Data in Brief 52 (2024) 109836

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Dataset of the complete mitogenome of the deep-sea sailfin roughshark, *Oxynotus paradoxus* Frade, 1929

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A R T I C L E I N F O

Article history:
Received 20 September 2023
Revised 31 October 2023
Accepted 16 November 2023
Available online 20 November 2023

Dataset link: Whole genome sequencing of Oxynotus paradoxus (Original data)
Dataset link: Oxynotus paradoxus isolate 4.93 mitochondrion, complete genome (Original data)
Dataset link: Oxynotus paradoxus voucher 4.93 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial (Original data)

A B S T R A C T

Chondrichthyans comprise a diverse group of vertebrate species with extraordinary ecological relevance. Yet, multiple members of this evolutionary lineage are associated with significant extinction risk. The sailfin roughshark *Oxynotus paradoxus* is a deep-water benthic shark currently listed as vulnerable due to population declines in parts of its range. Here we provide the first complete mitochondrial genome of *O. paradoxus*, comprising also the first record for the genus and family Oxynotidae. These data can facilitate future monitoring of the genetic diversity in this and related species. Genomic DNA was extracted from *O. paradoxus* collected in the eastern North Atlantic off western Portugal (37.59°N, 9.51°W) and sent for Illumina Paired-End (2 × 150 bp) library construction and whole genome sequencing on a Novaseq6000 platform. Trimmomatic (version 0.38) was used to remove

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https://doi.org/10.1016/j.dib.2023.109836

Keywords:
Chondrichthyes
Shark
Oxynotidae
Mitochondrial
Phylogeny

adapters and MitoZ (version 3.4) to assemble and annotate the mitogenome. This mitogenome with 17 100 bp has a total of 38 genes, 13 of which are protein-coding genes, 23 transfer RNA genes, and 2 ribosomal RNA genes. Eight transfer RNAs and 1 protein-coding gene (NADH dehydrogenase subunit 6, NAD6) are in the complementary strand. In the provided phylogenetic inference, with all available and verified Squalomorphii mitogenomes, the four orders are well separated, and as expected, *O. paradoxus* is placed in the Squaliformes order. This data reinforces the need for more genomic resources for the Oxynotidae family.

Specifications Table

Subject	Biological Sciences
Specific subject area	Bioinformatics, Marine Biology, Phylogeny and Evolution
Data format	Raw, analyzed
Type of data	Figures
Data collection	A specimen of *Oxynotus paradoxus* was collected at 37.59°N, 9.51°W in the eastern North Atlantic off western Portugal (Fig. 1). The species was identified at morphological and genetic levels. Genomic DNA was sent to Macrogen (Seoul, South Korea) for Illumina Paired-End (2 × 150 bp) library construction and whole genome sequencing on a Novaseq6000 platform. Adapters were removed using Trimmomatic (version 0.38) and the mitogenome was assembled and annotated with MitoZ (version 3.4). Genome coverage information was obtained by running BBMap (BBMap Guide - DOE Joint Genome Institute).
Data source location	One *O. paradoxus* specimen, collected at 37.59°N, 9.51°W, was deposited at Centre of Marine Sciences, Universidade do Algarve (Portugal) (CCMAR) (contact person: Sofia Graça Aranha, sgramos@ualg.pt) with voucher name 4.93.
Data accessibility	Repository name: GenBank Data identification number: Accession numbers OQ627801 and OQ645448, and BioProject accession number PRJNA1033629 Direct URL to data: https://www.ncbi.nlm.nih.gov/nuccore/OQ627801.1/ https://www.ncbi.nlm.nih.gov/nuccore/OQ645448 https://www.ncbi.nlm.nih.gov/sra/PRJNA1033629

1. Value of the Data

- The Class Chondrichthyes includes two sister groups: Holocephalans (or chimaeras) and Elasmobranchs (sharks and rays), distributed throughout the marine, brackish and freshwater ecosystems. Despite the importance of this group, the available genomic resources are still scarce. These are essential for assessing species diversity and population structure and applying conservation policies.
- Amongst Elasmobranchs, the sharks comprise roughly 50 % of the taxa in the group and include various orders, of which the Squaliformes is the second most diverse. The only family within the Squaliformes without mitochondrial genomes reported is the Oxynotidae.
- The data provided in this study comprises the first mitogenome of *O. paradoxus* which is also the first record for the genus *Oxynotus* and family Oxynotidae. These data can facilitate future monitoring of the genetic diversity in this and related species.
- Researchers, conservation managers, and policy-makers can benefit from these data.

