

MITOGENOME ANNOUNCEMENT

## The complete mitochondrial genome of the Japanese mud shrimp *Upogebia major* (Crustacea, Decapoda)

SANGHEE KIM<sup>1</sup>, TAEHO KIM<sup>2</sup>, HAN-GU CHOI<sup>1</sup>, JOONG-KI PARK<sup>3</sup>, DONG-HA AHN<sup>4</sup>, & GI-SIK MIN<sup>4</sup>

<sup>1</sup>Korea Polar Research Institute, Songdo Techno Park, Yeonsu-gu, Incheon 406-840, South Korea, <sup>2</sup>Department of Plant Medicine, College of Agriculture, Life, and Environmental Sciences, Chungbuk National University, Cheongju 361-763, South Korea, <sup>3</sup>Graduate Program in Cell Biology and Genetics, Department of Parasitology, College of Medicine, Chungbuk National University, Cheongju 361-763, South Korea, and <sup>4</sup>Department of Biological Sciences, Inha University, Incheon 402-751, South Korea

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### Abstract

We determined a full-length sequence of mitochondrial (mt) genome from *Upogebia major*. This is the first complete mt genome report for infraorder Thalassinidea in Decapoda, Crustacea. Our result showed that *U. major* generally followed a typical pancrustacean gene order but some tRNA genes showed a very unique gene arrangement such as duplication or translocation. Since none of the complete mt genome sequences in the infraorder Thalassinidea are available yet, this report will provide additional information in relation to mt genome diversity and evolution of the decapods.

**Keywords:** Complete mitochondrial genome, Decapoda, Japanese mud shrimp, *Upogebia major*

The Japanese mud shrimp, *Upogebia major* (de Haan, 1841) (Decapoda, Thalassinidea), live in burrows in the muddy intertidal flats of Korea and Japan. Recently, they have attracted increased attention in ecological studies due to their abundance and bioturbating activity and consequent effects on the benthic community structure (Mukai and Koike 1984; Dworschak 2000).

A fresh specimen of the Japanese mud shrimp was collected from the intertidal flat of Seosan, Chungcheongnam-do province, Korea, and the partial sequences of *cox1* and 16S rDNA were initially determined using previously published primers for *cox1* (Folmer et al. 1994) and newly designed 16S rDNA primers: Cru16S + 81 (5'-taggagatagaaaccra-cctgg-3') and Cru16S - 613 (5'-atgaccgtgcaaaggtagc-3'). The sequences from each gene fragment were then

used to design *U. major*-specific primers for the long PCR amplification. Genomic DNA extraction, sequencing and gene annotation for the complete mtDNA were carried out following the methods described by Min and Park (2009).

The complete mtDNA sequence of *U. major* was 16,119 bp in length (accession no. JF793665) with an overall A + T content of 70.8% (Table I). The mitochondrial (mt) genome of *U. major* contained 13 protein-coding genes, two rRNAs, 23 tRNAs, and a putative control region.

The gene arrangement and the transcriptional polarity of the 13 protein-coding genes were consistent with the pancrustacea (crustacea + hexapod) ground pattern (Liu and Cui 2011). However, six genes of tRNAs (*trnI*, *trnQ*, *trnC*, *trnY*, *trnM*, and *trnW*) had a unique gene arrangement in *U. major*. The *trnC* and

Correspondence: S. Kim, Korea Polar Research Institute, Songdo Techno Park, Yeonsu-gu, Incheon 406-840, South Korea. Tel: + 82 32 260 6164. Fax: + 82 32 260 6301. E-mail: sangheekim@kopri.re.kr

Table I. Organization of the mitochondrial genome of *Upogebia major*.

