

Mitochondrial DNA

The Journal of DNA Mapping, Sequencing, and Analysis

ISSN: 1940-1736 (Print) 1940-1744 (Online) Journal homepage: <http://www.tandfonline.com/loi/imdn20>

Complete mitogenome of the Graceful Shark *Carcharhinus amblyrhynchoides* (Carcharhiniformes: Carcharhinidae)

Pierre Feutry, Richard D. Pillans, Peter M. Kyne & Xiao Chen

To cite this article: Pierre Feutry, Richard D. Pillans, Peter M. Kyne & Xiao Chen (2016) Complete mitogenome of the Graceful Shark *Carcharhinus amblyrhynchoides* (Carcharhiniformes: Carcharhinidae), *Mitochondrial DNA*, 27:1, 314-315, DOI: 10.3109/19401736.2014.892094

To link to this article: <http://dx.doi.org/10.3109/19401736.2014.892094>



Published online: 11 Mar 2014.



Submit your article to this journal [↗](#)



Article views: 21



View related articles [↗](#)



View Crossmark data [↗](#)



Citing articles: 1 View citing articles [↗](#)

Full Terms & Conditions of access and use can be found at
<http://www.tandfonline.com/action/journalInformation?journalCode=imdn20>

MITOGENOME ANNOUNCEMENT

Complete mitogenome of the Graceful Shark *Carcharhinus amblyrhynchoides* (Carcharhiniformes: Carcharhinidae)Pierre Feutry¹, Richard D. Pillans², Peter M. Kyne¹, and Xiao Chen³¹Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, Northern Territory 0909, Australia, ²CSIRO Wealth from Oceans Flagship, 41 Boggo Road, Dutton Park, Queensland, 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 Near Threatened Graceful Shark *Carcharhinus amblyrhynchoides*. It is 16,705 bp in length, consists of two rRNA genes, 22 tRNA genes, 13 protein-coding genes and one control region with the typical gene arrangement pattern and translate orientation in vertebrates. The overall base composition is 31.4% A, 25.1% C, 13.2% G and 30.3% T. The shortest tRNA-*Ser2* cannot fold into a clover-leaf secondary structure due to the lack of the dihydrouridine arm.

Keywords

Carcharhinus amblyrhynchoides, genome, mitochondrion

History

Received 20 January 2014
Accepted 25 January 2014
Published online 11 March 2014

The Graceful Shark *Carcharhinus amblyrhynchoides* is a medium-sized shark of the family Carcharhinidae (whaler sharks). This species mostly inhabits open waters from close inshore to a depth of at least 50 m (Last & Stevens, 2009). It is patchily distributed in the tropical Indo-West Pacific, from the Arabian Sea to northern Australia and New Guinea (Last & Stevens, 2009), although the species' distribution may be more continuous through southern Asia than presently known (Simpfendorfer, 2009). This species is of relatively low abundance, except in estuaries and coastal environments of tropical northern Australia where it is common (unpublished data, RD Pillans). *Carcharhinus amblyrhynchoides* is listed as Near Threatened on the IUCN Red List of Threatened Species; there is currently no evidence it faces a high risk of extinction (Simpfendorfer, 2009). In this study we provide the first complete mitogenomic sequence for *C. amblyrhynchoides*.

A tissue sample (fin clip) was collected from a specimen of *C. amblyrhynchoides* captured and released in January 2012 in the estuary of the South Alligator River, Kakadu National Park, Northern Territory, Australia, under Kadadu Research Permit RK786. The experimental protocol and data analysis methods followed Chen et al. (2013).

The complete mitogenome of *C. amblyrhynchoides* is 16,705 bp in length (GenBank Accession No. KF956523). It consists of two rRNA genes, 22 tRNA genes, 13 protein-coding genes and one control region with the typical gene arrangement