- This dataset can be reused by other researchers when studying phylogenetic relationships in sharks and their genetic structure.

2. Data Description

Oxynotidae family comprises benthic deep-sea sharks with a wide distribution range and all belonging to the same genus, *Oxynotus*. Currently, this genus comprises five species, including *Oxynotus paradoxus* Frade, 1929 (sailfin rough shark) which is listed as vulnerable by the International Union for Conservation of Nature (IUCN). This article describes the mitochondrial genome of *O. paradoxus* (Fig. 1). This mitogenome has 17 100 bp with a gene content of 38 genes: 13 protein-coding genes, 23 transfer RNA genes and 2 ribosomal RNA genes (Fig. 2; Supplementary Material 1–3), as other elasmobranchs [1–3]. Of these 38 genes, 9 were in the complementary strand (8 transfer RNAs and 1 protein-coding gene (NADH dehydrogenase subunit 6, NAD6)). The phylogenetic analysis here presented separates with high node support the four taxonomic orders of Squalomorphii. *O. paradoxus* is placed within the Squaliformes clade, as expected, and in a separate branch basal to the families Squalidae and Somniosidae (Fig. 3).

Genome coverage information and graphical displays are available in Supplementary Materials 1–3. The mitogenome was deposited in GenBank with accession number OQ645448, and raw sequencing data was deposited in NCBI with BioSample accession SAMN38037946, BioProject number PRJNA1033629, and SRA study SRP469130.

3. Experimental Design, Materials and Methods

A female specimen (identified by the absence of claspers on the pelvic fin) of *O. paradoxus* was collected at 37.59°N, 9.51°W in the eastern North Atlantic off western Portugal (Fig. 1). The sex of the specimen does not influence the results of the study. The species was first identified at the morphological level. A further test was performed by amplifying the mitochondrial cytochrome oxidase subunit 1 (COI) gene. The sample was obtained in a dead state. Genomic DNA was extracted following a standard high-salt protocol [4], and the COI gene was amplified with LCOI and HCOI primers [5]. The PCR mixture (final volume of 25 µL) contained 2.5 µL of Invitrogen PCR buffer (Invitrogen, Waltham, MA, USA), 1.5 µL 50 mM $MgCl_2$ (Invitrogen, Waltham,

Fig. 1. Species reference image of *Oxynotus paradoxus* (photograph by Tiago Marsili).

