**Complete mitogenome of the Oven’s halosaur, Halosaurus ovenii (Elopomorpha; Notacanthiformes)**

David Barros-García, Andrés Gomes-dos-Santos, André M. Machado, L. Filipe C. Castro, Alejandro de Carlos, Rafael Bañón, Isabel Bruno, Juan C. Arronte and Elsa Froufe

*Terminal de Cruzeiros de Leixões, CILMAR/CIMAR – Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Matosinhos, Portugal; Department of Biology, Faculty of Sciences, University of Porto, Porto, Portugal; Departamento de Bioquímica, Xenética e Imunoloxía, Facultade de Bioloxia, Universidade de Vigo, Vigo, Spain; Servizo de Planificación, Consellería do Mar, Xunta de Galicia, Santiago de Compostela, Spain; Grupo de Estudos do Medio Maríno (GEMM), Ribeira, Spain; Instituto Español de Oceanografía, Centro Oceanográfico de Vigo, Vigo, Spain; Instituto Español de Oceanografía, Centro Oceanográfico de Cádiz, Cádiz, Spain*

**ABSTRACT**

The difficulties involved in the study of deep-sea species imply the existence of a wide gap in knowledge of this ecosystem. Here, we have obtained the mitogenome of the Oven’s halosaur, *Halosaurus ovenii*, for the first time using low coverage Illuma Paired-end (PE) sequencing. This species belongs to order Notacanthiformes, a poorly studied group of deep-sea fishes. Moreover, given their evolutionary placement, they are critical to investigate the early diversification of the Teleostei. The assembled mitogenome displays the expected gene arrangement for vertebrate mtDNA. Phylogenetic analyses combining all the available mitogenomes of the Order Notacanthiformes were performed. The evolutionary relationships among *H. ovenii* and the rest of the Halosauridae family were confirmed. This mitogenome provides a valuable baseline for future research of *H. ovenii*.

The Oven’s halosaur, *Halosaurus ovenii* Johnson, 1864, is a deep-sea marine fish species belonging to the family Halosauridae, a group of eel-shaped fish found worldwide but mainly distributed in the Atlantic Ocean (Bañón et al. 2016). Only three mitogenomes of halosaurid species have been published and none from the genus *Halosaurus*. In general, the economic costs related to deep-sea research limits the amount of knowledge related to these species. The mitogenome submitted in this manuscript is the first step toward a better understanding of the biology of this species.

The specimen was captured north of the Iberian Peninsula (42.2625° N; 9.4869° W) at 810.5 meters of depth during the DEMERSALES campaign 2019 and several tissue samples were stored in ethanol. Morphological identification was performed on board and later confirmed by means of COI mtDNA barcoding fragment. The specimen is stored at the Interdisciplinary Centre of Marine and Environmental Research (specimen code NOTAC0001).

Whole genomic DNA was obtained from a small portion of the fin tissue using Qiagen MagAttract HMW DNA extraction kit. Library preparation (i.e. 350 bp insert) and sequencing (i.e. 150 bp Paired-end reads) were performed by Novogene Europe. Mitogenome assembly and annotation were obtained using SPAdes v3.12.0 (Bankevich et al. 2012) and MitoZ v2.2.3 (Meng et al., 2019), respectively. All available mitogenomes of notacanthiform fish as well as six outgroup taxa were retrieved from GenBank (accessed in September 2020, Figure 1). Gene alignments of the 13 protein-coding genes (PCG) were produced using GUIDANCE2 (Sela et al. 2015) with MAFFT v 7.304 (Katoh and Standley 2013) and subsequently concatenated using FASconCAT-G (https://github.com/PatrickKueck/FASconCAT-G), resulting in a final alignment with 11,416 nucleotides. PartitionFinder2 (Lanfear et al. 2016) was used to estimate the best partition schemes and molecular evolutionary models for the phylogenetic Bayesian inference with MrBayes v3.2.6 (Ronquist et al. 2012), where two independent runs with four chains each were performed (10⁷ generations, sampling one tree for every 1000 generations). Partition schemes and molecular evolutionary models for Maximum Likelihood phylogenetic inference were obtained using IQ-TREE v1.6.12 (Nguyen et al. 2015; Kalyaanamothry et al. 2017). The *H. ovenii* complete mitogenome has been deposited in GenBank under the accession number MW077726. The total length of the assembled mitogenome is 16,647 bp, within the length observed on other species of the family, i.e., *Halosaurus macrochir* 16,655 bp; *Aldrovandra affinis* 16,649 bp; and *Aldrovandra oleosa* 16,653 bp. Gene content and orientation are the same as the other Halosauridae mitogenomes available: 13 PCGs, 22 transfer RNA (tm), 2 ribosomal RNA (rm) genes. NAD6 and 8 tRNAs are encoded on the light strand while the remaining genes are encoded on the heavy strand. The consensus tree...
obtained showed the relationships among the notacanthiform species (Figure 1). The mitogenome of *H. ovenii* is closely related to other Halosauridae species and located before the common ancestor of the Notacanthide family. The values of pairwise p-distances among *H. ovenii* and the other Halosauridae vary from a minimum of 13.7% with *H. macrochir* and a maximum of 14.2% with *A. oleosar*. Overall, this information will be useful to a better understanding of the biology of deep-sea species.

**Disclosure statement**

The authors declare that there is no conflict of interest.

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**ORCID**

David Barros-García [ORCID: 0000-0002-5283-2605](http://orcid.org/0000-0002-5283-2605)

André Gomes-dos-Santos [ORCID: 0000-0001-9973-4861](http://orcid.org/0000-0001-9973-4861)

Elsa Froufe [ORCID: 0000-0003-0262-0791](http://orcid.org/0000-0003-0262-0791)

**Figure 1.** Consensus tree of 13 mitogenomes, including seven notacanthiform species, obtained with BI and ML. Node values indicate posterior probabilities and bootstrap supports, respectively, with values above 95% represented with asterisks (*). The new mitogenome of *Halosaurus ovenii* is highlighted in bold.

**Data availability statement**

The data produced in this study are available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov), reference number MW077726. Raw data can be made available from the corresponding author; Barros-Garcia D.

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