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MITOGENOME REPORT

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# The complete mitochondrial genome of Chilean Jack Mackerel, *Trachurus murphyi* Nichols, 1920 (Teleostei, Carangidae)

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**ABSTRACT**

The Chilean jack mackerel (*Trachurus murphyi,* Nichols, 1920) is a pelagic fish of high fishery interest, with a global capture of 828,358 mt in 2021. We report the complete mitochondrial genome of *T. murphyi* (Teleostei, Carangidae), collected in Bahia de Zapallar, Chile (32°33′02.59″ S, 71°27′55.38″ W). The size of the mitogenome is 16,561 bp (H-strand composition: 25.9% A, 16.7% C, 29.8% G, and 27.5% T). The mitogenome has the classic vertebrate gene content of 13 protein-coding, two rRNA, and 22 tRNA genes, as found in Carangidae and other Teleostei families. Phylogenetic analysis using mitochondrial genomes of 22 related species revealed that *T. murphyi* formed a well-supported monophyletic group with the other *Trachurus* species, being *T. simmetricus* its closest relative. Sequencing the mitochondrial genome from *T. murphyi* is the first step in developing traceability tools based on DNA analysis to enforce fishing quotas and trace the processed food and foodstuff containing Chilean jack mackerel following the objective of the South Pacific Regional Fisheries Management Organization (SPRFMO).

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## Introduction

The Chilean jack mackerel (*Trachurus murphyi,* Nichols, 1920) belongs to the Carangidae family (jacks and pompanos) comprised of 32 genera, one of which is *Trachurus* (Froese and Pauly 2024). This genus contains 14 species: *T. capensis*, *T. declives*, *T. delagoa*, *T. indicus*, *T. japonicus*, *T. lathami*, *T. longimanus*, *T. mediterraneus*, *T. murphyi*, *T. novaezelandiae*, *T. picturatus*, *T. symmetricus*, *T. trachurus*, and *T. trecae* (Froese and Pauly 2024). *Trachurus murphyi* is a pelagic fishery resource of high interest (FAO 2024). It is distributed in the Southeastern Pacific from Ecuador to Chile (FAO fishery area 87) and in the Southwestern Pacific, New Zealand, and Tasmania (FAO fishery area 81) (Ferrada Fuentes et al. 2023). Due to its history life traits and marine pelagic life, *T. murphyi* shows a single reproductive population in the South-eastern Pacific when it was analyzed with mtDNA (Cárdenas et al. 2009) and microsatellite markers (Cárdenas et al. 2009; Galleguillos et al. 2012; Canales-Aguirre et al. 2024). The maximum global fishery landing was 4,955,186 mt reached in 1995, nevertheless it decreased to 354,898 mt in 2013 (FAO 2024), probably due to overfishing. Nowadays, the global capture quota is regulated by the South Pacific Regional Fisheries Management Organization (SPRFMO), leading to a steady recovery of the species abundance. Global capture was 828,358 mt in 2021 (FAO 2024; SPRFMO 2022). *T. murphyi* is a very nutritious fish; it is a good source of proteins of high biological value, PUFAs (polyunsaturated fatty acid), vitamins, and minerals (Bastías et al. 2017). In Chile, 69.5% of this resource is intended for direct human consumption: refrigerated (0.7%), frozen (57.0%), canned (10.6%), and oil (13.2%). The other 30.5% is processed to produce fish meal (SERNAPESCA 2022).

The mitogenomes of Carangidae fishes are similar to that of the rest of the vertebrates. Their number and type of genes are highly conserved: 13 protein-coding, two rRNA, and 22 tRNA genes (Satoh et al. 2016). The order in which those genes are located is also preserved: F,12S, V,16S, L1, ND1, I, Q, M, ND2, W, A, N, C, Y, COI, S1, D, COII, K, ATP8, ATP6, COIII, G, ND3, R, NAD4L, ND4, H, S2, L2, ND5, ND6, E, CYTb, T and P (Satoh et al. 2016). The total length of the Carangidae mitogenomes ranges between 16 and 17 Kbp.

