Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

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

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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 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 ($tRNA^{Ser2}$) to 75 bp ($tRNA^{Leu1}$). The control region is 1102 bp in length with high A + T (62.0%) and poor G (13.5%) content.

Keywords

Mitochondrial genome, *Pristis pectinata*, threatened species

History

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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 (Figure 1). The nucleotide composition of the coding strand was 31.1% A, 26.0% C, 13.1% G and 28.9% T. There were 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 that ranged from 1 to 8 bp ($tRNA^{Thr}$-$tRNA^{Pro}$).

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* were 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 were 965 and 1692 bp, respectively. The length of 22 tRNA genes range from 67 bp ($tRNA^{Ser2}$) to 75 bp ($tRNA^{Leu1}$). The nucleotide sequence similarities of tRNA genes between *P. pectinata* and *P. clavata* range from 90% ($tRNA^{Asp}$) to 98.65 ($tRNA^{Lys}$). The $tRNA^{Ser2}$ 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 $tRNA^{Asn}$ and $tRNA^{Cys}$ genes. It overlaps with $tRNA^{Cys}$ by 5 bp and can 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 $tRNA^{Pro}$ gene and formed a hairpin structure.

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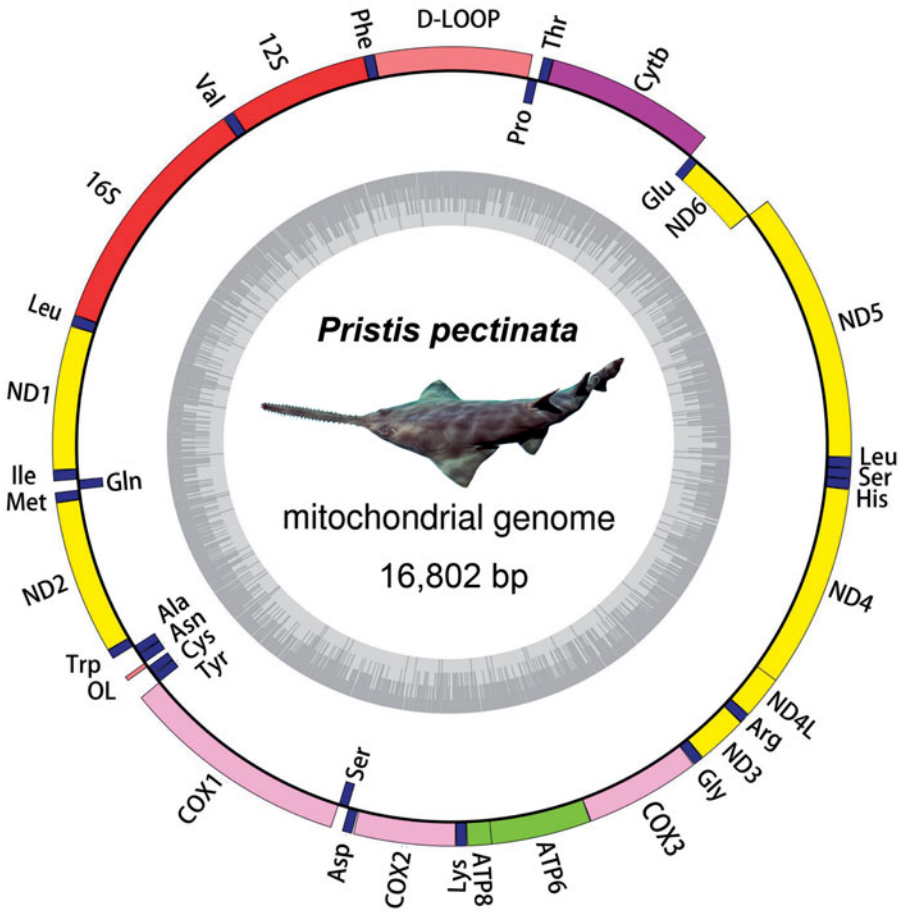

Figure 1. Mitogenomic map of *P. pectinata*. Photo credit: Kadu Pinheiro.

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Declaration of interest

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