



Mitochondrial DNA Part A

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the Violet-spotted reef lobster *Enoplometopus debelius* (Crustacea, Astacoidea, Enoplometopidae)

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Abstract

The violet-spotted reef lobster *Enoplometopus debelius* Holthuis, 1983 (Decapoda, Astacoidea, Enoplometopidae) is found in the tropical reef areas of the Indo-Pacific region, and is a highly prized and very popular species in the aquarium trade industry. The complete mitochondrial genome of *E. debelius* has 15,641 base pairs consisting of 13 protein-coding genes, 22 transfer RNAs, 2 ribosomal RNAs, and a control region of 746 bp. The base composition of *E. debelius* is 36.4% A, 35.3% T, 18.1% C, 10.3% G, and the species has an AT content of 71.7%. The *E. debelius* mitogenome was found to have a gene arrangement and transcriptional polarity identical to that of the *Homarus americanus* mitogenome, a representative of the arthropod ground pattern. Here, we present the complete mitogenome sequence of *E. debelius*, which is the first in the superfamily Enoplometopoidea. These data will provide a useful molecular resource for the phylogenetic study of the infraorder Astacoidea/order Decapoda.

Keywords

Astacoidea, Enoplometopidae, *Enoplometopus debelius*, mitogenome, reef lobster

History

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The violet-spotted reef lobster or Debelius' reef lobster *Enoplometopus debelius* Holthuis, 1983 belongs to the genus *Enoplometopus* (Decapoda, Astacoidea, Enoplometopidae) – all 12 species of the genus are known so far (De Grave et al., 2009; WoRMS-Editorial-Board, 2014). *E. debelius* is found in tropical reef areas of the Indo-Pacific region, including Indonesia, New Caledonia, Hawaii, and possibly Japan. This species inhabits coral or rocky reefs to depths of 12–25 m, and is a highly prized and very popular species in the aquarium trade industry (Chan & Wahle, 2013; Poupin, 2003). Recently, the mitochondrial genome (mitogenome) of family Enoplometopidae was published based on sequences from the Red reef lobster *E. occidentalis* (NC_020027) (Shen et al., 2013), but it was not fully determined owing to the absence of the entire *nad2* sequence, as well as some tRNAs (i.e. *trnW*, *trnC*, and *trnY*). In this study, we present the complete mitogenome sequence of *E. debelius*, the first to be fully described in the superfamily Enoplometopoidea.

A specimen of *E. debelius* was purchased from an online aquarium shop in California, USA. Genomic DNA extraction, sequencing, and gene annotation were performed according to the methods described by Kim et al. (2012). The complete mitogenome of *E. debelius* was 15,641 bp in size (GenBank accession number: KM488333) and comprises 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNAs (rRNAs), and a control region (CR), which is typical for most metazoans (Table 1). The base composition of *E. debelius* was 36.4% A, 35.3% T, 18.1% C, and 10.3% G. The total AT content

of the mitogenome was 71.7%, which was slightly higher among decapods (60.2–74.9%). Of the 13 PCGs, 10 PCGs have ATG as the initiation codon, whereas the *cox1* sequence was inferred to begin with ACG, and *nad3* and *nad6* were initiated with ATC and TAT, respectively. Two of the PCGs (*cox2* and *nad5*) terminated with an incomplete stop codon (T–), whereas the others contain the complete stop codons (TAA or TAG). The 22 tRNA genes ranged from 64 to 74 bp in length, and had typical clover-leaf secondary structures. The *rrnL* (16S) and *rrnS* (12S) are 1333 and 860 bp in length, respectively. The CR of 746 bp was located between *rrnS* (12S) and *trnI*.

The infraorder Astacoidea comprises four extant superfamilies (Enoplometopoidea, Nepropoidea, Astacoidea, and Parastacoidea). In mitogenome analysis of decapod crustacean phylogeny, Shen et al. (2013) reported that the infraorder Astacoidea was monophyletic, and that the superfamily Enoplometopoidea was the closest group to the superfamily Nepropoidea, even though only the partial mitogenome of *E. occidentalis* was analyzed. Here, we found that the complete mitogenome of *E. debelius* was identical, in terms of the typical arrangement and transcriptional polarity, to that of the American lobster *Homarus americanus* mitogenome (NC_015607, superfamily: Nepropoidea), a representative of the arthropod ground pattern (Kim et al., 2011). Thus, among the four superfamilies in Astacoidea, the mitogenome structures of Enoplometopoidea and Nepropoidea were identical, whereas the other two crayfish superfamilies, Astacoidea and Parastacoidea, have distinct arrangements from the former ones, as shown the result of Gan et al. (2014). We expect that our data will be a useful molecular resource for the more detailed study of phylogenetic relationships and mitogenome evolution in comparative mitogenomic studies of the infraorder Astacoidea/order Decapoda.