We are developing traceability tools for *T. murphyi* using mitochondrial barcode genes to enforce fishing quotas, trace the processed derived product, and check the truthfulness of the labeling information. The first step in this process is to

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obtain the complete mitochondrial genome of Chilean Jack Mackerel, *Trachurus murphyi,* Nichols, 1920 (Teleostei, Carangidae).

## Materials and methods

One *Trachurus murphyi* specimen (Figure 1) was collected (21 February 2024) in the Zapallar Bay, Chile (32°33′02.59′′ S, 71°27′55.38′′ W). According to the manufacturer's protocol, total DNA was extracted from fin clips using the E.Z.N.A.® Tissue DNA Kit (Omega BIO-TEK). The library was prepared using the Illumina DNA Prep Kit (Illumina Inc.©) following the manufacturer's instructions. The next-generation sequencing was performed in an Illumina iSeq100 system (Illumina Inc.©) at the Food Quality Research Center facilities, Universidad de Chile. 4,061.984 paired end reads (2 × 150 bp) were obtained and processed in Geneious Prime 2024.0.3 (https://www.geneious.com). Trimmed reads with BBDuk v. 38.84 were assembled *de novo* with Geneious assembler obtaining the mitogenome contig. We edited the overlapping ends and obtained the circularized mitogenome. The trimmed reads were mapped again to check the assembly and generate the final version. Genes were annotated by manually adjusting *Trachurus symmetricus* annotations (NC082545.1) to the consensus sequence. Annotations were confirmed with the other three *Trachurus* species mitogenomes available in GenBank: *T. japonicus* (NC002813.1), *T. lathami* (OP057107.2), and *T. trachurus* (NC006818.1).

The *T. murphyi* mitochondrial genome was aligned with four other species of *Trachurus* and 18 representatives from genera of the Carangidae family as outgroups, obtained from GenBank, using the MAFFT v7.490 plugin with default settings (Katoh and Standley 2013). The maximum-likelihood phylogenetic reconstruction was obtained using the plugin PhyML 3.3.20180621 with the following settings: substitution model = GTR, bootstrap = 1000, the proportion of invariable sites = estimated, gamma distribution parameter = estimate, optimize = Topology/length/rate (Guindon et al. 2010).

## Results

The complete mitochondrial genome of *T. murphyi* was assembled with 5507 reads (mean coverage 35.1, min 5, max 79, supplemental Figure S1), yielding a circular sequence of 16,561 bp (GenBank accession no. PP533446). Gene composition and structure were like other fish mitogenomes and comprised 13 protein-coding genes, two ribosomal RNA units, 22 tRNA genes, and the control region (Figure 2). The overall base composition was 25.9% A, 16.7% C, 29.8% G, and 27.5% T. The tRNA genes showed lengths ranging from 67 to 75 bp. The 16S rRNA genes (1,719 bp) and 12S rRNA (955 bp) were located between $tRNA^{Val}$ and $tRNA^{Leu}$ and between $tRNA^{Phe}$ and $tRNA^{Val}$, respectively. The protein-coding genes started with ATG, except for COI, which started with GTG. The stop codons of the protein-coding genes were TAA (ND1, COI, ATP8, ATP6, ND4L, ND5, and ND6), T—(ND2, COII, ND3, ND4, and Cytb), TA– (COIII) and TAG (ATP8). The control region (861 bp) was located between $tRNA^{Pro}$ and $tRNA^{Phe}$

All analyzed *Trachurus* species form a well-defined clade with two branches, the first including *T. murphyi* and *T. symmetricus* and the second grouping the other three species (Figure 3). *T. murphyi* showed 115 bp of difference (0.7%) with *T. symmetricus*, while with other *Trachurus* species, the difference percentages ranged between 1.4% and 2%. The

**Figure 1.** Representative photograph of a specimen of Chilean jack mackerel, *Trachurus murphyi* (photo credit: Cristian Araneda).

