

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the salmon shark, *Lamna ditropis* (Chondrichthyes, Lamnidae)

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Abstract

The complete mitochondrial genome of the salmon shark consists of 16,699 bp and includes 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, 1 replication origin region and 1 control region. The mitochondrial gene arrangement of the salmon shark is the same as that of most vertebrates. Base composition of the genome is A (29.6%), T (28.6%), C (27.1%), and G (14.8%).

Keywords

Complete mitochondrial genome, *Lamna ditropis*, salmon shark

History

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Salmon sharks, *Lamna ditropis*, are highly migratory apex predators in the North Pacific ecosystems, ranging from cold productive subarctic waters to warm subtropical waters (Weng et al., 2005). Like all lamnid sharks, salmon sharks are endothermic, maintaining body temperatures as high as 21°C above ambient water temperatures (Goldman et al., 2004). In this study, we sequenced the complete mitochondrial genome of a juvenile female salmon shark (KF 562053, 73 cm precaudal length) collected in Monterey Bay, California, USA (approximately 36.93°N 121.86°W), on 20 August 2010.

The salmon shark had a mitochondrial genome structure similar to that of other Lamniform species (Chang et al., 2013a,b,c,d,e; Chen et al., 2013; Huster et al., 2013). The salmon shark had entire sequence of 16,699 bp in its complete mitochondrial genome, which was composed 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). MITOS (Bernt et al., 2013) and the tRNAscan-SE v1.21 (Schattner et al., 2005), which were used to determine the positions of RNA genes, and the mitochondrial protein-coding genes of other Lamniform species were utilized to identify homologous ones in the salmon shark. The overall base composition of the entire genome had an A + T bias, with A comprising 29.6%, T 28.6%, C 27.1% and G 14.8%. Among the mitochondrial protein-coding genes, *ND5* was the longest, while *ATP8* was the shortest. The primary start codon was ATG with the exception of the *COI* gene, which used GTG, and the primary stop codons were TAA, TAG, AGG or T--.

Table 1. Characters of the salmon shark mitochondrial genome.

Gene	Position		Length (bp)	Codon		Intergenic nucleotides*	Strand†
	From	To		Start	Stop		
<i>tRNA^{Phe}</i>	1	70	70			–	H
12S rRNA	71	1028	958			0	H
<i>tRNA^{Val}</i>	1026	1097	72			–3	H
16S rRNA	1098	2770	1673			0	H
<i>tRNA^{Leu(UUR)}</i>	2770	2844	75			–1	H
<i>ND1</i>	2845	3819	975	ATG	TAA	0	H
<i>tRNA^{Ile}</i>	3822	3890	69			2	H
<i>tRNA^{Gln}</i>	3889	3960	72			–2	L
<i>tRNA^{Met}</i>	3961	4029	69			0	H
<i>ND2</i>	4030	5073	1044	ATG	TAA	0	H
<i>tRNA^{Trp}</i>	5073	5143	71			–1	H
<i>tRNA^{Ala}</i>	5145	5213	69			1	L
<i>tRNA^{Asn}</i>	5214	5286	73			0	L
O _L	5287	5319	33			0	–
<i>tRNA^{Cys}</i>	5320	5386	67			0	L
<i>tRNA^{Tyr}</i>	5388	5457	70			1	L
<i>COI</i>	5459	7012	1554	GTG	TAA	1	H
<i>tRNA^{Ser(UCN)}</i>	7015	7085	71			2	L
<i>tRNA^{Asp}</i>	7090	7159	70			4	H
<i>COII</i>	7164	7854	691	ATG	T--	4	H
<i>tRNA^{Lys}</i>	7855	7928	74			0	H
<i>ATP8</i>	7930	8097	168	ATG	TAA	1	H
<i>ATP6</i>	8088	8771	684	ATG	TAA	–10	H
<i>COIII</i>	8771	9556	786	ATG	TAA	–1	H
<i>tRNA^{Gly}</i>	9559	9628	70			2	H
<i>ND3</i>	9629	9979	351	ATG	TAG	0	H
<i>tRNA^{Arg}</i>	9978	10,047	70			–2	H
<i>ND4L</i>	10,048	10,344	297	ATG	TAA	0	H
<i>ND4</i>	10,338	11,718	1381	ATG	T--	–7	H
<i>tRNA^{His}</i>	11,719	11,787	69			0	H

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(continued)

Table 1. Continued

Gene	Position		Length (bp)	Codon		Intergenic nucleotides*	Strand†
	From	To		Start	Stop		
<i>tRNA^{Ser(AGY)}</i>	11,788	11,855	68			0	H
<i>tRNA^{Leu(CUN)}</i>	11,856	11,927	72			0	H
<i>ND5</i>	11,928	13,757	1830	ATG	TAA	0	H
<i>ND6</i>	13,753	14,274	522	ATG	AGG	−5	L
<i>tRNA^{Glu}</i>	14,275	14,344	70			0	L
<i>Cytb</i>	14,347	15,492	1146	ATG	TAG	2	H
<i>tRNA^{Thr}</i>	15,492	15,563	72			−1	H
<i>tRNA^{Pro}</i>	15,566	15,634	69			2	L
<i>D-loop</i>	15,635	16,699	1065			0	–

*Numbers correspond to the nucleotides separating different genes. Negative numbers indicate overlapping nucleotides between contiguous genes.

†H and L denote heavy and light strands, respectively.

control region, consisting of 1065 bp, did not contain any tandem repeat when 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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