Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Mitochondrial genome of Japanese angel shark *Squatina japonica* (Chondrichthyes: Squatinidae)

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Abstract

Squatina japonica belonging to the monogenetic family Squatinidae is endemic to the Northwest Pacific. The complete mitochondrial genome sequence of *S. japonica* is 16,689 bp long and comprises 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control region. The base composition of the genome is 31.10% A, 31.04% T, 24.42% C, and 13.43% G. The geographic clade and phylogenetic relationship of *S. japonica* are ambiguous. Therefore, studying the complete mitochondrial genome of *S. japonica* is highly important to understand the aforementioned aspect and to analyze the conservation genetics in the genus *Squatina*.

Keywords

Genome, mitochondrial, *Squatina japonica*

History

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Squatina japonica belongs to the monogenetic family Squatinidae, which comprises 23 valid species worldwide (FishBase). *Squatina japonica*, a ray-like benthic angel shark, is endemic to the Northwest Pacific, which includes the Sea of Japan, along the south eastern Japan coast, Yellow Sea, East China Sea, waters surrounding northern Taiwan and Taiwan Strait (Compagno et al., 2005; Walsh & Ebert, 2007). The IUCN Red List of Threatened Species (http://www.iucnredlist.org/) considered *S. japonica* as a Vulnerable species because of its limited geographic distribution, vulnerability to fishing pressure, and low-reproductive potential (Compagno et al., 2005; Holmes et al., 2009; Last & White, 2008; Walsh & Ebert, 2007).

In this study, the complete mtDNA of *S. japonica* was first amplified and sequenced by polymerase chain reaction with 22 primer pairs. Nucleotide sequences were deposited in GenBank (Accession Number KJ619663). The complete mtDNA of *S. japonica* was a closed circular molecule with a genome length of 16,689 bp. It comprises of 13 protein-coding genes, 22 tRNA, 2 rRNA genes (12S rRNA and 16S rRNA) and 1 control region.

Ten of the 13 protein-coding genes began with ATG, whereas *CO1* and *ND6* begin with GTG and CTA, respectively. Seven protein-coding genes ended with TAA; *ND1*, *ND2*, and *ND3* with TAG; *ND6* with CAT; and *CO2* and *ND4* with T (incomplete stop codon). The 22 tRNA genes had lengths ranging from 65 bp in $tRNA^{Cys}$ to 75 bp in $tRNA^{Lys}$ and $tRNA^{Leu}$. The 12S and 16S rRNA genes were 955 and 1665 bp long, respectively. These genes were located between $tRNA^{Phe}$ and $tRNA^{Leu}$, and separated by $tRNA^{Val}$. The control region was 1059 bp long and lies between $tRNA^{Pro}$ and $tRNA^{Phe}$. *ND5* was the longest gene with 1827 bp. The shortest gene was *ATP8* with only 168 bp. Thirteen protein-coding genes for 3800 amino acids were identified. The nucleotide composition was 31.10% A, 31.04% T, 24.42 % C, and 13.43% G. This composition shows considerable bias toward an A + T preference, which is 62.14%. The mitochondrial genes from *S. japonica* were overlapped in 26 bp at six locations and interleaved in 50 bp intergenic spacers at 12 locations (Table 1).

Over the past few decades, molecular techniques have been promoted for shark species identification and phylogeographic distribution (Holmes et al., 2009). mtDNA is a biomarker used to determine the phylogenetic relationships among individuals, populations, and even species (Naylor et al., 2005; Stelbrink et al., 2010). Stelbrink et al. (2010) discussed the phylogenetic reconstruction of 17 *Squatina* species with two mitochondrial markers (COI and 16S rRNA). However, the geographic clade and phylogenetic relationship of *S. japonica* are ambiguous. Therefore, studying the complete mitochondrial genome of *S. japonica* is important to clearly understand the aforementioned

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Table 1. Characteristics of the *S. japonica* mitochondrial DNA genome.

Gene names	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Sizes (bp)	No. of the codons	Start condon	Stop condon
tRNA^{Phe}	H	1	69			69			
12S rRNA	H	71	1025	1		955			
tRNA^{Val}	H	1026	1097			72			
12S rRNA	H	1098	2762			1665			
tRNA^{Leu}	H	2763	2837			75			
ND1	H	2838	3815			978	325	ATG	TAG
tRNA^{Ile}	H	3818	3887	2		70			
tRNA^{Gln}	L	3888	3959			72			
tRNA^{Met}	H	3960	4029			70			
ND2	H	4030	5076			1047	348	ATG	TAG
tRNA^{Trp}	H	5075	5143		2	69			
tRNA^{Ala}	L	5145	5213	1		69			
tRNA^{Asn}	L	5214	5286			73			
tRNA^{Cys}	L	5316	5380	29		65			
tRNA^{Tyr}	H	5381	5450			70			
CO1	H	5452	7008	1		1557	518	GTG	TAA
tRNA^{Ser}	L	7010	7080	1		71			
tRNA^{Asp}	H	7083	7152	2		70			
CO2	H	7159	7849	6		691	230	ATG	T––
tRNA^{Lys}	H	7850	7924			75			
ATP8	H	7926	8093	1		168	55	ATG	TAA
ATP6	H	8084	8767		10	684	227	ATG	TAA
CO3	H	8767	9552		1	786	261	ATG	TAA
tRNA^{Gly}	H	9555	9624	2		70			
ND3	H	9625	9975			351	116	ATG	TAG
tRNA^{Arg}	H	9974	10,042		2	69			
ND4L	H	10,043	10,339			297	98	ATG	TAA
ND4	H	10,333	11,713		7	1381	460	ATG	T––
tRNA^{His}	H	11,714	11,783			70			
tRNA^{Ser}	H	11,784	11,850			67			
tRNA^{Leu}	H	11,851	11,922			72			
ND5	H	11,923	13,749			1827	608	ATG	TAA
ND6	L	13,746	14,267		4	522	173	CTA	CAT
tRNA^{Glu}	L	14,268	14,337			70			
Cyt b	H	14,342	15,487	3		1146	381	ATG	TAA
tRNA^{Thr}	H	15,489	15,561	1		73			
tRNA^{Pro}	L	15,562	15,630			69			
D-loop	H	15,631	16,689			1059			

aspect and to analyze the conservation genetics in the genus *Squatina*.

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Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing style of this article. This study was funded by the National Natural Science Foundation of China (30970321; 31272287) and the JSPS Invitation Fellowship Program for Research in Japan.

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