



Mitochondrial DNA Part A

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MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of the Japanese fan lobster
Ibacus ciliatus (Crustacea, Achelata, Scyllaridae)**Dong-Ha Ahn¹, Sanghee Kim², Joong-Ki Park³, Sook Shin⁴, and Gi-Sik Min¹¹Department of Biological Sciences, Inha University, Incheon, South Korea, ²Division of Life Sciences, Korea Polar Research Institute, KIOST, Incheon, South Korea, ³Department of Parasitology, College of Medicine, Chungbuk National University, Cheongju, South Korea, and ⁴Department of Life Science, Sahmyook University, Seoul, South Korea**Abstract**

Slipper lobsters are a unique group of decapod crustaceans; they have cylindrical or flattened bodies and belong to the family Scyllaridae. The genus *Ibacus* (Leach, 1815) (Achelata, Scyllaridae, Ibacinae) consists of eight recognized species to date, all of which occur in the Indo-West Pacific Ocean and are commercially important seafood species. The complete mitochondrial genome of the Japanese fan lobster *Ibacus ciliatus* (Von Siebold, 1824) is 15,696 bp in size and consists of 13 protein-coding genes, 22 transfer RNAs, 2 ribosomal RNAs, and a control region of 783 bp. The base composition of *I. ciliatus* is 35.8% A, 34.7% T, 19.0% C, and 10.5% G, with an overall AT content of 70.5%. The mitogenome of *I. ciliatus* was found to have gene arrangement and transcriptional polarity identical to that of the American lobster *Homarus americanus*, showing the pancrustacean ground pattern. Here, we present the complete mitogenome sequence of *I. ciliatus*; it is the first mitogenome information from the subfamily Ibacinae, and represents the second for the family Scyllaridae.

KeywordsAchelata, Ibacinae, *Ibacus ciliatus*, Japanese fan lobster, mitogenome, Scyllaridae**History**

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Slipper lobsters are a unique group of decapod crustaceans; they have cylindrical or flattened bodies, and are found in all warm oceans. Slipper lobsters belong to the family Scyllaridae, which is currently divided into four subfamilies (Arctidinae, Ibacinae, Scyllarinae, and Theninae). According to morphological and molecular phylogenetic analyses, all the subfamilies are monophyletic, except for Ibacinae, which is paraphyletic (Yang et al., 2012). The genus *Ibacus* (Leach, 1815) (Achelata, Scyllaridae, Ibacinae) is a group of slipper lobsters, which currently consists of eight recognized species (De Grave et al., 2009; WoRMS-Editorial-Board, 2014). These are all commercially important seafood species, and occur in the Indo-West Pacific Ocean. Of these, the Japanese fan lobster *Ibacus ciliatus* (Von Siebold, 1824) are distributed rather broadly from the east coast of the Philippines to the southern Korean Peninsula (Korea Strait) and southern Japan. This species inhabits on soft sandy- or muddy-substrates at a depth range of 49–324 m (Holthuis, 1985, 1991). In this study, we determined the complete mitochondrial genome (mitogenome) of *I. ciliatus*. This is the first mitogenome sequence from the subfamily Ibacinae, and represents the second for the family Scyllaridae. The *I. ciliatus* mitogenome was compared with other species of the infraorder Achelata.

A specimen of *I. ciliatus* was purchased at the fish market in Jeju, South Korea. Genomic DNA extraction, sequencing, and

gene annotation were performed according to the methods described by Kim et al. (2012). The complete mitogenome of *I. ciliatus* was 15,696 bp (GenBank accession number: KM488334), and contains 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNAs (rRNAs), and a control region (CR) (Table 1). The AT content of the entire sequence was 70.5% (35.8% A, 34.7% T, 19.0% C, and 10.5% G), which is higher than that of *Scyllarides latus* (67.5%). Nine PCGs use ATG as the initiation codon, whereas *nad3* and *nad6* started with ATT, and *cox1* and *atp8* started with ACG and ATC, respectively. In termination codon, some PCGs terminated with an incomplete stop codon T (*cox2*, *nad5*, and *cytb*) or TA (*nad4*), whereas the remaining terminated with TAA (eight of the 13 PCGs) or TAG (*atp8*). The 22 tRNA genes ranged from 63 to 74 bp in size and conform to the typical cloverleaf-shaped secondary structure. The *rrnL* (16 S) and *rrnS* (12 S) were 1331 and 863 bp in length, respectively. The CR of 783 bp, was located between the *rrnS* (12 S) and *trnI* genes, and was slightly longer than that of *S. latus* (710 bp).

