Phylogenetic position of the Atlantic Gnomefish, *Scombrops oculatus* (Teleostei: Scombropidae), within the genus *Scombrops*, inferred from the sequences of complete mitochondrial genome and cytochrome c oxidase subunit I genes

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**ABSTRACT**

We determined the complete mitochondrial genome of the Atlantic Gnomefish, *Scombrops oculatus* (Scombropidae). The total length of mitochondrial DNA (mtDNA) was 16,515 bp and included 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes, and one control region. The gene arrangement of *S. oculatus* was identical to those of three Japanese scombropid species and those of other teleosts. The phylogenetic analysis using the whole mtDNA, excluding the control region, indicates the Atlantic species is distinct from the Japanese clade, whereas that using cytochrome c oxidase subunit I gene showed the Atlantic species is most closely related to the African species.

The Atlantic Gnomefish, *Scombrops oculatus* (Poey 1860), is one of five species in *Scombrops*, which is the monotypic genus in the family Scombropidae (Itoi et al. 2018, 2020; Oyama et al. 2019). Although *S. oculatus* is speculated to be distributed worldwide in tropical regions based on their morphological similarities (Robins and Ray 1986), several reports indicate that this species is confined to the localities described below. The scombropid fishes are classified into *Scombrops* boops (Houttuyn 1782), *Scombrops gilberti* (Jordan & Snyder 1901), and *Scombrops* sp. in the northwestern Pacific Ocean (Yasuda et al. 1971; Mochizuki 1979, 1984; Shao 1987; Itoi et al. 2008, 2010, 2011, 2018, 2020), *Scombrops dubius* Gilchrist 1922 in the southwestern Indian Ocean (Heemstra 1986; Oyama et al. 2019), and *S. oculatus* in the western Atlantic Ocean, including the Caribbean Sea (Poey 1860). In these, no genetic information of the Atlantic Gnomefish, *S. oculatus*, has been available. Here, we sequenced the whole mitochondrial genome of *S. oculatus* and inferred its phylogenetic relationship among scombropid species.

The specimen of *S. oculatus* was collected on 23 July 1999 at 363°424 m depth, 43 nautical miles due east of Jupiter, Palm Beach Country, Florida, USA (26°56′N, 79°35′W), via hook-and-line, and stored in the Ichthyology Collection of the Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute (https://myfwc.com/research, Eric Post, Eric.Post@MyFWC.com) under catalog number FSBC 19124 (Ruiz-Carus et al. 2003). Total genomic DNA was extracted from a scale using QiAamp FFPE Tissue Kit (Qiagen), and libraries were prepared using Nextera XT DNA Library Prep Kit (Illumina). Next-generation sequencing (NGS) was performed using MiSeq (Illumina), and sequences were assembled by SPAdes v3.14.1 (Bankevich et al. 2012) after trimming raw reads using fastp v0.20.1 (Chen et al. 2018). Several parts that could not be determined by NGS were sequenced by the Sanger method with a 3130xl Genetic Analyzer (Applied Biosystems). Gene annotation, including ribosomal RNA (rRNA) estimation and transfer RNA (tRNA) prediction, was conducted using MitoFish (http://mitofish.aori.u-tokyo.ac.jp/) and Mitos WebServer (http://mitos.bioinf.uni-leipzig.de/index.py; Bernt et al. 2013), and the results of this annotation were manually verified using BLAST searches (http://blast.ncbi.nlm.nih.gov; Altschul et al. 1997). The phylogenetic tree was constructed via the maximum likelihood method using MEGA X ver. 10.2.2 (Kumar et al. 2018).

The total mitochondrial DNA (mtDNA) length of the Atlantic Gnomefish was 16,515 bp composed of 27.92% adenine, 29.59% cytosine, 26.03% thymine and 16.46% guanine. In this sequence, the heavy-strand contained 12 protein-coding genes, two rRNA genes, 14 tRNA genes and one control region, whereas the light-strand contained the remaining genes including one protein-coding gene and eight tRNA genes (DDBJ accession number LC603186). The arrangement of the mitochondrial genes was identical to that of three Japanese scombropids (Tsunashima, Itoi et al. 2016; Carus et al. 2003).
Figure 1. Phylogenetic relationship of the Atlantic Gnomefish *Scombrops oculatus* in related teleosts inferred from (a) whole mitochondrial genome excluding the control region and (b) partial sequence of *COI* gene. Tree was generated by maximum likelihood analysis under the nucleotide substitution models GTR + G + I for whole mitochondrial genome and HKY + I for *COI* gene. Numbers at branches denote the bootstrap percentages from 1000 replicates. Only bootstrap values exceeding 50% are presented. LC603186 in parentheses indicates the accession number deposited in the DDBJ/EMBL/GenBank databases in this study and accession numbers for reference sequences are shown in parentheses. The sequences of *Takifugu rubripes* and *Emmelichthys struhsakeri* are used as the outgroups for trees of whole mitochondrial genome and *COI* gene, respectively.
Bio-Sample numbers are PRJDB12050, DRA012467, and SAMD00394227, openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/.

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under the accession no. LC603186. The associated BioProject, SRA, and Bio-Sample numbers are PRJDB12050, DRA012467, and SAMD00394227, respectively.

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