

MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of the sand tiger shark, *Carcharias taurus* (Chondrichthyes, Odontaspidae)**

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**Abstract**

The complete mitochondrial genome of the sand tiger shark consists of 16,773 bp and including 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 sand tiger shark is the same as the one observed in most vertebrates. Base composition of the genome is A (31.8%), T (28.7%), C (26.3%) and G (13.2%).

**Keywords**

*Carcharias taurus*, complete mitochondrial genome, sand tiger shark

**History**

Received 5 September 2013  
Revised 8 September 2013  
Accepted 14 September 2013  
Published online 24 January 2014

The sand tiger shark, *Carcharias taurus*, is a large Lamniforme shark belonging to the Odontaspidae family (Campagno, 1984). This family consists of two genera, *Odontaspis* and *Carcharias*, the latter comprised of only one species – the sand tiger shark, *C. taurus*. The sand tiger shark is a coastal shark that can reach a maximum total length of 318 cm and is usually found in most subtropical and warm temperate seas (Campagno, 1984). It is generally considered a common species in areas in which it is found with a known distribution extending from waters of the Atlantic, Indian and western Pacific Oceans, as well as the Mediterranean Sea (Campagno, 1984; Gilmore et al., 1983). In the western Indian Ocean, this species has been reported from Yemen, Pakistan and India (Pollard & Smith, 2009) with more recent records extending its distribution to the Persian Gulf (Jabado et al., 2013; Krupp et al., 2000; Moore et al., 2007). The sand tiger shark can occur as solitary individuals or in small to large aggregations and commonly occurs in shallow bays, and around inshore rocky reefs and islands at up to 200 m depth (Campagno, 1984). Around the world, several populations of sand tiger sharks have shown severe declines due to fishing pressures and their life history characteristics, which includes a low fecundity with only two pups per litter (Campagno, 1984; Pollard & Smith, 2009). It is therefore listed on the IUCN Red List as “Vulnerable” (IUCN, 2012).

In this study, the complete mitochondrial genome of the sand tiger shark (KF 569943), incidentally captured by fishermen off the coast of Dalma island in Abu Dhabi, United Arab Emirates, on 18 March 2012 (Jabado et al., 2013) is sequenced.

The sand tiger shark had a similar mitochondrial genome structure to that of other Lamniformes species such as *Megachasma pelagios* (Chang et al., 2013a), *Alopias superciliosus* (Chang et al., 2013b), *Carcharodon carcharias* (Chang et al., 2013c) and *Isurus oxyrinchus* (Chang et al., 2013d). The sand tiger shark had 16,773 bp in its complete mitochondrial genome composed of 2 rRNA genes, 22 tRNA genes, 13 protein-coding genes, 1 replication origin region (O<sub>L</sub>) and 1 control region (D-loop) (Table 1). The MITOS (Bernt et al., 2012) and the tRNAscan-SE v1.21 (Schattner et al., 2005) were recruited for predicting the positions of RNA genes and the protein-coding genes of *Mitsukurina owstoni* (NC\_011825) were utilized to identify the ones of homologous protein-coding genes.

Table 1. Mitochondrial genome of the sand tiger shark, *C. taurus*.

Gene	Position		Length (bp)	Codon		Inter-genetic nucleotides <sup>a</sup>	Strand <sup>b</sup>
	From	To		Start	Stop		
tRNA <sup>Phe</sup>	1	70	70			–	H
12S rRNA	71	1023	953			0	H
tRNA <sup>Val</sup>	1021	1092	72			–3	H
16S rRNA	1093	2763	1671			0	H
tRNA <sup>Leu(UUR)</sup>	2763	2837	75			–1	H
<i>ND1</i>	2838	3812	975	ATG	TAA	0	H
tRNA <sup>Ile</sup>	3815	3883	69			2	H
tRNA <sup>Gln</sup>	3882	3953	72			–2	L
tRNA <sup>Met</sup>	3954	4022	69			0	H
<i>ND2</i>	4023	5066	1044	ATG	TAA	0	H
tRNA <sup>Trp</sup>	5066	5134	69			–1	H
tRNA <sup>Ala</sup>	5196	5264	69			61	L
tRNA <sup>Asn</sup>	5265	5337	73			0	L
O <sub>L</sub>	5338	5370	33			0	–
tRNA <sup>Cys</sup>	5371	5437	67			0	L
tRNA <sup>Tyr</sup>	5438	5506	69			0	L
<i>COI</i>	5508	7061	1554	GTG	TAA	1	H

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Table 1. Continued.

Gene	Position		Length (bp)	Codon		Inter-genetic nucleotides <sup>a</sup>	Strand <sup>b</sup>
	From	To		Start	Stop		
tRNA <sup>Ser(UCN)</sup>	7064	7134	71			2	L
tRNA <sup>Asp</sup>	7139	7208	70			4	H
<i>COII</i>	7213	7903	691	ATG	T- -	4	H
tRNA <sup>Lys</sup>	7904	7977	74			0	H
<i>ATP8</i>	7979	8146	168	ATG	TAA	1	H
<i>ATP6</i>	8137	8820	684	ATG	TAA	-10	H
<i>COIII</i>	8820	9605	786	ATG	TAA	-1	H
tRNA <sup>Gly</sup>	9608	9677	70			2	H
<i>ND3</i>	9678	10,055	378	ATG	TAA	0	H
tRNA <sup>Arg</sup>	10,027	10,096	70			-29	H
<i>ND4L</i>	10,097	10,393	297	ATG	TAA	0	H
<i>ND4</i>	10,387	11,767	1381	ATG	T- -	-7	H
tRNA <sup>His</sup>	11,768	11,836	69			0	H
tRNA <sup>Ser(AGY)</sup>	11,837	11,903	67			0	H
tRNA <sup>Leu(CUN)</sup>	11,904	11,975	72			0	H
<i>ND5</i>	11,976	13,805	1830	ATG	TAA	0	H
<i>ND6</i>	13,801	14,322	522	ATG	AGA	-5	L
tRNA <sup>Glu</sup>	14,323	14,392	70			0	L
<i>Cytb</i>	14,395	15,540	1146	ATG	TAG	2	H
tRNA <sup>Thr</sup>	15,540	15,610	71			-1	H
tRNA <sup>Pro</sup>	15,646	15,714	69			35	L
D-loop	15,715	16,773	1059			0	-

<sup>a</sup>Numbers correspond to the nucleotides separating different genes. Negative numbers indicate overlapping nucleotides between contiguous genes.

<sup>b</sup>H and L respectively denote heavy and light strands.

The overall base composition of the entire genome was A (31.8%), T (28.7%), C (26.3%) and G (13.2%), which demonstrated a A + T 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 except for the *COI* gene using the GTG; the usage of the stop one was TAA, TAG, AGA, or T- -. The control region, consisting of 1059 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 article.

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