Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Critically Endangered speartooth shark *Glyphis glyphis* (Carcharhiniformes: Carcharhinidae)

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Abstract

In this study we present the first complete mitogenome for the speartooth shark *Glyphis glyphis*, a rare euryhaline elasmobranch from northern Australia and Papua New Guinea. The mitogenome is 16,702 bp in length and the overall base composition is 31.5% A; 26.0% C; 13.0% G and 29.5% T. It includes 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, 13 protein-coding genes and a putative 1066 bp long control region. The *COI* gene is initiated by GTG codon whereas the remaining protein-coding genes started with the ATG codon. This study will help elucidate the taxonomy of this poorly known group of sharks.

Keywords

Glyphis glyphis, mitogenome, river sharks, threatened species

History

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The speartooth shark *Glyphis glyphis*, listed as Critically Endangered on the Australian *Environment Protection and Biodiversity Conservation Act*, and Endangered on the IUCN Red List of Threatened Species (Compagno et al., 2009), is found in tropical rivers and Estuarine waters of northern Australia and Papua New Guinea. This species belongs to the rare and poorly known group of river sharks (*Glyphis*: Carcharhinidae). The systematics of the group have been poorly understood due to the paucity of specimens collected so far and the subsequent lack of morphological or molecular data for those fish, although recent work has improved our knowledge (e.g. Compagno et al., 2008; Wynen et al., 2009). The mitogenome of *G. glyphis* described here is the first complete mitochondrial sequence available for this genus and, to the best of our knowledge, the third for the family Carcharhinidae (GenBank Accessed 09 May 2013). This information is a starting point to better understand the taxonomy and the phylogenetic relationships in this group.

One specimen of *G. glyphis* was caught from the South Alligator River, Kakadu National Park, Northern Territory, Australia, under Kakadu Research Permit RK805. A fin clip was preserved in 95% ethanol before the fish was released. The experimental protocol and data analysis were done as described elsewhere (Chen et al., 2013).

The complete mitogenome of *G. glyphis* is 16,702 bp in length (GenBank accession number: KF006312). Overall, the base compositions were as follows: 31.5% A; 26.0% C; 13.0% G and 29.5% T. The gene order and transcriptional orientation of *G. glyphis* mitogenome are given in Table 1. There are a total of 21 bp short intergenic spacers located at 10 gene junctions ranging in size from 1 bp to 7 bp (tRNA-*Asp*-*COII*). In addition, 35 bp overlaps were found at 8 gene junctions ranging in size from 1 bp to 10 bp (*ATP8*-*ATP6*). The 12S rRNA (953 bp) and 16S rRNA (1668 bp) genes were located between the tRNA-*Phe* and tRNA-*Leu* genes, and separated by the tRNA-*Val* gene. The 22 tRNA genes spread in the mitogenome ranged from 67 bp (tRNA-*Ser2*) to 75 bp (tRNA-*Leu1*) and formed three conserved clusters (IQM, WANCY and HSL). A 35 bp inserted sequence was identified as the origin of L-strand replication (OL) between tRNA-*Asn* and tRNA-*Cys* genes within the WANCY cluster. All tRNA genes could be folded in the typical cloverleaf structure except tRNA-*Ser2*, which has lost the dihydrouridine stem and replaced it with a simple loop. Except for the *COI* gene started with the GTG codon, the remaining protein-coding genes started with the ATG codon. In addition, the *ND2*, *ND3* and *Cytb* genes ended with the TAG codon, while the other protein-coding genes ended with TAA or complete T (Table 1). The control region of *G. glyphis* is 1066 bp in length, which was located between the tRNA-*Pro* and tRNA-*Phe* genes. The termination associated sequence (TAS) and the conserved sequence blocks (CSB1-3) were identified in the control region, which is involved in the replication and transcription of the mitogenome (Falkenberg et al., 2007).

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Table 1. Organization of the mitogenome in *Glyphis glyphis*.

