

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the longfin mako shark, *Isurus paucus* (Chondrichthyes, Lamnidae)

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Abstract

Here we describe the complete mitochondrial genome sequence of the longfin mako, *Isurus paucus*, which is a pelagic shark found in temperate and tropical waters. The circle genome (16,704 bp) consists of 13 protein coding, 22 tRNA, 2 rRNA genes and 1 control region. It has the typical vertebrate mitochondrial gene arrangement.

Keywords

Complete mitochondrial genome, *Isurus paucus*, longfin mako shark

History

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Longfin mako *Isurus paucus* (Guitart-Manday, 1966) is considered a Vulnerable species by IUCN Red List for its apparent rarity, large body size, low fecundity and continued bycatch in intensive oceanic fisheries (Reardon et al., 2006). Its slender body and long broad pectoral fins suggests that the longfin mako is a less active predator than its better-known relative, the shortfin mako shark (*I. oxyrinchus*). Here we present the complete mitochondrial genome of *I. paucus* that was deposited in GenBank with the accession number KJ616742. The specimen used for this study was caught off Taitung County, eastern Taiwan on 22, Nov. 2012, which was identified by the second author. The organization of mitochondrial genome of *I. paucus* is shown in Table 1, which had a similar mitochondrial genome structure to that of other Lamniform species (Chang et al., 2013a,b,c,d, 2014a,b). It was sequenced and determined to be 16,704 bp in size, including 13 typical vertebrate protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and a control region. All genes were encoded on the H-strand with the exception of one protein-coding gene (*ND6*) and eight tRNA genes [*tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA^{Ser(UCN)}*, *tRNA^{Glu}*, and *tRNA^{Pro}*]. The base composition was counted using MEGA6 (Tamura et al., 2013). The overall base composition in descending order was A (29.14%), T (27.1%), C (28.56%), G (15.2%) with 43.76% GC content. The positions of RNA genes were predicted by the MITOS (Bernt et al., 2013) and the locations of protein-coding genes were identified by comparing with the homologous genes of shortfin mako *I. oxyrinchus* (KF361861; Chang et al., 2013d) and megamouth

Table 1. Characteristics of the mitochondrial genome of *Isurus paucus*.

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	1026	956			0	H
<i>tRNA^{Val}</i>	1024	1096	73			–3	H
<i>16S rRNA</i>	1097	2770	1674			0	H
<i>tRNA^{Leu(UUR)}</i>	2770	2844	75			–1	H
<i>ND1</i>	2845	3819	975	ATG	TAG	0	H
<i>tRNA^{Ile}</i>	3822	3891	70			2	H
<i>tRNA^{Gln}</i>	3890	3961	72			–2	L
<i>tRNA^{Met}</i>	3966	4034	69			4	H
<i>ND2</i>	4035	5078	1044	ATG	TAA	0	H
<i>tRNA^{Trp}</i>	5078	5148	71			–1	H
<i>tRNA^{Ala}</i>	5150	5218	69			1	L
<i>tRNA^{Asn}</i>	5219	5291	73			0	L
<i>OL</i>	5292	5324	33			0	–
<i>tRNA^{Cys}</i>	5325	5391	67			0	L
<i>tRNA^{Tyr}</i>	5393	5462	70			1	L
<i>COI</i>	5464	7017	1554	GTG	TAA	1	H
<i>tRNA^{Ser(UCN)}</i>	7020	7090	71			2	L
<i>tRNA^{Asp}</i>	7095	7164	70			4	H
<i>COII</i>	7171	7861	691	ATG	T–	6	H
<i>tRNA^{Lys}</i>	7862	7935	74			0	H
<i>ATP8</i>	7937	8104	168	ATG	TAA	1	H
<i>ATP6</i>	8095	8778	684	ATG	TAA	–10	H
<i>COIII</i>	8778	9563	786	ATG	TAA	–1	H
<i>tRNA^{Gly}</i>	9566	9635	70			2	H
<i>ND3</i>	9636	9986	351	ATG	TAG	0	H
<i>tRNA^{Arg}</i>	9985	10,055	71			–2	H
<i>ND4L</i>	10,056	10,352	297	ATG	TAA	0	H
<i>ND4</i>	10,346	11,726	1381	ATG	T–	–7	H
<i>tRNA^{His}</i>	11,727	11,795	69			0	H
<i>tRNA^{Ser(AGY)}</i>	11,796	11,862	67			0	H
<i>tRNA^{Leu(CUN)}</i>	11,863	11,934	72			0	H
<i>ND5</i>	11,935	13,764	1830	ATG	TAA	0	H
<i>ND6</i>	13,760	14,281	522	ATG	AGG	–5	L
<i>tRNA^{Glu}</i>	14,282	14,351	70			0	L

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(continued)

Table 1. Continued

Gene	Position		Length (bp)	Codon		Intergenic nucleotides	Strand
	From	To		Start	Stop		
<i>Cytb</i>	14,354	15,499	1146	ATG	TAG	2	H
<i>tRNA^{Thr}</i>	15,499	15,570	72			–1	H
<i>tRNA^{Pro}</i>	15,573	15,641	69			2	L
<i>D-loop</i>	15,642	16,704	1063			0	–

shark *M. pelagios* (KC702506; Chang et al., 2013a). The 22 tRNA genes ranged from 67 to 75 bp in length and can fold into a typical cloverleaf secondary structure that was estimated by the online software tRNAscan-SE v1.21 (Schattner et al., 2005), except for *tRNA^{Ser(AGY)}*. The two ribosomal RNA genes, *12S rRNA* (956 bp) and *16S rRNA* (1674 bp), located between *tRNA^{Phe}* and *tRNA^{Leu(UUR)}* genes and were separated by the *tRNA^{Val}* gene as seen in other vertebrates (Table 1). *ND5* and *ND6* overlap by 5 nucleotides, whereas they were encoded on the opposing strand. Except for *COI* with a GTG start codon, the remaining 12 protein-coding genes started with an ATG codon. Eleven protein-coding genes in longfin mako mitochondrial genome end with complete stop codons, TAA (*ND2*, *COI*, *ATP8*, *ATP6*, *COIII*, *ND4L* and *ND5*), AGG (*ND6*) and TAG (*ND1*, *ND3*, and *Cyt b*). The remaining protein-coding genes end with the incomplete stop codons representing as ‘‘T’’ (*COII* and *ND4*). The origin of L-strand replication (O_L), in *I. paucus* was located between the *tRNA^{Asn}* and *tRNA^{Cys}* genes within a cluster of five tRNA genes (WANCY region, Table 1) as in most vertebrates, which is 33 bp long. *D-loop* is 1063 bp long and no repeat set was found (in total 15,642–16,704; checked by online software ‘‘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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