

---

Charles Darwin University

## Complete mitochondrial genome of the Critically Endangered Smalltooth Sawfish *Pristis pectinata* (Rajiformes: Pristidae)

Chen, Xiao; Wiley, Tonya; Kyne, Peter M.; Feutry, Pierre

*Published in:*  
Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis

*DOI:*  
[10.3109/19401736.2015.1018208](https://doi.org/10.3109/19401736.2015.1018208)

Published: 01/01/2016

*Document Version*  
Peer reviewed version

[Link to publication](#)

### *Citation for published version (APA):*

Chen, X., Wiley, T., Kyne, P. M., & Feutry, P. (2016). Complete mitochondrial genome of the Critically Endangered Smalltooth Sawfish *Pristis pectinata* (Rajiformes: Pristidae). *Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis*, 27(5), 3331-3332. <https://doi.org/10.3109/19401736.2015.1018208>

### **General rights**

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

### **Take down policy**

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

**Complete mitochondrial genome of the Critically Endangered Smalltooth  
Sawfish *Pristis pectinata* (Rajiformes: Pristidae)**

Xiao Chen<sup>1</sup>, Tonya Wiley-Lescher<sup>2</sup>, Peter M. Kyne<sup>3</sup>, and Pierre Feutry<sup>3</sup>

<sup>1</sup>*Guangxi Key Lab for Mangrove Conservation and Utilization, Guangxi  
Mangrove Research Center, Beihai, PR China*

<sup>2</sup>*Haven Worth Consulting, 2925 Terra Ceia Bay Boulevard #2502, Palmetto,  
Florida, USA*

<sup>3</sup>*Research Institute for the Environment and Livelihoods, Charles Darwin  
University, Darwin, Northern Territory, Australia*

Correspondence: P. Feutry, Research Institute for the Environment and  
Livelihoods, Charles Darwin University, Darwin, Northern Territory 0909, Australia.

Tel: +61 3 6232 5095. Fax: +61 3 6232 5000. E-mail: Pierre.Feutry@csiro.au

**Abstract:**

In this study we describe the first complete mitochondrial sequence of the Critically Endangered Smalltooth Sawfish *Pristis pectinata*. It is 16,802 bp in length and contains all 37 genes found in typical vertebrate mitogenomes. The nucleotide composition of the coding strand is 31.1% A, 26.0% C, 13.1% G, and 28.9% T. There are 29 bp overlaps and 38 bp short intergenic spaces dispersed in the mitogenome. Two start codons (ATG and GTG) and two stop codons (TAG and TAA/T) were found in the protein-coding genes. The length of the 22 tRNA genes range from 67 bp (tRNA<sup>Ser2</sup>) to 75 (tRNA<sup>Leu1</sup>) bp. The control region is 1,102 bp in length with high A+T (62.0%) and poor G (13.5%) content.

**Keywords:** mitochondrial genome, *Pristis pectinata*, threatened species

The Smalltooth Sawfish *Pristis pectinata* once had a widespread distribution throughout coastal tropical and subtropical marine and brackish waters of the Atlantic Ocean (Carlson et al., 2013). Populations have been extirpated from large areas of its former range and it is now known to occur only in a restricted number of core areas of the western Atlantic. Contemporary records from the eastern Atlantic are very rare and often unconfirmed (Faria et al., 2013). It is listed as Critically Endangered on the IUCN Red List of Threatened Species (Carlson et al., 2013). In this study we provide the first complete mitogenomic sequence for *P. pectinata*.

A tissue sample (fin clip) was collected from a *P. pectinata* captured and released on 23 January 2008, in the Turner River, Everglades National Park, Florida, USA, under Endangered Species Act (ESA) permit #1352 and Everglades National Park (ENP) permit #EVER-2007-SCI-0039. The experimental protocol and data analysis methods follow Chen et al. (2013).

The complete nucleotide sequence of the L strand of the *P. pectinata* mitogenome was determined to be 16, 802 bp long (GenBank Accession No. KP400584). It contains all 37 genes found in typical vertebrate mitogenomes: 13 protein-coding genes, two ribosomal RNA (rRNA) genes and 22 transfer RNA (tRNA) genes. The nucleotide composition of the coding strand is 31.1% A, 26.0% C, 13.1% G and 28.9% T. There are 29 bp overlaps located in 7 gene junctions ranging from 1 to 10 bp (*ATP8-ATP6*), and 38 bp short intergenic spaces located in 13 gene junctions ranging from 1 to 8 bp (tRNA<sup>Thr</sup>-tRNA<sup>Pro</sup>).

Two start codons (ATG and GTG) and two stop codons (TAG and TAA/T) were found in the protein-coding genes in *P. pectinata*. The lengths of protein-coding genes of *P. pectinata* are almost identical to *P. clavata* (Feutry et al., 2013) except the *ATP6* gene: the *ATP6* gene of *P. pectinata* has 3 bp shorter than that of *P. clavata* by losing one CAA codon before the stop codon. Furthermore, the *ND6* gene used TAG as the stop codon in *P. pectinata* instead the AGG in *P. clavata*; the usage of the other start and stop codons in *P. pectinata* and *P. clavata* are identical.

The 12S and 16S rRNA genes are 965 and 1, 692 bp, respectively. The length of 22 tRNA genes range from 67 bp (tRNA<sup>Ser2</sup>) to 75 bp (tRNA<sup>Leu1</sup>). The nucleotide similarities of tRNA genes between *P. pectinata* and *P. clavata* range from 90% (tRNA<sup>Asp</sup>) to 98.65 (tRNA<sup>Lys</sup>). The tRNA<sup>Ser2</sup> can not be folded into a typical cloverleaf structure by lacking the dihydrouridine arm. The origin of L-strand replication (OL, 39 bp) was identified between the tRNA<sup>Asn</sup> and tRNA<sup>Cys</sup> genes. It overlaps with tRNA<sup>Cys</sup> by 5 bp and be folded to a hairpin structure (13 bp stem and 13 bp loop). In the control region, the termination-associated sequence (TAS) was found close to the tRNA<sup>Pro</sup> gene and formed a hairpin structure.

## **Acknowledgements**

The authors thank Kadu Pinheiro for access to the *P. pectinata* photograph.

## **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 by the National Marine Fisheries Service (NMFS) under solicitation# WC133F-07-RP-0152. 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.

Carlson J, Wiley T, Smith K. (2013). *Pristis pectinata*. In: IUCN 2013. IUCN Red List of Threatened Species. Version 2014.3. <[www.iucnredlist.org](http://www.iucnredlist.org)>. Downloaded on 02 December 2014.

Faria VV, McDavitt MT, Charvet P, Wiley TR, Simpfendorfer CA, Naylor GJ. (2013). Species delineation and global population structure of Critically Endangered sawfishes (Pristidae). *Zool J Linn Soc* 167:136–164.

Feutry P, Kyne PM, Grewe PM, Chen X, Liu M. (2013). Whole mitogenome of the Endangered dwarf sawfish *Pristis clavata* (Rajiformes: Pristidae). Mitochondr DNA, early online.

---

Figure 1. Mitogenomic map of *Pristis pectinata*. Photo credit: Kadu Pinheiro.

