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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Pigeye Shark *Carcharhinus amboinensis* (Carcharhiniformes: Carcharhinidae)

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Abstract

In this manuscript we describe the first complete mitochondrial sequence for the Data Deficient Pigeye Shark *Carcharhinus amboinensis*. The mitogenome is 16,704 bp long and consists of 1 control region, 2 rRNA genes, 22 tRNA genes and 13 protein-coding genes with an overall base composition of 31.6% A, 24.9% C, 13.1% G and 30.4% T. The gene arrangement pattern and transcriptional direction were typical for a vertebrate species. The tRNA-*Ser2* lacks the dihydrouridine arm and forms a simple loop, therefore it cannot be folded into the typical cloverleaf secondary structures like other tRNAs.

Keywords

Carcharhinus amboinensis, genome, mitochondrion

History

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The Pigeye Shark *Carcharhinus amboinensis* is a wide-ranging medium-sized whaler shark (family Carcharhinidae) of tropical and subtropical waters (Last & Stevens, 2009). Its distribution is patchy and its occurrence in several geographic areas requires resolution, partially due to confusion with the morphologically similar Bull Shark *C. leucas* (Cliff, 2009; Last & Stevens, 2009). Globally, the absence of information on population status has resulted in a Data Deficient listing on the IUCN Red List of Threatened Species (Cliff, 2009). Here we provide the whole mitogenome of *C. amboinensis*.

One specimen of *C. amboinensis* was collected from the mouth of the South Alligator River, Kakadu National Park, Northern Territory, Australia, under Kakadu Research Permit RK805.The species was morphologically identified using keys in Last & Stevens (2009). The specimen was caught using a baited line and a biopsy was taken from the caudal peduncle using a muscle punch. The sample was immediately frozen in liquid nitrogen at −196 °C before the fish was released. Connective tissue from the lower dermal layer was sectioned from the biopsy and analysed. The experimental protocol and data analysis methods were followed according to Chen et al. (2013).

The complete mitochondrial genome of *C. amboinensis* was found to be 16,704 bp in length, and consists of 13 protein-coding genes, 22 tRNA genes, two rRNA genes and 1 control region (GenBank accession No. KM921745; Figure 1). The gene arrangement and transcriptional direction in the *C. amboinensis* mitogenome are identical to most vertebrates. The overall base composition of the mitogenome in *C. amboinensis* is 31.6% A, 24.9% C, 13.1% G and 30.4% T. A total of 32 bp short overlaps have been found at 9 gene junctions, from 1 to 10 bp. In addition, 22 noncoding nucleotides were observed in 11 unassigned intergenic spacers, from 1 to 7 bp. Except for the *COI* gene initiated by the GTG codon, the remaining 12 protein-coding genes started with the ATG codon. The *ND6* gene was terminated by the AGG codon; the *ND2*, *ND3* and *Cyt b* genes were terminated by the TAG codon; the remaining 9 genes used TAA (*ND1*, *COI*, *ATP8*, *ATP6*, *COIII*, *ND4L* and *ND5*) or incomplete T (*ND4* and *COII*) as the stop codon. The 12S and 16S rRNA genes are 956 and 1671 bp in length, respectively, separated by the tRNA-*Val* gene. The 22 tRNA genes ranged from 67 bp (tRNA-*Cys* and tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*) in length. The tRNA-*Ser2* lacks the dihydrouridine arm and forms a simple loop, therefore it cannot be folded into the typical cloverleaf secondary structures like other tRNAs. A 38 bp noncoding sequence was identified as the origin of L-strand replication (OL) between tRNA-*Asn* and tRNA-*Cys*. It could form a hairpin structure (13 bp pairs stem and 12 bp loop) to initiate the replication of L-strand. The control region is 1,067 bp in length, located between tRNA-Pro and tRNA-Phe. It is rich in AT (63.1%) and poor in G (14.1%). No tandem repeat motifs were found in the control region.

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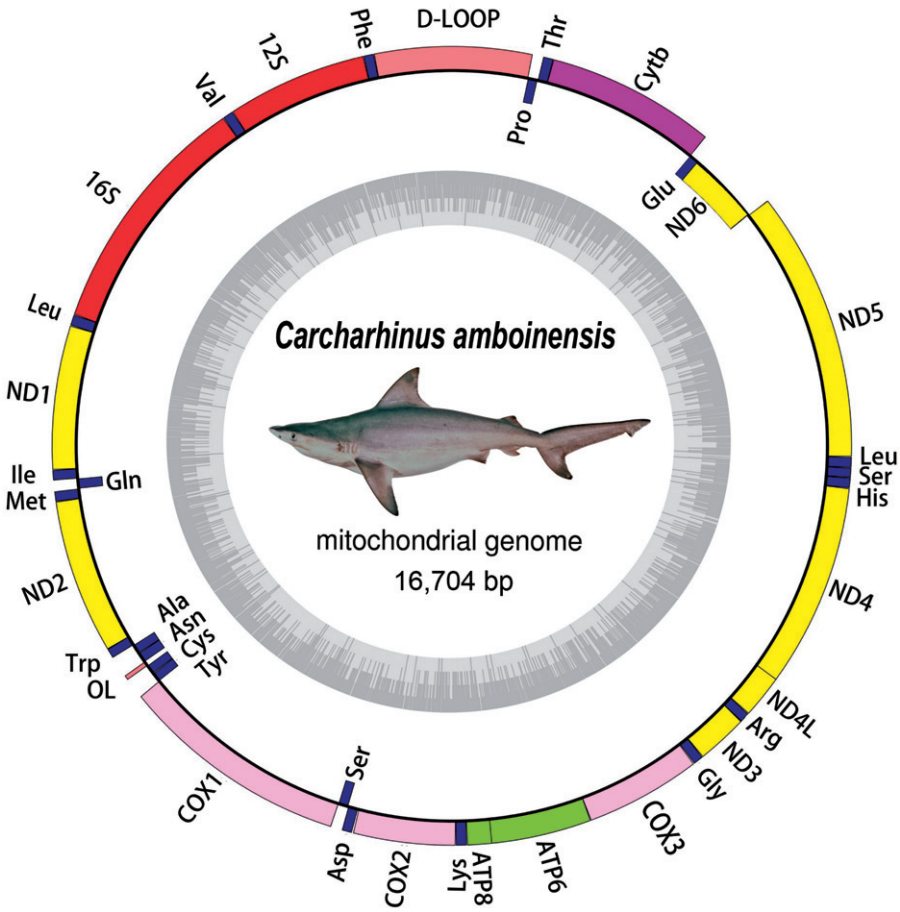

Figure 1. Mitogenomic map of *Carcharhinus amboinensis.* Photo credit: Australian National Fish Collection, CSIRO.

Declaration of interest

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