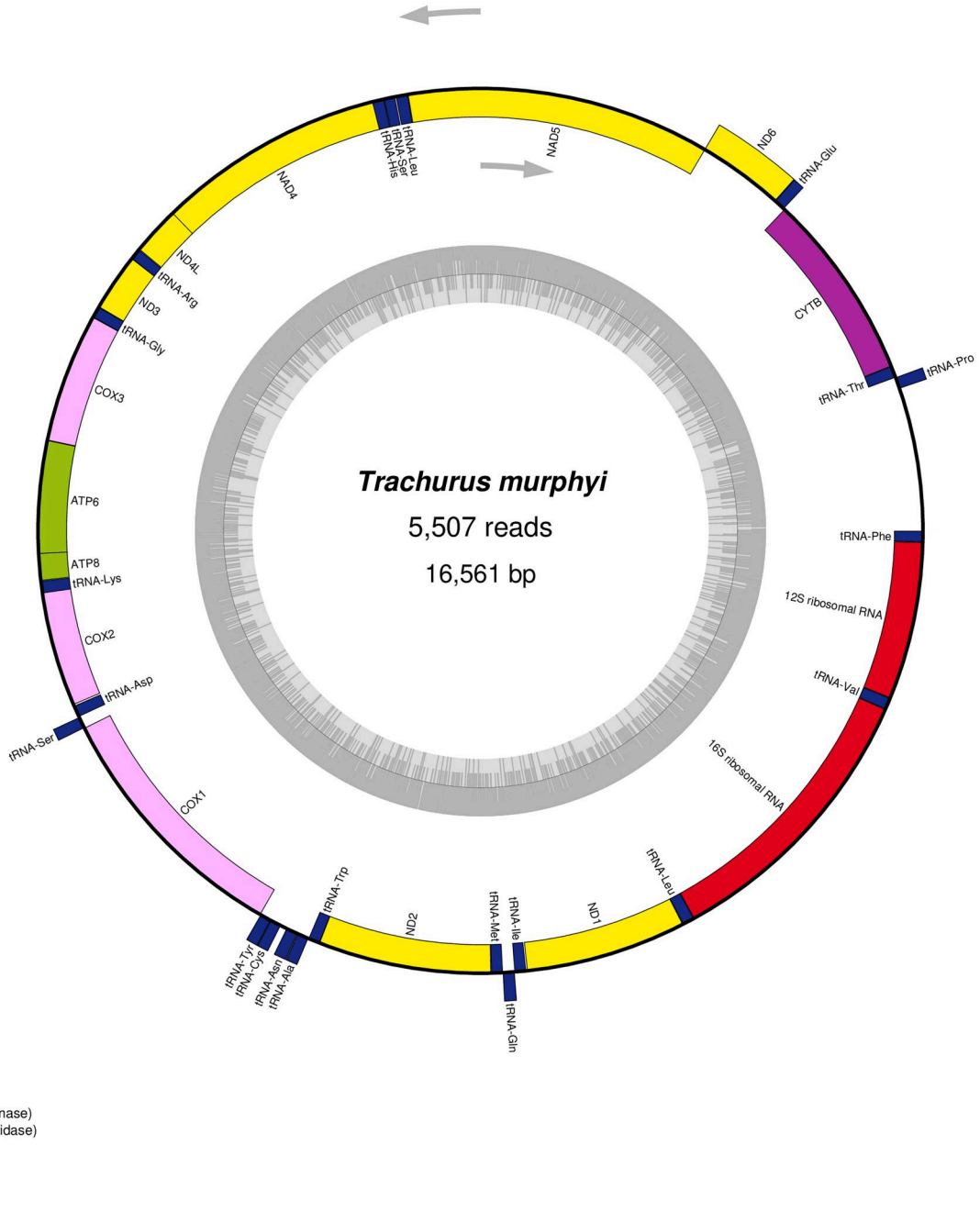


**Figure 2.** Mitochondrial genome map of *Trachurus murphyi*. Genes oriented in the reverse direction are indicated in the outermost concentric ring and genes in the forward orientation are in the second outermost ring. The innermost rings of the image represent %GC per every 5 bp of the mitogenome; longer lines indicate higher %GC.

differences with other genera within Carangidae were greater than 10%.

