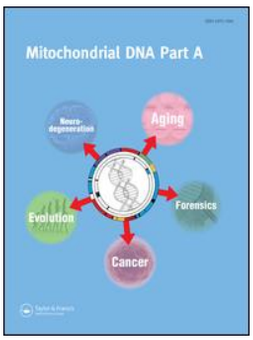

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Endangered Narrow Sawfish *Anoxypristis cuspidata* (Rajiformes: Pristidae)

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Abstract

In this study, we describe the first complete mitochondrial sequence for the Endangered Narrow Sawfish *Anoxypristis cuspidata*. It is 17,243 bp in length and contains 13 protein-coding genes, two rRNA genes, 22 tRNA genes, and a control region with the common vertebrate mitogenomic organization. A total of 30 bp overlaps and 28 bp short intergenic spaces are located between all genes. The overall base composition is 32.7% A, 25.7% C, 12.9% G, and 28.6% T. Two start codons (ATG and GTG) and two stop codons (TAG and TAA/T) were used in all protein-coding genes. The origin of L-strand replication (OL) sequence (38 bp) formed a hairpin structure (13 bp stem and 12 bp loop) to initiate the replication of L-strand.

Keywords

Anoxypristis cuspidata, mitochondrial genome, threatened species

History

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The Narrow Sawfish *Anoxypristis cuspidata* inhabits estuarine, inshore, and offshore areas of the Indo-West Pacific. This species has a widespread distribution from the Persian Gulf to northern Australia and Japan (D'Anastasi et al., 2013; Last & Stevens, 2009). It is the most productive of the sawfish species (family Pristidae) but like all sawfishes, has suffered population declines across its range (D'Anastasi et al., 2013). It is listed as Endangered on the IUCN Red List of Threatened Species (D'Anastasi et al., 2013). In this study, we provide the first complete mitogenomic sequence for *A. cuspidata*.

A tissue sample (fin clip) was collected from a specimen of *A. cuspidata* captured and released on 20 January 2012 in the South Alligator River estuary, Kakadu National Park, Northern Territory, Australia, under Kakadu Research Permit RK786. The experimental protocol and data analysis methods followed Chen et al. (2013) with slight modifications.

The complete sequence of the L-strand of the *A. cuspidata* mitogenome was determined to be 17,243 bp in length (GenBank accession number: KP233202). It contained 13 protein-coding genes, two rRNA genes, 22 tRNA genes, and a control region (Figure 1). The structural organization and direction of each feature in the genome conform to the common vertebrate mitogenomic model. The mitochondrial genes are overlapped by a total of 30 bp in seven different locations from 1 to 10 bp. In addition, a total of 28 bp short intergenic spaces were located in 13 gene junctions ranging from 1 to 4 bp. The overall base composition (32.7% A, 25.7% C, 12.9% G, and 28.6% T) reflected the observed vertebrate bias against G and rich A + T on the L-strand.

The 13 protein-coding genes of the *A. cuspidata* mitogenome were similar in length to those of its relatives *Pristis clavata* (Feutry et al., 2014) and *Rhinobatos schlegelii* (Chen et al., 2014). They all started with the ATG codon except for the *COI* gene, which used the GTG codon. Two stop codons (TAG and TAA/T) were found in all protein-coding genes. The *COII* and *ND4* genes terminated by the incomplete stop codon T, which would generate the entire TAA by polyadenylation of the corresponding mRNAs (Ojala et al., 1981). The 12S and 16S rRNA genes were 964 bp and 1689 bp, respectively, exhibited the typical location between tRNA-*Phe* and tRNA-*Leu1*, and separated by tRNA-*Val*. The 22 tRNA genes were interspersed between rRNA and protein-coding genes, and ranged from 67 bp (tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*). All tRNA genes could be folded into the typical cloverleaf secondary structures except for the tRNA-*Ser2*, which lost the dihydrouridine arm and was replaced by a simple loop. The origin of L-strand replication (OL) sequence (38 bp) was identified between tRNA-*Asn* and tRNA-*Cys* genes, which formed a hairpin

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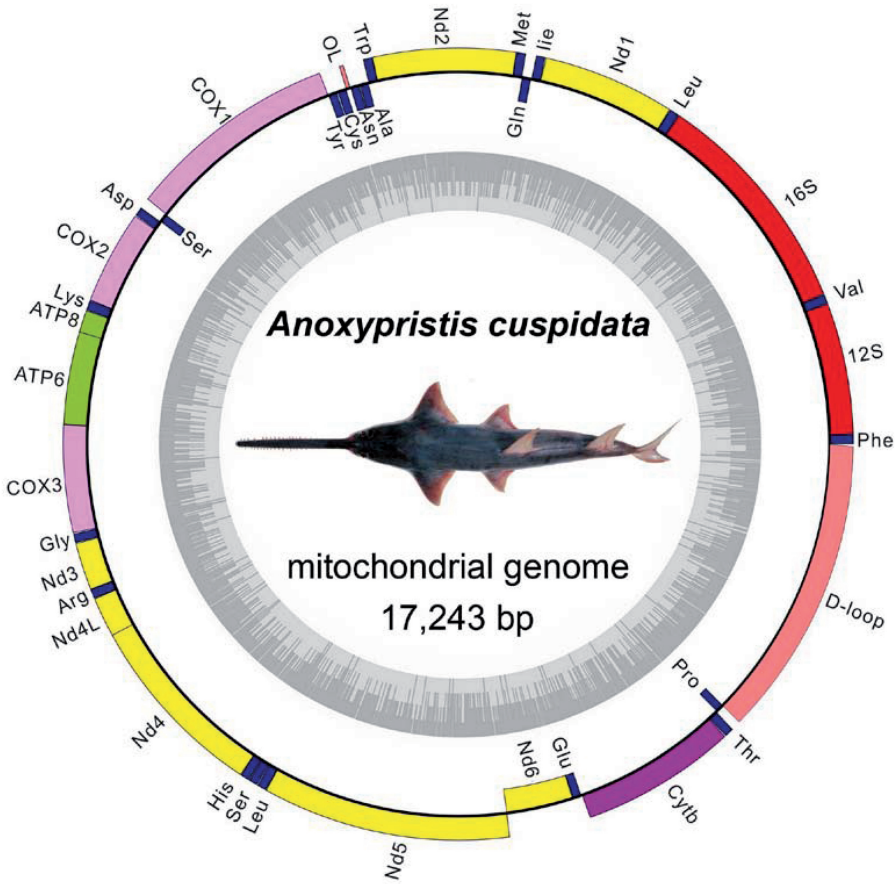

Figure 1. Mitogenomic map of *Anoxypristis cuspidata*. Photo credit: Australian National Fish Collection, CSIRO.

structure (13 bp stem and 12 bp loop) to initiate the replication of L-strand. The control region (1567 bp) was located between the tRNA-*Pro* and tRNA-*Phe* genes. It had the highest A + T (68.9%) and lowest G (10.7%) content in all features due to many poly A and poly T.

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Declaration of interest

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