

MITOGENOME ANNOUNCEMENTS

The complete mitochondrial genome of the great white shark, *Carcharodon carcharias* (Chondrichthyes, Lamnidae)

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Abstract

The complete mitochondrial genome of the great white shark having 16,744 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 great white shark is the same as the one observed in the most vertebrates. Base composition of the genome is A (30.6%), T (28.7%), C (26.9%) and G (13.9%).

Keywords

Carcharodon carcharias, complete mitochondrial genome, great white shark

History

Received 18 April 2013
Revised 25 April 2013
Accepted 3 May 2013
Published online 10 July 2013

The great white shark (GWS) [*Carcharodon carcharias* (Linnaeus, 1758)] is a species of large lamniform shark which characterized by large broadly triangular serrated upper teeth. The great white shark can be found in the coastal surface waters of all the major oceans and is mainly known for its size, with the largest individuals known to exceed 6.4 m in total length and 3324 kg in weight (Tricas & McCosker, 1984) which makes them the world's largest known predatory fish and one of the primary predators of marine mammals. Being ranked as first in having the most attacks on humans, the shark received large attention in different aspects. Without accurate population numbers are available, the IUCN now lists the great white shark as "vulnerable" (IUCN, 2012) and the great white shark is also included in CITES Appendix II (CITES, 2012).

In this study, the complete mitochondrial genome of the great white shark (KC914387), caught from the coast of Taitung County, Taiwan on 14 November 2012 is sequenced, and the tissue sample was deposited in the Biodiversity Research Center, Academia Sinica, Taiwan (ASIZP0915913).

The great white shark had a similar mitochondrial genome structure to that of the other Lamniformes species, for example, *Megachama pelagios* (Chang et al., 2013a) and *Alopias superciliosus* (Chang et al., 2013b). The great white shark had 16,744 bp in its complete mitochondrial genome 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). The MITOS (Leipzig, Germany) (Bernt et al., 2012) and the tRNAscan-SE v1.21 (Santa Cruz, CA) (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. The overall base composition of the entire

Table 1. Mitochondrial genome of the great white shark, *Carcharodon carcharias*.

| Gene | Position | | Length (bp) | Codon | | Intergenic nucleotides* | Strand† |
|--------------------------------|----------|--------|-------------|-------|------|-------------------------|---------|
| | From | To | | Start | Stop | | |
| <i>tRNA^{Phe}</i> | 1 | 71 | 71 | | | – | H |
| <i>12S rRNA</i> | 72 | 1027 | 956 | | | 0 | H |
| <i>tRNA^{Val}</i> | 1025 | 1096 | 72 | | | –3 | H |
| <i>16S rRNA</i> | 1097 | 2767 | 1671 | | | 0 | H |
| <i>tRNA^{Leu(UUR)}</i> | 2767 | 2841 | 75 | | | –1 | H |
| <i>ND1</i> | 2842 | 3816 | 975 | ATG | TAA | 0 | H |
| <i>tRNA^{Ile}</i> | 3819 | 3887 | 69 | | | 2 | H |
| <i>tRNA^{Gln}</i> | 3886 | 3957 | 72 | | | –2 | L |
| <i>tRNA^{Met}</i> | 3959 | 4027 | 69 | | | 1 | H |
| <i>ND2</i> | 4028 | 5071 | 1044 | ATG | TAA | 0 | H |
| <i>tRNA^{Trp}</i> | 5071 | 5141 | 71 | | | –1 | H |
| <i>tRNA^{Ala}</i> | 5143 | 5211 | 69 | | | 1 | L |
| <i>tRNA^{Asn}</i> | 5212 | 5284 | 73 | | | 0 | L |
| O _L | 5285 | 5317 | 33 | | | 0 | – |
| <i>tRNA^{Cys}</i> | 5318 | 5384 | 67 | | | 0 | L |
| <i>tRNA^{Tyr}</i> | 5385 | 5453 | 69 | | | 0 | L |
| <i>COI</i> | 5455 | 7008 | 1554 | GTG | TAA | –1 | H |
| <i>tRNA^{Ser(UCN)}</i> | 7011 | 7081 | 71 | | | 2 | L |
| <i>tRNA^{Asp}</i> | 7086 | 7154 | 69 | | | 4 | H |
| <i>COII</i> | 7159 | 7849 | 691 | ATG | T– | –4 | H |
| <i>tRNA^{Lys}</i> | 7850 | 7923 | 74 | | | 0 | H |
| <i>ATP8</i> | 7925 | 8092 | 168 | ATG | TAA | 1 | H |
| <i>ATP6</i> | 8083 | 8766 | 684 | ATG | TAA | –10 | H |
| <i>COIII</i> | 8766 | 9551 | 786 | ATG | TAA | –1 | H |
| <i>tRNA^{Gly}</i> | 9554 | 9623 | 70 | | | 2 | H |
| <i>ND3</i> | 9624 | 9974 | 351 | ATG | TAG | 0 | H |
| <i>tRNA^{Arg}</i> | 9973 | 10,043 | 71 | | | –2 | H |
| <i>ND4L</i> | 10,044 | 10,340 | 297 | ATG | TAA | 0 | H |
| <i>ND4</i> | 10,334 | 11,714 | 1381 | ATG | T– | 7 | H |
| <i>tRNA^{His}</i> | 11,715 | 11,783 | 69 | | | 0 | H |
| <i>tRNA^{Ser(AGY)}</i> | 11,784 | 11,850 | 67 | | | 0 | H |
| <i>tRNA^{Leu(CUN)}</i> | 11,851 | 11,922 | 72 | | | 0 | H |

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Table 1. Continued

| Gene | Position | | Length (bp) | Codon | | Intergenic nucleotides* | Strand† |
|---------------------------|----------|--------|----------------|-------|------|----------------------------|---------|
| | From | To | | Start | Stop | | |
| <i>ND5</i> | 11,923 | 13,752 | 1830 | ATG | TAA | 0 | H |
| <i>ND6</i> | 13,748 | 14,269 | 522 | ATG | AGG | –5 | L |
| <i>tRNA^{Glu}</i> | 14,270 | 14,339 | 70 | | | 0 | L |
| <i>Cytb</i> | 14,342 | 15,487 | 1146 | ATG | TAA | 2 | H |
| <i>tRNA^{Thr}</i> | 15,487 | 15,558 | 72 | | | –1 | H |
| <i>tRNA^{Pro}</i> | 15,561 | 15,629 | 69 | | | 2 | L |
| D-loop | 15,630 | 16,744 | 1115 | | | 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.

genome is A (30.6%), T (28.7%), C (26.9%) and G (13.9%), which demonstrated a A + T (59.3%) rich feature. The tRNA genes range from 67 ~ 75 bp in size, and only *tRNA^{Ser(AGY)}* could not fold into a distinctive cloverleaf secondary structure estimating by the tRNAscan-SE v1.21 (Schattner et al., 2005). Among the mitochondrial protein-coding genes, the *ND5* is the longest, while the *ATP8* is 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, AGG or T–. The control region had 2.5 set of repeat (period size = 54 bp, 88% matches) in position 454–585 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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