## Discussion and conclusion

The arrangement and number of genes in the mitochondrial genome of *T. murphyi* was like that of most other fish, as does the use of ATG as a start codon for most protein-coding genes (Satoh et al. 2016). The stop codons of most of the protein-coding genes also correspond to the majority of those found in fish, except for ND6 where the codon is TAA and not TAG (Satoh et al. 2016). The number of bases of the protein-coding genes was also within the most frequent ranges found in fish, except for ND3 and COII, which were longer (351 and 699 bp, respectively) (Satoh et al. 2016).

The phylogenetic analysis using the complete mitochondrial genome agrees with the analysis carried out with the control region and *cytochrome oxidase b* (Cárdenas et al. 2005; Tianfeng and Shigui 2011), as well as with the phylogenetic analysis carried out with the meristic characters (Shaboneyev 1981). We obtained the highest bootstrap support between *T. murphyi* and *T. symmetricus*; this clade also shows a 100% bootstrap value that separates it from the rest of the *Trachurus* species (Figure 3). Our results lend further evidence that *T. murphyi* is a sibling species of *T. symmetricus*

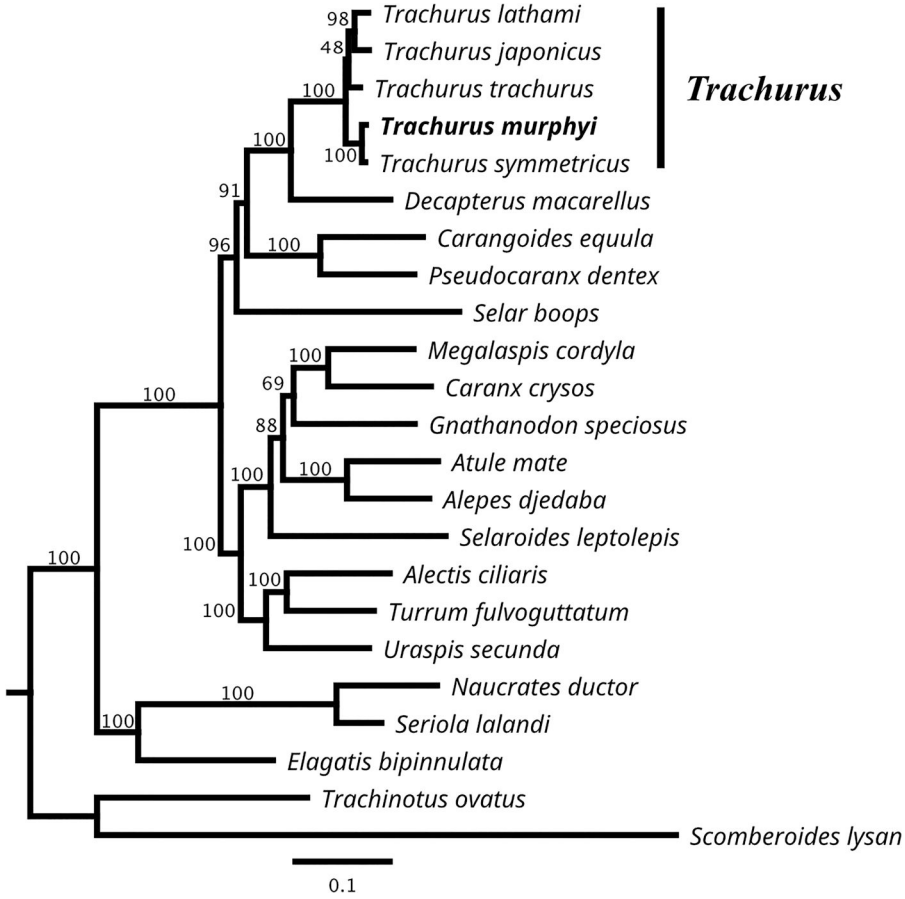


**Figure 3.** Maximum-likelihood phylogenetic reconstruction based on the complete mitochondrial genome (substitution model = GTR, bootstrap = 1000, proportion of invariable sites = estimated, gamma distribution parameter = estimate, optimize = Topology/lenght/rate). The complete mitogenome from five representatives of other *Trachurus* species were used: *T. murphy* (PP533446, this study), *T. lathami* (OP057107.2, unpublished), *T. japonicus* (NC002813.1, Mabuchi et al. 2007), *T. trachurus* (NC006818.1, Takashima et al. 2006), *T. symmetricus* (NC082545.1, unpublished). Representatives from other Carangidae genera were used as outgroups: *Decapterus macarellus* (NC026718.1, Zou et al. 2016), *Carangoides equula* (NC025644.1, Zou and Li 2015), *Pseudocaranx dentex* (NC058961.1, Li et al. 2021), *Selar boops* (NC060760.1, unpublished), *Megalapsis cordyla* (NC025565.1, Li et al. 2016), *Caranx crysos* (NC057648.1, unpublished), *Gnathanodon speciosus* (NC054367.1, unpublished), *Atule mate* (NC026222.1, Li et al. 2016b), *Alepes djedaba* (NC037049.1, unpublished), *Selaroides