Gene/region	Position		Size		Codons		Intergenic sequence
	Start	Finish	No. of nt	No. of aa	Initiation	Termination	
<i>cox1</i>	1	1548	1548	515	ATC	TAA	0
<i>trnL2</i>	1548	1615	68				-1
<i>trnL1</i>	1617	1681	65				1
<i>cox2</i>	1689	2393	705	234	ATG	TAA	7
<i>trnK</i>	2374	2441	68				-20
<i>trnD</i>	2441	2506	66				-1
<i>atp8</i>	2507	2665	159	52	ATG	TAA	0
<i>atp6</i>	2659	3333	675	224	ATG	TAA	-7
<i>cox3</i>	3333	4122	790	263	ATG	T	-1
<i>trnG</i>	4123	4187	65				0
<i>nad3</i>	4188	4541	354	117	ATT	TAA	0
<i>trnA</i>	4540	4604	65				-2
<i>trnR</i>	4605	4667	63				0
<i>trnN</i>	4667	4737	71				-1
<i>trnS1</i>	4737	4805	69				-1
<i>trnE</i>	4806	4873	68				0
<i>trnF</i>	4940	4874	67				0
<i>nad5</i>	6669	4941	1729	576	ATG	T	0
<i>trnH</i>	6734	6670	65				0
<i>nad4</i>	8074	6734	1341	446	ATG	TAG	-1
<i>nad4L</i>	8367	8068	300	99	ATG	TAA	-7
<i>trnT</i>	8369	8436	68				1
<i>trnP</i>	8501	8437	65				0
<i>nad6</i>	8510	9019	510	169	ATT	TAA	8
<i>cob</i>	9019	10,153	1135	378	ATG	T	-1
<i>trnS2</i>	10,154	10,221	68				0
<i>trnI</i>	10,224	10,291	68				2
<i>nad1</i>	11,251	10,310	942	313	ATG	TAG	18
<i>trnL1</i>	11,333	11,275	59				23
<i>rrnL</i>	12,688	11,334	1355				0
<i>trnV</i>	12,758	12,689	70				0
<i>rrnS</i>	13,587	12,759	829				0
<i>NCR1</i>	13,588	13,825	238				0
<i>trnQ</i>	13,894	13,826	69				0
<i>NCR2</i>	13,895	14,796	902				0
<i>trnC</i>	14,862	14,797	66				0
<i>trnY</i>	14,931	14,863	69				0
<i>trnM</i>	14,990	15,058	69				58
<i>nad2</i>	15,059	16,060	1002	333	ATT	TAA	0
<i>trnW</i>	16,059	16,113	55				-2

Note: The genes that are encoded on the light strand are underlined in the table.

*trnY* were located between *trnQ* and *trnM*, which differ from the pancrustacean ground pattern, where they are positioned between *trnW* and *cox1*. The position of *trnI* between *trnS2* and *nad1* in *U. major* was also very unique among all other pancrustaceans reported so far. Interestingly, *U. major* has an extra *trnL1*. One *trnL1* was located between *trnL2* and *cox2*, and another between *nad1* and *rrnL*. Except *Pagurus longicarpus*, where *trnL1* is located between *cox1* and *trnL2*, the *trnL1* for all other known decapods are after the *nad1* gene. Therefore, the presence of *trnL1* between *trnL2* and *cox2* seems to be a duplicate. The identification of extra genes in decapods is very rare and the only other case where this has been reported was for *Geothelphusa dehaani* (Brachyura), which also had a duplicated *trnL1* (Segawa and Aotsuka 2005).

The majority of protein-coding genes (9 of 13 genes) start with ATG, whereas *cox1* starts with ATC, and *nad2*, *nad3* and *nad6* start with ATT. It is also interesting to note that three of the 13 protein-coding genes were shown to terminate with an incomplete stop codon T (*cox3*, *nad5*, and *cob*), whereas the other 10 genes ended with a complete stop codon TAA or TAG.

The non-coding region (NCR1 and NCR2) of *U. major* mtDNA, which was separated by *trnQ*, was 1140 bp in length and contained a high A + T composition (85.6%).

Since none of the complete mt genome sequences in the infraorder Thalassinidea are available yet, this report will provide additional information in relation to mt genome diversity and the evolution of the decapods.

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