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MITOGENOME ANNOUNCEMENT

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

Pierre Feutry¹, Sharon L. Every¹,², Peter M. Kyne¹, Renjie Sun³, and Xiao Chen³

¹Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, Australia, ²North Australia Marine Research Alliance, Arafura-Timor Sea Research Facility, Brinkin, Australia, and ³Guangxi Key Lab for Mangrove Conservation and Utilization, Guangxi Mangrove Research Center, Guangxi Academy of Sciences, Beihai, PR China

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.

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, ATP6, COII, 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-Leu) 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.
Declaration of interest

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