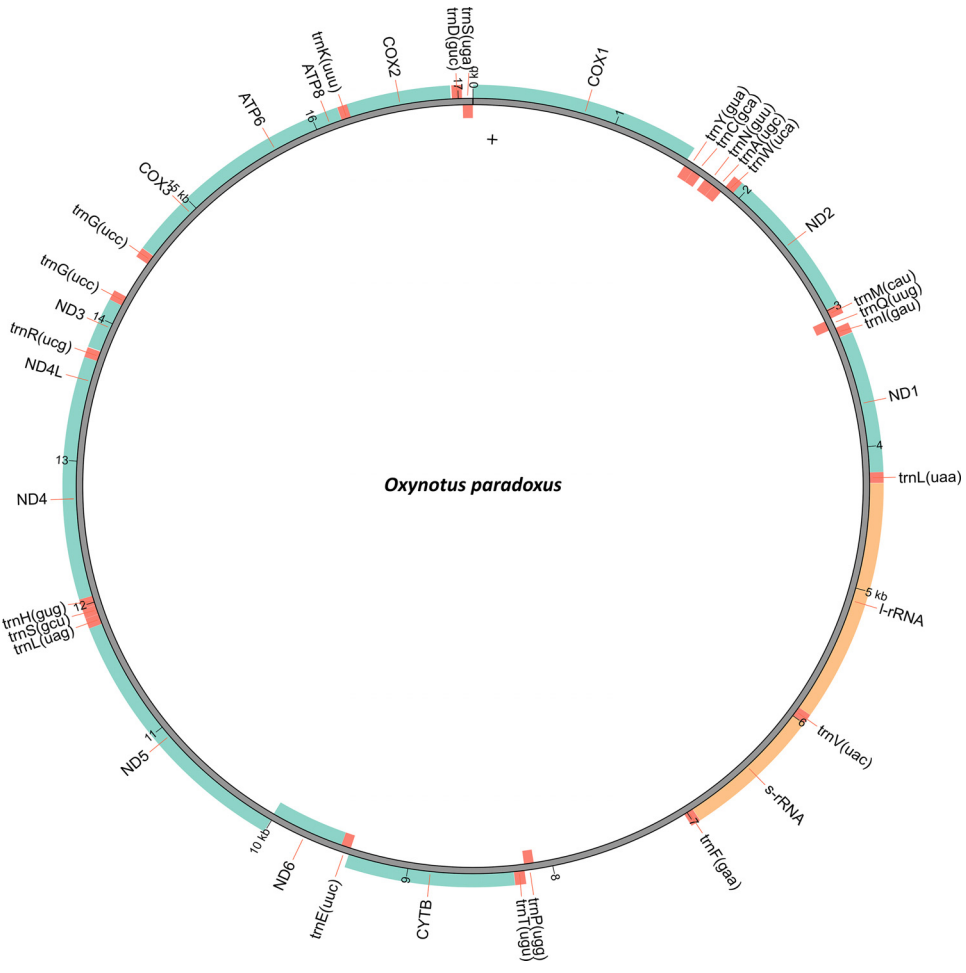

Fig. 2. Mitogenome map of *Oxynotus paradoxus*.

MA, USA), 0.5 µL 10 mM dNTPs, 0.5 µL of each primer (10 mM), 0.1 µL Invitrogen Taq DNA Polymerase (Invitrogen, Waltham, MA, USA) and 1 µL of genomic DNA. The PCR program consisted of an initial denaturation at 94 °C for 3 min followed by 38 cycles at 94 °C for 30 s, 45 °C for 40 s, and 72 °C for 1 min, with a final extension at 72 °C for 10 min. PCR product was sequenced in both directions by Macrogen (Madrid, Spain), using the same primers. The obtained sequence was submitted to GenBank under the accession number OQ627801.

CIIMAR ethical committee and CIIMAR Managing Animal Welfare Body (ORBEA), according to the European Union Directive 2010/63/EU, approved the present work. *Oxynotus. paradoxus* specimen was deposited at Centre of Marine Sciences, Universidade do Algarve (CCMAR) (contact person: Sofia Graça Aranha, sgramos@ualg.pt) with voucher name 4.93.

The extracted genomic DNA was sent to Macrogen (Seoul, South Korea) for Illumina Paired-End (2 × 150 bp) library construction and whole genome sequencing on a Novaseq6000 platform. Trimmomatic (version 0.38) was used to remove adapters in the raw PE sequencing reads, using parameters leading and trailing set to 5, minlen of 36, and a “sliding window” set to 4 bp with the required quality of 15 [6]. The mitogenome was assembled and annotated with MitoZ (version 3.4) [7], using the clean PE reads and default parameters. Genome coverage informa-