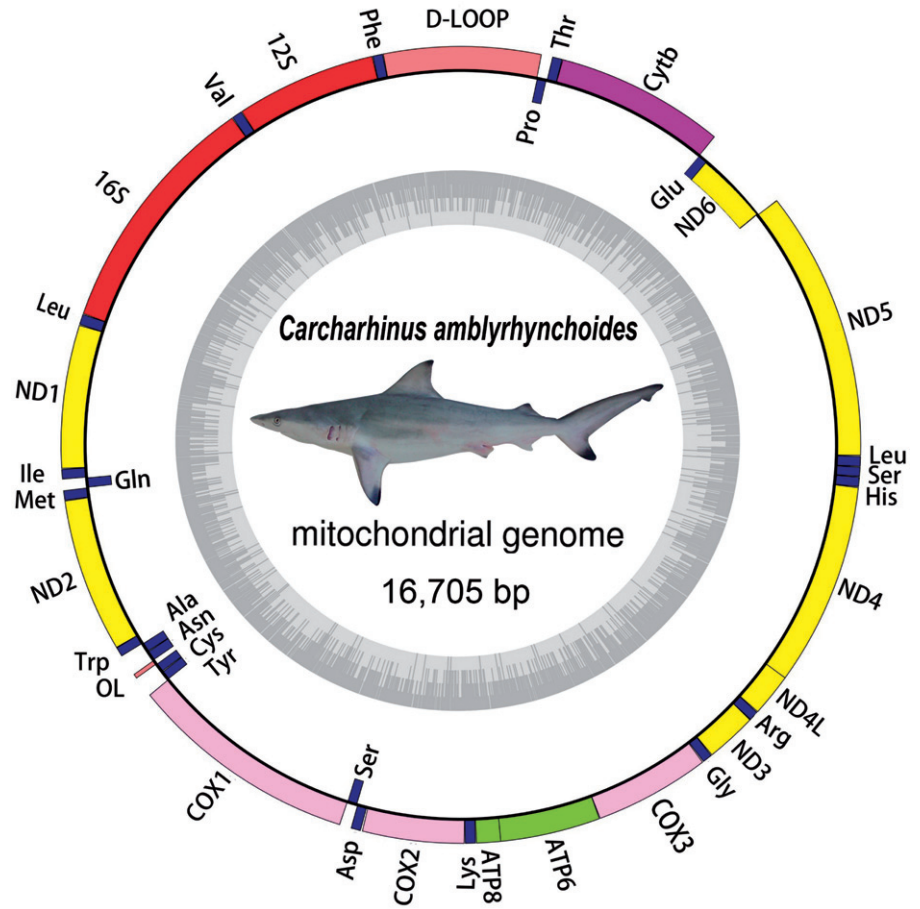
pattern and translate orientation in vertebrates (Figure 1). There were 21 bp short intergenic spacers located in 10 gene junctions with length ranging from 1 to 7 bp, and a total of 29 bp overlaps located in 8 gene junctions ranging from 1 to 10 bp. The overall base composition is 31.4% A, 25.1% C, 13.2% G and 30.3% T.

The *12S* and *16S* rRNA genes are 956 and 1668 bp in length, respectively, separated by the tRNA-*Val* gene. Except for the *COI* gene using GTG as the initiation codon, the remaining protein-coding genes started with the ATG codon. The *ND6* gene is terminated by the AGG codon, the remaining protein-coding genes stopped with the typical TAG, TAA or incomplete T codon.

All tRNA genes intersperse along the mitochondrial genome, ranging from 67 bp (tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*) and formed three conserved tRNA clusters (IQM, WANCY, and HSL). Among them, 21 tRNA genes were predicted to fold into the typical clover-leaf secondary structures, only the shortest tRNA-*Ser2* cannot fold into a clover-leaf secondary structure due to the lack of the dihydrouridine arm. The origin of L-strand replication (OL) was identified between tRNA-*Asn* and tRNA-*Cys* genes within the WANCY cluster.

The 1067 bp control region was located between the tRNA-*Pro* and tRNA-*Phe* genes with considerable polyA and polyT, which is the main reason causing the high A + T content in the control region. The conserved sequence blocks (CSB-1~3) were found in the control region.

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



Declaration of interest

This study was supported by the Marine Biodiversity Hub, a collaborative partnership supported through funding from the Australian Government's National Environmental Research Program (NERP), and the National Natural Sciences Foundation of China (41006080). Researcher PF was partly supported by the North Australia Marine Research Alliance (NAMRA). Researcher PMK was partly supported by the NERP Northern Australia Hub. The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

References

- Chen X, Ai W, Ye L, Wang X, Lin Yang S. (2013). The complete mitochondrial genome of the grey bamboo shark (*Chiloscyllium griseum*) (Orectolobiformes: Hemiscylliidae): genomic characterization and phylogenetic application. *Acta Oceanol Sinica* 32:59–65.
- Last PR, Stevens JD. (2009). *Sharks and Rays of Australia*. 2nd ed. Collingwood: CSIRO Publishing.
- Simpfendorfer C. (2009). *Carcharhinus amblyrhynchoides*. In: IUCN 2013. IUCN Red List of Threatened Species. Version 2013.2. Available at: <www.iucnredlist.org> (Accessed 11 December 2013).