leptolepis* (NC029184, unpublished), *Alectis ciliaris* (NC025566.1, Li et al. 2016), *Turrum fulvoguttatum* (NC082849.1, unpublished), *Uraspis secunda* (NC029488.1, -(Ma et al. 2017), *Naucrates ductor* (NC083043.1, unpublished), *Seriola lalandi* (NC016869.1, Iguchi et al. 2012), *Elagatis bipinnulata*-NC029880.1, -(Ma et al. 2017), *Trachinotus ovatus* (NC022707.1, Xie et al. 2015), *Scomberoides lysan* (NC063497.1, unpublished).

(Shaboneyev 1981; Cárdenas et al. 2005; Tianfeng and Shigui 2011). Both species and *T. pictoratus* form a mackerel group that is morphologically characterized by having low body depth, many scutes, and inhabiting areas beyond the continental shelf (Shaboneyev 1981). The five *Trachurus* species form a monophyletic group separated from its closest genus, *Decapterus*, with 100% bootstrap support (Figure 3). Sequencing the complete mitogenome of *T. murphyi* also represents a first step for developing traceability tools investigating the authenticity of food products containing Chilean Jack mackerel (e.g. Canned food and fishmeal).

In summary, *T. murphyi* mitochondrial genome has the classical characteristics of one belonging to fish, and its phylogenetic reconstruction confirmed *T. symmetricus* as its closest relative.

## Author contributions

The research project was designed by MAL and CA. The specimen was collected by CA; DNA extraction and sequencing were performed by CA; annotation and phylogenetic analysis were completed by CMA. The paper was written by CMA with contributions from CA and MAL.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

## Ethical approval

All research followed protocols approved under ID 23697-CQyF-UCH by the Institutional Animal Care and Use Committee, University of Chile ('Comité Institucional de Cuidado y Uso de Animales (CICUA)'. This project was performed in adherence with ARRIVE guidelines (https://arrive-guidelines.org/arrive-guidelines).

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## Data availability statement

The mitochondrial genome sequence data that support this study's findings are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov under accession no. PP533446. The associated BioProject, SRA, and BioSample numbers are PRJNA1104261, SRS21115476, and SAMN41074106.

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