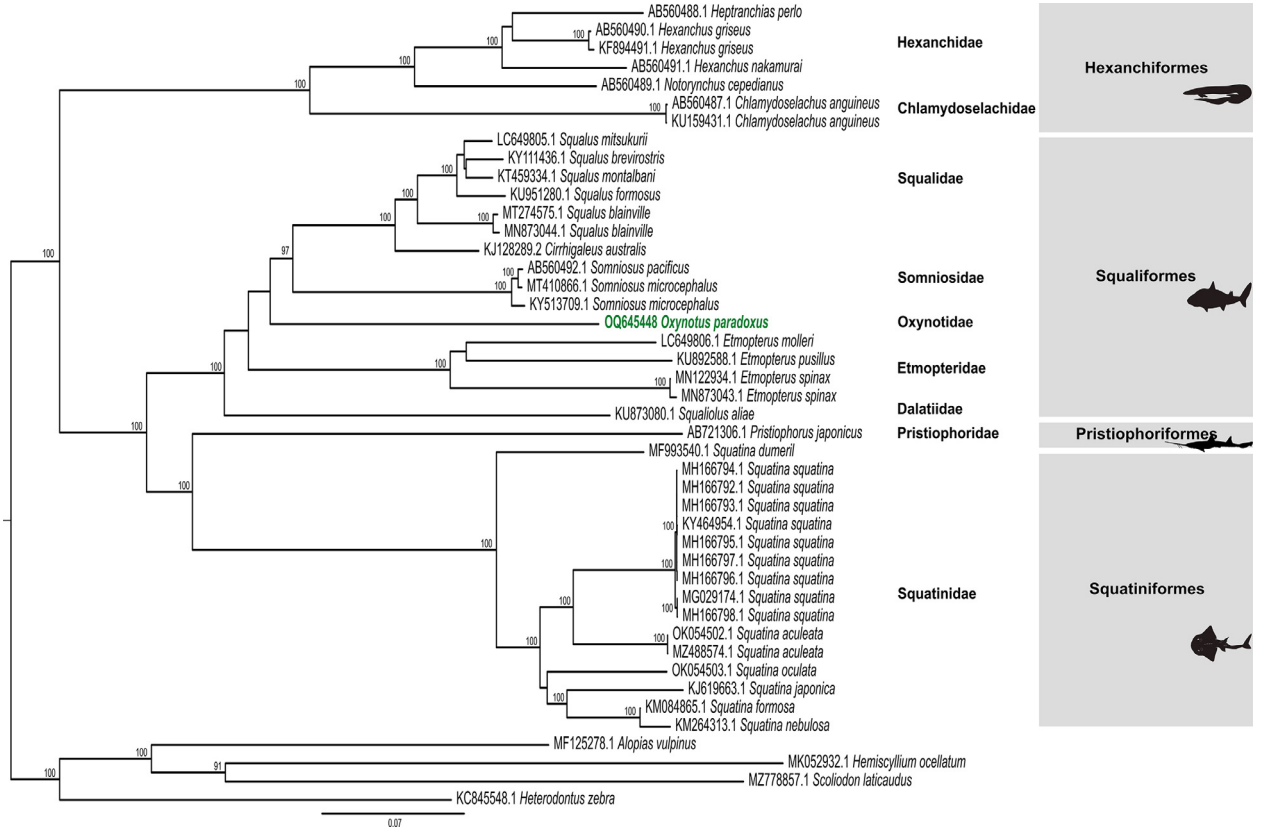

Fig. 3. Maximum Likelihood phylogenetic inference obtained with the sequences of all protein-coding genes from the 43 verified and available Squalomorphii mitogenomes. Bootstraps above 90 % are shown, above the nodes.

tion was obtained by running BBMap (BBMap Guide - DOE Joint Genome Institute) (splice-aware global aligner for DNA and RNA sequencing reads) and a graphical display produced using the genome browser Artemis [8] (Supplementary Material 1 and Supplementary Material 2) and following the Generating Sequencing Depth and Coverage Map for Organelle Genomes protocol [9] (Supplementary Material 3).

All available and verified Squalomorphii mitogenomes ($n = 43$) were downloaded from GenBank (accession date: 08/02/2023). Furthermore, four mitogenomes representing the shark orders Heterodontiformes, Orectolobiformes, Lamniformes, and Carcharhiniformes were also downloaded from GenBank as outgroup taxa. The 13 protein-coding genes of the downloaded mitogenomes were aligned with MAFFT (version 7.505) [10]. The resulting alignment was trimmed and concatenated with trimAL (version 1.2) [11] and FasConCAT-G (version 1.05.1) [12], respectively, resulting in a final alignment of 22 866 bp. The identification of partition-scheme, their best-fit nucleotide substitution models and Maximum Likelihood phylogenetic inference were conducted on IQ-TREE (version 1.6.12) [13,14].

Limitations

Not applicable.

Ethics Statement

The authors have read and followed the ethical requirements for publication in Data in Brief. The authors confirm the current work does not involve human subjects, animal experiments, or any data collected from social media platforms. CIIMAR ethical committee and CIIMAR Managing Animal Welfare Body (ORBEA), according to the European Union Directive 2010/63/EU, approved the present work.

Data Availability

Whole genome sequencing of Oxynotus paradoxus (Original data) (ncbi)
Oxynotus paradoxus isolate 4.93 mitochondrion, complete genome (Original data) (GenBank)
Oxynotus paradoxus voucher 4.93 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial (Original data) (GenBank).

CRediT Author Statement

Ana Matos: Methodology, Investigation, Software, Writing – original draft, Writing – review & editing; **André Gomes-dos-Santos:** Methodology, Investigation, Software, Writing – original draft, Writing – review & editing; **Sofia Graça Aranha:** Methodology, Writing – original draft, Writing – review & editing; **Ester Dias:** Methodology, Writing – original draft, Writing – review & editing; **Ana Veríssimo:** Methodology, Writing – original draft, Writing – review & editing; **Alexandra Teodósio:** Methodology, Writing – original draft, Writing – review & editing; **Ivone Figueiredo:** Methodology, Writing – original draft, Writing – review & editing; **L. Filipe C. Castro:** Conceptualization, Supervision, Writing – original draft, Writing – review & editing; **Elsa Froufe:** Conceptualization, Supervision, Writing – original draft, Writing – review & editing.

Acknowledgements

We thank the vessel owner, crew, and skipper for allowing us to join their daily activities and collect data; to the company OLSPS Marine and International Lda. for developing and providing

the software Olrac DDL® to collect and store data onboard; to Tiago Marsili and Pedro da Rocha for assisting during the fieldwork; to the Sustainable Horizons SHEs a European Union's Horizon Europe project (No. 101071300).

