Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Whole mitogenome of the Endangered dwarf sawfish *Pristis clavata* (Rajiformes: Pristidae)

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Abstract

In this study, we describe the first complete mitochondrial sequence for the Endangered dwarf sawfish *Pristis clavata*. The base composition of the 16,804 bp long mitogenome is 31.9% A, 26.5% C, 13.3% G and 28.3% T and the gene arrangement and transcriptional direction are the same as those found in most vertebrates. All protein-coding genes start with ATG except the *COI* gene, which starts with GTG. Stop codons include incomplete T, AGG and TAA; however, TAG is not found in the mitogenome of this euryhaline elasmobranch species.

Keywords

Mitochondrial genome, *Pristis clavata*, threatened species

History

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Sawfishes (family Pristidae) are one of the most threatened families of fishes with all five species listed as Endangered or Critically Endangered on the IUCN Red List of Threatened Species (IUCN, 2013). Globally, their populations have been severely depleted by gill net and trawl fisheries (Simpfendorfer, 2000). The dwarf sawfish *Pristis clavata* is listed as Endangered on the IUCN Red List (Kyne et al., 2013) and as Vulnerable on the Australian *Environment Protection and Biodiversity Conservation Act*. This species is now considered to be restricted to Australian estuarine and coastal areas, although it was once more widespread in the Indo-West Pacific Oceans (Kyne et al., 2013). Here, we provide the whole mitogenome of *P. clavata*, the first complete mitochondrial sequence of a sawfish (GenBank accessed 13 May 2013).

A tissue sample (fin clip) was collected from a specimen of *P. clavata* captured and released in the South Alligator River, Kakadu National Park, Northern Territory, Australia, under Kadadu Research Permit RK805. The experimental protocol and data analysis methods followed Chen et al. (2013). The complete mitogenome of *P. clavata* is 16,804 bp in length (GenBank accession No. KF381507) and contains 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes and a putative control region (D-loop). The gene arrangement and transcriptional direction are identical to those of most vertebrates (Figure 1).

In the mitogenome, there are 13 short intergenic spaces (SIS) and 6 overlaps ranging from 1 to 8 bp and from 1 to 10 bp, respectively. The cumulated length of the SIS is 36 bp, whereas the overlaps represent 25 bp in total.

The overall base composition of the mitogenome in *P. clavata* is 31.9% A, 26.5% C, 13.3% G and 28.3% T. Except for the *COI* gene using GTG as the initiation codon, the remaining protein-coding genes started with the typical ATG codon. Interestingly, the typical stop codon TAG is not found in the protein-coding genes; the *ND6* gene used special AGG stop codon and the others used TAA codon or incomplete T. The 12S and 16S rRNA genes are 964 bp and 1698 bp in length, respectively. The 22 tRNAs ranged from 67 bp (tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*) in length and formed three conserved clusters (IQM, WANCY, and HSL). One 34 bp inserted sequence was found between the tRNA-*Asn* and tRNA-*Cys* genes within the WANCY cluster. It was considered the origin of L-strand replication (OL) by folding a hair-pin structure (8 bp stem and 13 bp loop) to initiate the replication of L-strand. All tRNAs can be folded into the typical cloverleaf secondary structures except the tRNA-*Ser2*, which lost the dihydrouridine arm and was replaced by a simple loop. The control region of *P. clavata* is located between the tRNA-*Pro* and tRNA-*Phe* genes. It is 1103 bp in length with high A + T (62.6%) and poor G (14.1%) content.

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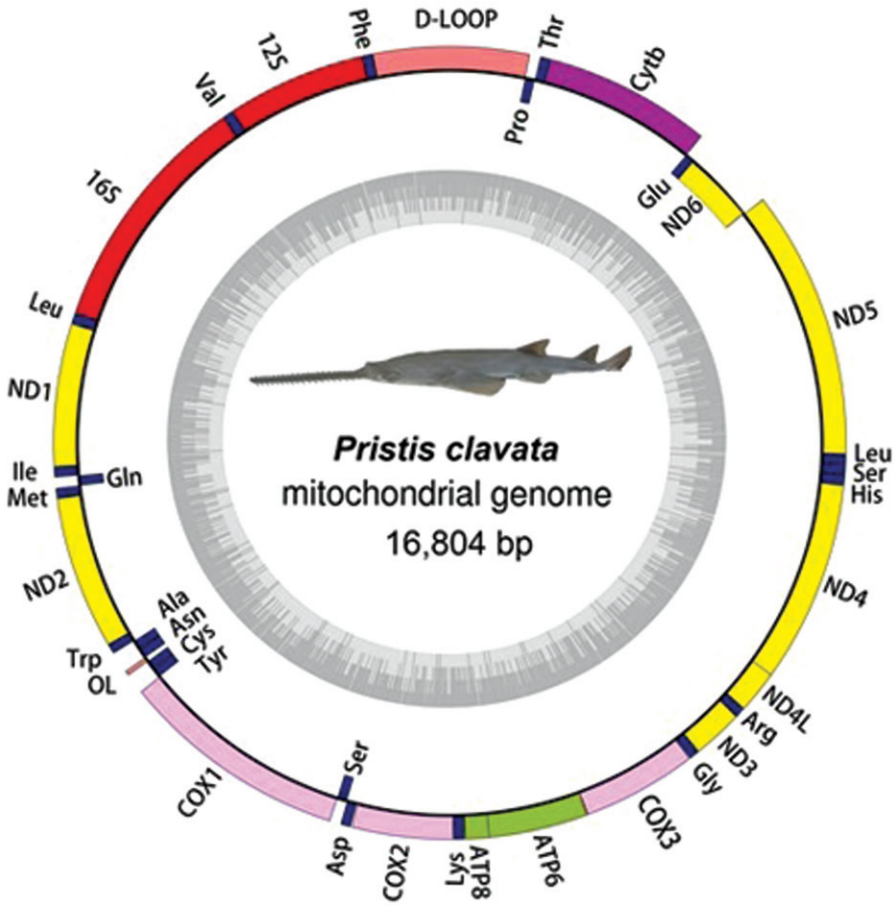

Figure 1. Mitogenomic map of *Pristis clavata*.

The termination-associated sequence (TAS) was found near the tRNA-*Pro* and the conserved sequence blocks (CSB1-3) were identified near the tRNA-*Phe*.

Declaration of interest

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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.

IUCN 2013. IUCN Red List of Threatened Species. Version 2013.1. Available at: http://www.iucnredlist.org (Accessed 15 July 2013).

Kyne PM, Rigby C, Simpfendorfer CA. (2013). *Pristis clavata*. In: IUCN 2013. IUCN Red List of Threatened Species. Version 2013.1. Available at: http://www.iucnredlist.org (Accessed 15 July 2013).

Simpfendorfer CA. (2000). Predicting population recovery rates for endangered western Atlantic sawfishes using demographic analysis. Env Biol Fish 58:371–7.