Complete mitochondrial genome and phylogenetic analysis of the copper shark *Carcharhinus brachyurus* (Günther, 1870)

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**ABSTRACT**

Copper shark (*Carcharhinus brachyurus* Günther, 1870) is one of the most widely distributed but least known species in the family Carcharhinidae. Herein, we report the first complete mitogenome of *C. brachyurus*. The overall structure of the 16,704 bp *C. brachyurus* mitogenome was similar to that of other *Carcharhinus* species and showed the highest average nucleotide identity (97.1%) with the spinner shark (*Carcharhinus brevipinna*). Multigene phylogeny using 13 protein-coding genes (PCGs) in the mitogenome resolved *C. brachyurus* clustered with other species within the genus; the overall tree topology was congruent with recent phylogenetic studies of this species. These results provide important information for conservation genetics and further evolutionary studies of sharks.

Genomic DNA was extracted using the DNeasy Blood & Tissue Kit (Qiagen Korea Ltd., Seoul, Korea) according to the manufacturer’s instructions and subjected to direct PCR-based sequencing. Fifteen primer pairs, designed from the mitogenome of a related species in the family Carcharhinidae, the spinner shark (*Carcharhinus brevipinna*, NC_027081.1), were used to amplify the *C. brachyurus* mitogenome. All PCR primers and amplification conditions are listed in [Supplementary Table 1](#supplementary). The obtained partial sequences of *C. brachyurus* were assembled using Geneious R11.1.5 (Kearse et al. 2012), and the final complete mitogenome was annotated as previously described (Kim et al. 2017).

The complete *C. brachyurus* mitogenome (MT995631) was 16,704 bp long, with a 61.7% A + T content. It consisted of a typical set of 37 genes (2 rRNAs, 22 tRNAs, and 13 protein-coding genes [PCGs]), and the overall structure was similar to the mitogenomes of other sharks in Carcharhinidae available in MitoFish ([http://mitofish.aori.u-tokyo.ac.jp/](http://mitofish.aori.u-tokyo.ac.jp/)). A putative D-loop (1061 bp, 66.4% A + T content) was located between *tRNA<sup>Pro</sup>* and *tRNA<sup>Phe</sup>* and the replication origin (35 bp) was located on the H-strand between *tRNA<sup>Asn</sup>* and *tRNA<sup>Ser</sup>* ([Supplementary Table 2](#supplementary)). The two rRNAs were 955 bp (12S rRNA) and 1676 bp (16S rRNA) long and separated by *tRNA<sup>Thr</sup>*. The size of the 22 tRNAs varied from 67 bp (*tRNA<sup>Ser</sup>* and *tRNA<sup>Cys</sup>* to 75 bp (*tRNA<sup>Arg</sup>*), with a total length of 1550 bp.

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Except for ND6, all PCGs were encoded on the H-strand of the genome. The 12 PCGs had the typical ATG initiation codon, whereas GTG was the initiation codon in COX1. Four types of stop codons were detected: TAA (ND1, COX1, ATP8, COX3, ND4L, and ND5), AGG (ND6), and the incomplete stop codons TA- (ATP6 and CYTB) and T- (ND2, COX2, ND3, and ND4) (Supplementary Table 2).

Orthologous average nucleotide identity (OrthoANI) values were analyzed with other related sharks in the family Carcharhinidae as previously described (Kim et al. 2017). The overall OrthoANI values between C. brachyurus and other sharks in the genus Carcharhinus were >93%, with the highest value (97.1%) obtained for spinner shark (C. brevipinna, KM244770); other genera in the family showed <92% identity (Supplementary Table 3). Thirty-three complete mitogenomes of other related species in Carcharhinidae were obtained from GenBank and used for multigene phylogenetic analysis. The concatenated sequences of the 13 PCGs were aligned as previously described (Kim et al. 2017), and the maximum likelihood tree was reconstructed using MEGAX version 10.0 (Kumar et al. 2018). In the resultant tree, copper shark was clustered with other Carcharhinus species (Figure 1). Our tree topology was congruent with previous phylogenetic analyses based on nuclear or mitochondrial genes, which clustered blue shark (Prionace glauca) and whitetip reef shark (Triaenodon obesus) with other sharks in the genus Carcharhinus (Dosay-Akbulut 2008; Li et al. 2016), indicating that taxonomic assignment of the two species warrants further reevaluation. The mitogenome and associated genomic data of C. brachyurus provide important insights into biodiversity and address phylogenetic relationships within the genus Carcharhinus.
Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The data that support the findings of this study are openly available in the NCBI GenBank database at https://www.ncbi.nlm.nih.gov, reference number MT995631.

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