Table 1. Mitochondrial genome organization of *E. debelius* (15,641 bp).

| Gene/region | Position | | Size | | Codons | | Intergenic sequence |
|---------------------|----------|--------|-----------|------------|------------|-------------|---------------------|
| | Start | End | No. of nt | No. of aa* | Initiation | Termination | |
| <i>cox1</i> | 1 | 1539 | 1539 | 512 | ACG | TAA | -6 |
| <i>trnL2</i> | 1534 | 1601 | 68 | | | | -1 |
| <i>cox2</i> | 1601 | 2288 | 688 | 229 | ATG | T-- | -1 |
| <i>trnK</i> | 2288 | 2356 | 69 | | | | 0 |
| <i>trnD</i> | 2357 | 2423 | 67 | | | | -1 |
| <i>atp8</i> | 2423 | 2581 | 159 | 52 | ATG | TAG | -7 |
| <i>atp6</i> | 2575 | 3249 | 675 | 224 | ATG | TAA | -1 |
| <i>cox3</i> | 3249 | 4040 | 792 | 263 | ATG | TAA | 2 |
| <i>trnG</i> | 4043 | 4109 | 67 | | | | -1 |
| <i>nad3</i> | 4109 | 4462 | 354 | 117 | ATC | TAG | -3 |
| <i>trnA</i> | 4460 | 4524 | 65 | | | | 2 |
| <i>trnR</i> | 4527 | 4590 | 64 | | | | 0 |
| <i>trnN</i> | 4591 | 4657 | 67 | | | | 0 |
| <i>trnS1</i> | 4658 | 4725 | 68 | | | | 0 |
| <i>trnE</i> | 4726 | 4790 | 65 | | | | -2 |
| <i>trnF</i> | 4856 | 4789 | 68 | | | | -1 |
| <u><i>nad5</i></u> | 6584 | 4856 | 1729 | 576 | ATG | T-- | 0 |
| <u><i>trnH</i></u> | 6650 | 6585 | 66 | | | | -1 |
| <u><i>nad4</i></u> | 7990 | 6650 | 1341 | 446 | ATG | TAG | -7 |
| <u><i>nad4L</i></u> | 8286 | 7984 | 303 | 100 | ATG | TAA | 1 |
| <i>trnT</i> | 8288 | 8353 | 66 | | | | -2 |
| <i>trnP</i> | 8419 | 8352 | 68 | | | | -17 |
| <i>nad6</i> | 8403 | 8939 | 537 | 178 | TAT | TAA | -1 |
| <i>cytb</i> | 8939 | 10,075 | 1137 | 378 | ATG | TAG | -3 |
| <i>trnS2</i> | 10,073 | 10,144 | 72 | | | | 24 |
| <i>nad1</i> | 11,113 | 10,169 | 945 | 314 | ATG | TAA | 21 |
| <u><i>trnL1</i></u> | 11,204 | 11,135 | 70 | | | | 0 |
| <u><i>rrnL</i></u> | 12,537 | 11,205 | 1333 | | | | 0 |
| <u><i>trnV</i></u> | 12,611 | 12,538 | 74 | | | | 1 |
| <u><i>rrnS</i></u> | 13,472 | 12,613 | 860 | | | | 0 |
| <i>CR</i> | 13,473 | 14,218 | 746 | | | | 0 |
| <i>trnI</i> | 14,219 | 14,284 | 66 | | | | -3 |
| <u><i>trnQ</i></u> | 14,350 | 14,282 | 69 | | | | 0 |
| <i>trnM</i> | 14,351 | 14,421 | 71 | | | | -1 |
| <i>nad2</i> | 14,421 | 15,422 | 1002 | 333 | ATG | TAA | -3 |
| <i>trnW</i> | 15,420 | 15,491 | 72 | | | | 12 |
| <u><i>trnC</i></u> | 15,570 | 15,504 | 67 | | | | -1 |
| <u><i>trnY</i></u> | 15,637 | 15,570 | 68 | | | | 4 |

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

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work 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) for G.-S. Min, and the Basic Research Program of the Korea Polar Research Institute (PE14020) for S. Kim.

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