

MITOGENOME ANNOUNCEMENT

Mitochondrial genome of *Dasyatis bennettii* (Chondrichthyes: Dasyatidae)

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Abstract

Dasyatis bennettii is a bottom-dweller that inhabits in the coastal waters of the Indian and Pacific Oceans as well as the freshwaters of Southern China. In this study, we determined the complete mitochondrial genome of this species of stingrays. The results showed that the total length of the mitogenome was 17,668 bp as a circular DNA and contained 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 control region. The base composition of the complete mitochondrial DNA was 31.1% A, 28.7% T, 26.7% C, and 13.5% G. All the genes in *D. bennettii* were distributed on the H-strand, except for the *ND6* subunit gene and eight tRNA genes which were encoded on the L-strand.

Keywords: *Dasyatis bennettii*, mitochondrion, genome

Dasyatis bennettii belongs to the genus *Dasyatis* (Dasyatidae, Myliobatiformes, Batoidea), which comprises more than 40 valid species worldwide (Nishida and Nakaya 1990; Compagno 1999). This species is a bottom-dweller that inhabits in the coastal waters of the Indian and Pacific Oceans as well as the freshwaters of Southern China (Schwartz 2007; Zhang et al. 2010). Habitat degradation and over-exploitation declined the population of fish resources sharply, especially in chondrichthyans (Port et al. 2012). As a member of extant chondrichthyans, *D. bennettii* is considered to be particularly vulnerable to overexploitation as a result of its K-selected life history strategies, which is generally characterized by low fecundity, slow growth, late age at maturity, and long life spans (White and Kyne 2010). Despite its low resilience (Bijukumar and Deepthi 2009), there is no sufficient information to assess its conservation status using molecular approach. Thus, a lack of data and

complicated jurisdictional issues present particular challenges for assessing and conserving high seas biodiversity (Dulvy et al. 2008).

The evolutionary substitution rate of mitochondrial DNA (mtDNA) is much higher than nuclear DNA (Kocher et al. 1989). It is a valuable molecule for understanding the evolutionary relationships among individuals, populations, and species (Irwin et al. 1991). Except for a few species, family Rivulidae, for example, mtDNA of fishes is similar with other vertebrates (Lee et al. 2001).

In this study, we sequenced the entire mitogenome of *D. bennettii* by polymerase chain reaction (PCR) with 16 pairs of primers. Nucleotide sequences were deposited in GenBank (accession number KC196067). The complete mitochondrial genome of *D. bennettii* is 17,668 bp, containing 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 control region. The nucleotide

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Table I. Characteristics of the *D. bennettii* mtDNA genome.

Gene name	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Size (bp)	No. of codons	Start codon	Stop codon
<i>tRNA^{Phe}</i>	H	1	69			69			
<i>12S rRNA</i>	H	70	1033			964			
<i>tRNA^{Val}</i>	H	1034	1105	1		72			
<i>16S rRNA</i>	H	1107	2811		3	1705			
<i>tRNA^{Leu}</i>	H	2810	2884	1		75			
<i>ND1</i>	H	2886	3863	3		978	325	ATG	TAA
<i>tRNA^{Ile}</i>	H	3867	3936	4		70			
<i>tRNA^{Gln}</i>	L	3941	4012			72			
<i>tRNA^{Met}</i>	H	4013	4083			71			
<i>ND2</i>	H	4084	5130		2	1047	348	ATG	TAA
<i>tRNA^{Trp}</i>	H	5130	5199			70			
<i>tRNA^{Ala}</i>	L	5200	5268	1		69			
<i>tRNA^{Asn}</i>	L	5270	5342	36		72			
<i>tRNA^{Cys}</i>	L	5379	5446	6		68			
<i>tRNA^{Tyr}</i>	L	5453	5521	1		69			
<i>CO1</i>	H	5523	7079	9		1557	518	GTG	TAA
<i>tRNA^{Ser}</i>	L	7089	7159			71			
<i>tRNA^{Asp}</i>	H	7160	7230	3		71			
<i>CO2</i>	H	7234	7924			691	230	ATG	T-
<i>tRNA^{Lys}</i>	H	7925	7998	1		74			
<i>ATP8</i>	H	8000	8167		10	168	55	ATG	TAA
<i>ATP6</i>	H	8158	8841		1	684	227	ATG	TAA
<i>CO3</i>	H	8841	9626	5		786	261	ATG	TAA
<i>tRNA^{Gly}</i>	H	9632	9703			72			
<i>ND3</i>	H	9704	10,052			349	116	ATG	T-
<i>tRNA^{Arg}</i>	H	10,053	10,123			71			
<i>ND4L</i>	H	10,124	10,420		5	297	98	ATG	TAA
<i>ND4</i>	H	10,414	11,794			1381	460	ATG	T-
<i>tRNA^{His}</i>	H	11,795	11,863	1		69			
<i>tRNA^{Ser}</i>	H	11,865	11,932	2		68			
<i>tRNA^{Leu}</i>	H	11,935	12,006			72			
<i>ND5</i>	H	12,007	13,851		4	1845	614	ATG	TAA
<i>ND6</i>	L	13,848	14,369	1		522	173	CTA	CAT
<i>tRNA^{Glu}</i>	L	14,371	14,439	7		69			
<i>Cyt b</i>	H	14,447	15,589	6		1143	380	ATG	TAA
<i>tRNA^{Thr}</i>	H	15,596	15,668	9		73			
<i>tRNA^{Pro}</i>	L	15,678	15,746			69			
<i>D-loop</i>	H	15,747	17,668			1922			

composition showed considerable bias toward an A + T preference as 59.8%. All protein-coding genes are found in H-strand, except *ND6*, which is found in L-strand (Table I). The 21 tRNAs can fold into a typical cloverleaf secondary structure except for tRNA^{Ser}. The mitochondrial genes from *D. bennettii* were overlapped in a total of 25 bp at six locations, as well as interleaved with a total of 97-bp intergenic spacers at 18 locations.

Thirteen protein-coding genes for 3805 amino acids were identified. The longest one is *ND5* gene with 1845 bp, and the shortest one is *ATP8* with only 168 bp. Eleven of the 13 protein-coding genes require ATG as the start codon, while *CO1* and *ND6* utilize GTG and CTA, respectively. The *CO1* gene having GTG instead of ATG as a start codon seems to be a tendency in fish mitochondrial genomes (Miya and Nishida 1999). Nine use TAA as stop codons. The *ND6* ends with CAT, and *CO2*, *ND3*, and *ND4* use T as an incomplete stop codon. The 22 tRNA genes range in size from 75 bp in tRNA^{Leu} to 68 bp in

tRNA^{Cys} and tRNA^{Ser}. The 12S and 16S rRNA genes are 964 and 1705 bp, respectively, and are located between the tRNA^{Phe} and tRNA^{Leu} genes and separated by the tRNA^{Val} gene. The control region is 1922 bp long and lies between the tRNA^{Pro} and tRNA^{Phe} genes.

Mitochondrial genome sequences have been proven to be very useful for phylogenetic relationships at several taxonomic levels; we expect this study to provide a useful database for analyzing the phylogenetic relationship and conservation genetics in family Dasyatidae.

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