institute of Oceanography (IEO-CSIC) on board the R/V Miguel Oliver (Ministry of Agriculture, Fisheries and Food, Spain). We are very grateful to Ana Antolínez (IEO-CSIC) for her assistance with the dissection of specimens.

Submitted: September 10, 2025 EDT. Accepted: October 21, 2025 EDT. Published: October 21, 2025 EDT.

## REFERENCES

- Bañón, R., D. Barros-García, F. Baldó, M. Cojan, and A. de Carlos. 2024. “Unveiling Taxonomic Diversity in the Deep-Sea Fish Genus *Notacanthus* (Notacanthiformes: Notacanthidae) with Description of *Notacanthus Arronte* n. Sp.” *J. Fish Biol* 104 (6): 1910–23. <https://doi.org/10.1111/jfb.15734>.
- Bolger, A. M., M. Lohse, and B. Usadel. 2014. “Trimmomatic: A Flexible Trimmer for Illumina Sequence Data.” *Bioinformatics* 30 (15): 2114–20. <https://doi.org/10.1093/bioinformatics/btu170>.
- Carrasón, M., and J. Matallanas. 2002. “Feeding Strategies of *Polyacanthonotus Rissoanus* (Pisces: Notacanthidae) in the Deep Western Mediterranean.” *Journal of Marine Biology Association of the United Kingdom* 82:665–71. <https://doi.org/10.1017/S0025315402006033>.
- Chen, J. N., S. Samadi, and W. J. Chen. 2015. “Elopomorpha (Teleostei) as a New Model Fish Group for Evolutionary Biology and Comparative Genomics.” In *Evolutionary Biology: Biodiversification from Genotype to Phenotype*, edited by P. Pontarotti. Cham: Springer. [https://doi.org/10.1007/978-3-319-19932-0\\_17](https://doi.org/10.1007/978-3-319-19932-0_17).
- Coggan, R. A., J. D. M. Gordon, and N. R. Merret. 1998. “Abundance, Distribution, Reproduction and Diet of Notacanthid Fishes from the North-East Atlantic.” *Journal of Fish Biology* 52:1038–57. <https://doi.org/10.1111/j.1095-8649.1998.tb00602.x>.
- Devine, J., K. Baker, and R. Haedrich. 2006. “Deep-Sea Fishes Qualify as Endangered.” *Nature* 439:29. <https://doi.org/10.1038/439029a>.
- Gomes-dos-Santos, A., A. M. Machado, F. Baldó, J. C. Arronte, L. F. C. Castro, and D. Barros-García. 2025. “A ‘Light in the Darkness’: First Transcriptomic Data from Deep-Sea Spiny Eels (Notacanthidae).” *Marine Genomics* 80:101182. <https://doi.org/10.1016/j.margen.2025.101182>.
- Luo, R., B. Liu, Y. Xie, Z. Li, W. Huang, J. Yuan, G. He, et al. 2012. “SOAPdenovo2: An Empirically Improved Memory-Efficient Short-Read de Novo Assembler.” *GigaScience* 1 (1): 18. <https://doi.org/10.1186/2047-217X-1-18>.
- Nelson, J. S., T. C. Grande, and M. V. H. Wilson. 2016. *Fishes of the World*. 5th ed. Wiley.
- Vedishcheva, E. V., A. M. Orlov, S. Y. Orlova, et al. 2016. “First Data on the Age, Growth Processes, and Otoliths of Snub-Nosed Spiny Eel *Notacanthus Chemnitzii* (Notacanthidae).” *Journal of Ichthyology* 56:890–98. <https://doi.org/10.1134/S0032945216060102>.