This work is a result of the project ATLANTIDA (ref. NORTE-01-0145-FEDER-000040), supported by the Norte Portugal Regional Operational Programme (NORTE 2020), under the PORTUGAL 2020 Partnership Agreement and through the European Regional Development Fund (ERDF). The project ATLANTIDA (NORTE-01-0145-FEDER-000040) also supported AGS with the grant 2023_033_BI_ATLANTIDA. This work was also funded by the Save our Seas Foundation (SOSF 501), the EEA Grants (PT-Innovation-0007), and supported by national funds through FCT projects - Foundation for Science and Technology within the scope of UIDB/04423/2020, UIDP/04423/2020, UIDB/04326/2020, UIDP/04326/2020 and LA/P/0101/2020 which also supported SGA (SFRH/BD/147493/2019) and EF (CEECINST/00027/2021/CP2789/CT0003).

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] S. Johri, N. Dunn, T.K. Chapple, D. Curnick, V. Savolainen, E.A. Dinsdale, B.A. Block, Mitochondrial genome of the Silvertip shark, Carcharhinus albimarginatus, from the British Indian Ocean Territory, Mitochondrial DNA Part B 5 (2020) 2085–2086, doi:10.1080/23802359.2020.1765210.
[2] J. Pearce, M.W. Fraser, A.M.M. Sequeira, P. Kaur, State of shark and ray genomics in an era of extinction, Front. Mar. Sci. 8 (2021) 1497, doi:10.3389/fmars.2021.744986.
[3] J. Kim, S.M. Jang, E. Choi, E. Jo, S.J. Lee, S.H. Kim, Y.M. Chi, J.H. Kim, H. Park, The complete mitochondrial genome of Eaton's skate, Bathyraja eatonii (Rajiformes, Arhynchobatidae), Mitochondrial DNA Part B 6 (2021) 91–92, doi:10.1080/23802359.2020.1847608.
[4] J. Sambrook, E.R. Fritsch, T. Maniatis, Molecular Cloning: A Laboratory Manual, Cold Harbor Spring Press, New York, 1989.
[5] O. Folmer, M. Black, W. Hoeh, R. Lutz, R. Vrijenhoek, DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates, Mol. Mar. Biol. Biotechnol. 3 (1994) 294–299 http://www.ncbi.nlm.nih.gov/pubmed/7881515.
[6] A.M. Bolger, M. Lohse, B. Usadel, Trimmomatic: a flexible trimmer for Illumina sequence data, Bioinformatics 30 (2014) 2114–2120, doi:10.1093/bioinformatics/btu170.
[7] G. Meng, Y. Li, C. Yang, S. Liu, MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization, Nucleic Acids Res. 47 (2019) e63, doi:10.1093/nar/gkz173.
[8] T. Carver, S.R. Harris, M. Berriman, J. Parkhill, J.A. McQuillan, Artemis: an integrated platform for visualization and analysis of high-throughput sequence-based experimental data, Bioinformatics 28 (2012) 464–469, doi:10.1093/bioinformatics/btr703.
[9] Y. Ni, J. Li, C. Zhang, C. Liu, Generating sequencing depth and coverage map for organelle genomes, APR 15 (2023) 2023, doi:10.17504/PROTOCOLS.IO.4R3L27JKXG1Y/V1.
[10] K. Katoh, D.M. Standley, MAFFT multiple sequence alignment software version 7: improvements in performance and usability, Mol. Biol. Evol. 30 (2013) 772–780, doi:10.1093/molbev/mst010.
[11] S. Capella-Gutiérrez, J.M. Silla-Martínez, T. Gabaldón, trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses, Bioinformatics 25 (2009) 1972–1973, doi:10.1093/bioinformatics/btp348.
[12] P. Kück, G.C. Longo, FASconCAT-G: extensive functions for multiple sequence alignment preparations concerning phylogenetic studies, Front. Zool. 11 (2014) 81, doi:10.1186/s12983-014-0081-x.
[13] L.-T. Nguyen, H.A. Schmidt, A. von Haeseler, B.Q. Minh, IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies, Mol. Biol. Evol. 32 (2015) 268–274, doi:10.1093/molbev/msu300.
[14] S. Kalyaanamoorthy, B.Q. Minh, T.K.F. Wong, A. von Haeseler, L.S. Jermiin, ModelFinder: fast model selection for accurate phylogenetic estimates, Nat. Meth. 14 (2017) 587–589, doi:10.1038/nmeth.4285.