Gene	Strand	Position	Size (bp)	Start codon	Stop codon	Intergenic spacer
tRNA-Phe	H	01–70	70			0
12S rRNA	H	71–1023	953			0
tRNA-Val	H	1024–1095	72			0
16S rRNA	H	1096–2763	1668			0
tRNA-Leu1 (UAA)	H	2764–2838	75			0
ND1	H	2839–3813	975	ATG	TAA	0
tRNA-Ile	H	3814–3883	70			1
tRNA-Gln	L	3885–3956	72			0
tRNA-Met	H	3957–4025	69			0
ND2	H	4026–5072	1047	ATG	TAG	−2
tRNA-Trp	H	5071–5141	71			1
tRNA-Ala	L	5143–5211	69			0
tRNA-Asn	L	5212–5284	73			0
OL	–	5285–5319	35			0
tRNA-Cys	L	5320–5387	68			1
tRNA-Tyr	L	5389–5457	69			1
COI	H	5459–7015	1557	GTG	TAA	0
tRNA-Ser1 (UGA)	L	7016–7086	71			3
tRNA-Asp	H	7090–7159	70			7
COII	H	7167–7857	691	ATG	T	0
tRNA-Lys	H	7858–7931	74			1
ATP8	H	7933–8100	168	ATG	TAA	−10
ATP6	H	8091–8774	684	ATG	TAA	−1
COIII	H	8774–9559	786	ATG	TAA	2
tRNA-Gly	H	9562–9631	70			0
ND3	H	9632–9982	351	ATG	TAG	−2
tRNA-Arg	H	9981–10,050	70			0
ND4L	H	10,051–10,347	297	ATG	TAA	−7
ND4	H	10,341–11,727	1387	ATG	T	−6
tRNA-His	H	11,722–11,790	69			0
tRNA-Ser2 (GCU)	H	11,791–11,857	67			0
tRNA-Leu2 (UAG)	H	11,858–11,929	72			0
ND5	H	11,930–13,759	1830	ATG	TAA	−6
ND6	L	13,754–14,276	523	ATG	T	0
tRNA-Glu	L	14,277–14,346	70			2
Cytb	H	14,349–15,494	1146	ATG	TAG	−1
tRNA-Thr	H	15,494–15,565	72			2
tRNA-Pro	L	15,568–15,636	69			0
Control region	–	15,637–16,702	1066			

Intergenic spacer: negative number indicates that adjacent genes overlap.

Declaration of interest

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References

Chen X, Ai W, Ye L, Wang X, Lin Yang S. (2013). The complete mitochondrial genome of the grey bamboo shark (*Chiloscyllium griseum*) (Orectolobiformes: Hemiscylliidae): Genomic characterization and phylogenetic application. Acta Oceanol Sin 32:59–65.

Compagno LJV, Pogonoski J, Pollard D. (2009). *Glyphis glyphis*. In: IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. Available at: http://www.iucnredlist.org (Accessed 9 May 2013).

Compagno LJV, White WT, Last PR. (2008). *Glyphis garricki* sp. nov., a new species of river shark (Carcharhiniformes: Carcharhinidae) from northern Australia and Papua New Guinea, with a redescription of *Glyphis glyphis* (Müller & Henle, 1839). In: Last PR, White WT, Pogonoski JJ, editors. Descriptions of New Australian Chondrichthyans. *CSIRO Marine and Atmospheric Research Paper* No. 022. Hobart, Tasmania: CSIRO Marine and Atmospheric Research. p 203–25.

Falkenberg M, Larsson NG, Gustafsson CM. (2007). DNA replication and transcription in mammalian mitochondria. Annu Rev Biochem 76: 679–99.

Wynen L, Larson H, Thorburn D, Peverell S, Morgan D, Field I, Gibb K. (2009). Mitochondrial DNA supports the identification of two endangered river sharks (*Glyphis glyphis* and *Glyphis garricki*) across northern Australia. Mar Freshw Res 60:554–62.