The infraorder Achelata was a monophyletic group composed of two main families, Palinuridae and Scyllaridae (De Grave et al., 2009; Palero et al., 2009). To date, the mitogenomes of Achelata lobsters are known for seven species: six from Palinuridae (*Panulirus homarus* [NC_016015], *P. japonicus* [NC_004251], *P. ornatus* [NC_014854], *P. stimpsoni* [NC_014339], *P. versicolor* [NC_017868], *Palinurellus wieneckii* [NC_021753]), and one from Scyllaridae (*S. latus* [NC_020022]) (Liu & Cui, 2011; Qian et al., 2011; Shen et al., 2013; Yamauchi et al., 2002; Yang et al., 2014). The gene order of the *I. ciliatus* mitogenome was similar to those known for the Palinuridae and Scyllaridae families, and is

Table 1. Mitochondrial genome organization of *I. ciliatus* (15,696 bp).

Gene/region	Position		Size		Codons		Intergenic sequence
	Start	End	No. of nt	No. of aa*	Initiation	Termination	
<i>cox1</i>	1	1539	1,539	512	ACG	TAA	−6
<i>trnL2</i>	1534	1600	67				5
<i>cox2</i>	1606	2293	688	229	ATG	T	0
<i>trnK</i>	2294	2357	64				0
<i>trnD</i>	2358	2420	63				0
<i>atp8</i>	2421	2579	159	52	ATC	TAG	−7
<i>atp6</i>	2573	3253	681	226	ATG	TAA	−1
<i>cox3</i>	3253	4044	792	263	ATG	TAA	−1
<i>trnG</i>	4044	4110	67				0
<i>nad3</i>	4111	4464	354	117	ATT	TAA	3
<i>trnA</i>	4468	4531	64				0
<i>trnR</i>	4532	4597	66				0
<i>trnN</i>	4598	4663	66				0
<i>trnS1</i>	4664	4730	67				−1
<i>trnE</i>	4730	4800	71				1
<u><i>trnF</i></u>	4868	4802	67				−4
<u><i>nad5</i></u>	6596	4865	1732	577	ATG	T	0
<u><i>trnH</i></u>	6661	6597	65				−1
<u><i>nad4</i></u>	8000	6661	1340	446	ATG	TA	−7
<u><i>nad4L</i></u>	8296	7994	303	100	ATG	TAA	2
<i>trnT</i>	8299	8364	66				−1
<i>trnP</i>	8432	8364	69				1
<i>nad6</i>	8434	8949	516	171	ATT	TAA	−1
<i>cytb</i>	8949	10,083	1135	378	ATG	T	−1
<i>trnS2</i>	10,083	10,150	68				32
<u><i>nad1</i></u>	11,127	10,183	945	314	ATG	TAA	29
<u><i>trnL1</i></u>	11,227	11,157	71				0
<u><i>rrnL</i></u>	12,558	11,228	1331				0
<u><i>trnV</i></u>	12,632	12,559	74				0
<u><i>rrnS</i></u>	13,495	12,633	863				0
<i>CR</i>	13,496	14,278	783				0
<i>trnI</i>	14,279	14,344	66				−3
<i>trnQ</i>	14,410	14,342	69				12
<i>trnM</i>	14,423	14,490	68				1
<i>nad2</i>	14,492	15,496	1,005	334	ATG	TAA	−3
<i>trnW</i>	15,494	15,563	70				−1
<u><i>trnC</i></u>	15,626	15,563	64				4
<u><i>trnY</i></u>	15,694	15,631	64				2

Genes encoded on the light strand are underlined. *, Stop codons were not included. nt, nucleotide; aa, amino acid.

identical to that of *Homarus americanus* (NC_015607), an additive evidence of the pancrustacean ground pattern (Kim et al., 2011). Nucleotide sequence comparison of *I. ciliatus* mtDNA showed a 76.8% similarity to that of *S. latus*. Our results will provide useful information for understanding the phylogenetic relationships and mtDNA evolution among the members of the decapods infraorder Achelata.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the manuscript. This study was supported by the Basic Science Research Program of the National Research Foundation of Korea (NRF), funded by the Ministry of Education, Science and Technology (2012R1A1A2006835); the program on Management of Marine Organisms causing Ecological Disturbance and Harmful Effects, funded by KIMST/MOF; and Basic Research Program of the Korea Polar Research Institute (PE14020) for S. Kim.

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