

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the shortfin mako, *Isurus oxyrinchus* (Chondrichthyes, Lamnidae)

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Abstract

The complete mitochondrial genome of the shortfin mako (*Isurus oxyrinchus*) was determined by using a PCR-based method. The total length of mitochondrial DNA is 16,701 bp and includes 13 protein-coding genes, 2 ribosomal RNA, 22 transfer RNA genes, 1 replication origin region, and 1 control region. The mitochondrial gene arrangement of the tiger tail seahorse is also matching the one observed in the most vertebrate creatures. Base composition of the genome is A (28.8%), T (28.0%), C (28.0%), and G (15.2%) with an A+T rich hallmark as that of other vertebrate mitochondrial genomes.

Keywords

Complete mitochondrial genome, *Isurus oxyrinchus*, shortfin mako

History

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The mackerel shark family Lamnidae, including five shark species, is one of seven families in the Laniformes. In the Lamnidae, the shortfin mako (*Isurus oxyrinchus*) can be distinguished from its only congeners (*Isurus paucus*) by the morphological characters, such as the pointed snout and the pectoral fin considerably shorter than head length and the pale underside of head. The epipelagic shortfin mako mainly dwells in coastal areas in temperate and tropical waters and is commonly collected by longline fishery. The largest size measured was about 4 m in total length and the body weight estimated is over 300 kg (Compagno, 2001). The IUCN currently lists this species in the Red List Category as vulnerable (IUCN, 2013).

In this study, we sequenced the complete mitochondrial genome of the shortfin mako (GenBank accession number KF361861). The shortfin mako specimen was identified by Dr. M. R. de Carvalho and was collected from the Tashi fish market (I-lan County, Taiwan). A piece of tissue was taken before the fixation of the specimen, and the head of this shark was deposited at Museu de Zoologia, Universidade de São Paulo, Brazil. The shortfin mako had a similar mitochondrial genome structure to that of the Lamniformes species, for example, *Megachama pelagios* (Chang et al., 2013a), *Carcharodon carcharias* (Chang et al., 2013b) and *Alopias superciliosus* (Chang et al., 2013c), and had 16,701 bp in its complete mitochondrial genome which consisted of 2 rRNA genes, 22 tRNA genes, 13 protein-coding genes, 1 replication origin region (O_L) and 1 control region (D-loop) (Table 1). The positions of RNA genes were predicted by the MITOS (Bernt et al., 2012),

Table 1. Mitochondrial genome of the shortfin mako, *Isurus oxyrinchus*.

Gene	Position		Length (bp)	Codon		Intergenic nucleotides*	Strand†
	From	To		Start	Stop		
<i>tRNA^{Phe}</i>	1	70	70			–	H
<i>12S rRNA</i>	71	1027	957			0	H
<i>tRNA^{Val}</i>	1025	1096	72			–3	H
<i>16S rRNA</i>	1097	2768	1672			0	H
<i>tRNA^{Leu(UUR)}</i>	2768	2842	75			–1	H
<i>ND1</i>	2843	3817	975	ATG	TAA	0	H
<i>tRNA^{Ile}</i>	3820	3889	70			2	H
<i>tRNA^{Gln}</i>	3888	3959	72			–2	L
<i>tRNA^{Met}</i>	3960	4028	69			0	H
<i>ND2</i>	4029	5072	1044	ATG	TAA	0	H
<i>tRNA^{Trp}</i>	5072	5142	71			–1	H
<i>tRNA^{Ala}</i>	5144	5212	69			1	L
<i>tRNA^{Asn}</i>	5216	5288	73			3	L
O _L	5289	5321	33			0	–
<i>tRNA^{Cys}</i>	5322	5388	67			0	L
<i>tRNA^{Tyr}</i>	5390	5459	70			1	L
<i>COI</i>	5461	7014	1554	GTG	TAG	1	H
<i>tRNA^{Ser(UCN)}</i>	7017	7087	71			2	L
<i>tRNA^{Asp}</i>	7092	7162	71			4	H
<i>COII</i>	7169	7859	691	ATG	T–	6	H
<i>tRNA^{Lys}</i>	7860	7933	74			0	H
<i>ATP8</i>	7935	8102	168	ATG	TAA	1	H
<i>ATP6</i>	8093	8776	684	ATG	TAA	–10	H
<i>COIII</i>	8776	9561	786	ATG	TAA	–1	H
<i>tRNA^{Gly}</i>	9564	9633	70			2	H
<i>ND3</i>	9634	10,011	378	ATG	TAA	0	H
<i>tRNA^{Arg}</i>	9983	10,052	70			–29	H
<i>ND4L</i>	10,053	10,349	297	ATG	TAA	0	H
<i>ND4</i>	10,343	11,723	1381	ATG	T–	–7	H
<i>tRNA^{His}</i>	11,724	11,792	69			0	H
<i>tRNA^{Ser(AGY)}</i>	11,793	11,859	67			0	H
<i>tRNA^{Leu(CUN)}</i>	11,860	11,931	72			0	H
<i>ND5</i>	11,932	13,761	1830	ATG	TAA	0	H

(continued)

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Table 1. Continued

Gene	Position		Length (bp)	Codon		Intergenic nucleotides*	Strand†
	From	To		Start	Stop		
<i>ND6</i>	13,757	14,278	522	ATG	AGG	–5	L
<i>tRNA^{Glu}</i>	14,279	14,348	70			0	L
<i>Cytb</i>	14,351	15,496	1146	ATG	TAA	2	H
<i>tRNA^{Thr}</i>	15,496	15,566	71			–1	H
<i>tRNA^{Pro}</i>	15,569	15,637	69			2	L
D-loop	15,638	16,701	1064			0	–

*Numbers correspond to the nucleotides separating different genes. Negative numbers indicate overlapping nucleotides between contiguous genes; †H and L, respectively, denote heavy and light strands.

and the locations of protein-coding genes were identified by comparing with the homologous genes of other Lamiformes sharks. The overall base composition of the entire genome was as follows: A (28.8%), T (28.0%), C (28.0%) and G (15.2%), which demonstrated an A + T (56.8%)-rich feature. Among the mitochondrial protein-coding genes, the *ND5* was the longest, while the *ATP8* was the shortest. The usage of the start codon was mainly ATG in the most of mitochondrial protein-coding genes, besides the *COI* gene employing the GTG; the usage of the stop one was either complete or incomplete. The control region was 1064bp in size and had no repeats inspected by the program ‘‘TANDEM REPEATS FINDER (Benson, 1999)’’.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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