

Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the hydrothermal vent ghost shrimp *Paraglypturus tonganus* (Crustacea, Axiidea, Callianassidae)Se-Joo Kim¹, Jonguk Kim¹, Dong-Ha Ahn², Se-Jong Ju^{1,3}, Gi-Sik Min², and Sanghee Kim⁴¹Deep-sea and Seabed Resources Research Division, Korea Institute of Ocean Science & Technology, Gyeonggi-do, Korea, ²Department of Biological Sciences, Inha University, Incheon, Korea, ³Department of Marine Biology, Korea University of Science & Technology, Daejeon, Korea, and ⁴Division of Life Sciences, Korea Polar Research Institute, Yeosu-gu, Incheon, Korea**Abstract**

Ghost shrimps are burrowing decapods that serve as bioturbators and habitat providers in seafloor environments. The hydrothermal vent ghost shrimp, *Paraglypturus tonganus*, was collected from a hydrothermal vent in the Tonga Arc. This species has a mitochondrial genome (mitogenome) of 15,924 bp in length with an AT content of 66.1%. The mitogenome was identical to the typical gene arrangement and transcriptional polarity of the infraorder Axiidea. *Paraglypturus tonganus* showed 65.3–70.1% nucleotide similarity with the known mitogenomes of other axiid shrimps. These results are useful for understanding the phylogenetic relationships among the members of Axiidea within the decapods.

Keywords

Axiidea, complete mitochondrial genome, hydrothermal vent, *Paraglypturus tonganus*, Tonga Arc

History

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Ghost shrimps (or mud shrimps) are burrowing decapods, and are an important fossil species (Ngoc-Ho, 2003; Karasawa, 2011). They serve as bioturbators and habitat providers in the seafloor environments (Felder, 2001; Mukai & Koike, 1984; Posey et al., 1991). The original infraorder Thalassinidea was recently divided into the two infraorders, Axiidea and Gebiidea, based on molecular data. However, their phylogenetic position within decapods remains unclear (Lin et al., 2012). Although some ghost shrimp species have been identified in hydrothermal fields, little is known about their ecological niche or mitochondrial genome (mitogenome).

Specimens of a new species of an axiid shrimp, named as *Paraglypturus tonganus* by Ahn et al. (under review), were collected from a hydrothermal vent field (volcano #19; referred from ISA GIS map (<http://www.mapserver.isa.org.jm/GIS/>)) of the Tonga Arc (24°48'S and 177°00'W) in the southwestern Pacific Ocean during the environmental baseline survey for the project titled "Exploration of Seafloor Hydrothermal Deposits in Tongan Waters" in February 2012. We analyzed the mitogenome of *P. tonganus* to better understand the phylogenetic relationships of vent ghost shrimps. Genomic DNA extraction, sequencing, and gene annotation were performed by the methods of Kim et al. (2012).

The complete mitogenome of *P. tonganus* was 15,924 bp in length (accession no. KJ820739) and encoded 13 protein-coding genes (PCGs), 2 rRNAs, 22 tRNAs, and a control region (CR). The overall AT content was 66.1% (64.9% in the 13 PCGs, 71.7% in the 2 rRNAs, 71.6% in the 22 tRNAs, and 68.7% in the CR). Twelve PCGs had ATN as the initiation codon, whereas ND2 was inferred to begin with GTG. In contrast, two PCGs (ND4 and ND4L) terminated with an incomplete stop codon (T–), whereas the others contained complete stop codons (TAA or TAG). The 16S and 12S rRNAs were 1329 and 802 bp in length, respectively. All tRNA genes ranged in length from 63–73 bp and had typical cloverleaf secondary structures. The CR of 1,035 bp was located between *tRNA^{Ile}* and *tRNA^{Gln}* and displayed the unique structural feature of inverted repeat sequences at both ends. The terminal repeats were 76 bp and contained a "TATA-box" in the upstream region, a pair of 15 matching nucleotides in the stem region, and 4 bases in the loop region (Figure 1).

The complete mitogenomes were recently determined for four species of Axiidea (Kim et al., 2013; Lin et al. 2012; Shen et al., 2013). The mitogenome of *P. tonganus* was identical to the typical arrangement and transcriptional polarity of Axiidea, but it contained a longer CR (1,035 bp) than other species (91–610 bp). The mitogenome of *P. tonganus* showed the following nucleotide sequence similarities with other species: *Nihonotrypaea japonica* (accession no. NC_020351), 70.1%; *Nihonotrypaea thermophile* (NC_019610), 69.4%; *Corallianassa coutierei* (NC_020025), 69.3%; and *Neaxius glyptocercus* (NC_019609), 65.3%.

Although there have been reports of mitochondrial phylogenomics for resolving taxonomic uncertainties of ghost shrimps, it remains unclear whether the infraorders Axiidea and Gebiidea are a monophyletic group (Kim et al., 2013; Lin et al., 2012). Our findings will facilitate elucidation of the phylogenetic

(A)

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13, 481  GAAAGGAGAA AGGGGGGTTA TTAATATAT AAGCTAGCTT ATATATTTAA TATAGCTTAT ATATCTAGTA ATAATAGGAT TGGTGTATC ATGACTATAT
13, 581  AATTAATAC ACCCAGAGGG GGTATAGAAT TTTATATGAC ATATTAGAAG TTAATATATA AGTTTTATTA TTACATAATC CTACAAGGAA TACATACAGA
13, 681  ACGTTAGTTG TAAATTAATA CAATATAAGC AAGGCAGGAT TTAGGACCTT GATCCCCGAC AAGTGAGGAA GCGAGGTCCG TATCGAATCC TGCCCCTACC
13, 781  GACATGATAC TATATTAGCA CGGAAACTTG GTGAACGGTC ACTGTAATGG TAGACCGTGG AGAATGTATT TGGGTATAAA GATTCTTACC TATGTGACGA
13, 881  TAAATCTTAG TTGTAGGCAT TGATAACGTA GTTTAATTGT ATACAGCAAT ATAAGTTATA GATCATAAGT AAAGTATATA ATATGAGGGG GAGAATTAAT
13, 981  GAAGAGTTTG TATTATACAG ATTAGTTTCT GTATTACTAC TATATGATTT ACTTTACTTA GGTGGGGGGA ACTATATATA CATTATATA TACAATAATG
14, 081  CTTAATTTAC ATCTGGACAT AATGCTATAG AAACGACTAA GTTAATGTCA ACTGGAACAG TACAAGTGCT TTAGGAGAGA CCCCATATAC CACAATACTG
14, 181  TCCTCGTCTA GAGTAAACAG TATTGTGGTA TATGGGGTCT TAAGTAGACT TAACCTGCTC CTTTCTTGA TTCATGTACT GGAACAAAGA GTAGCCTTCT
14, 281  ATATACGTAT AACATGAACG ATCAAGTTAA GTCTATAACG AGAGTCAAGT GGTAACCTT AGAGTATACA ATAATAACCT AAACATATAT TAAACATATA
14, 381  AACAAGCCAT AAAAGTTAAA TTACATGTAT ATAAAATCAT GAGGCAAACA TATAAGTTAT ATTATTACTA GATATATAAG CTATATTTAA TATATAAGCT
14, 481  AGCTTATATA TTTAATAACC CCCCTTTCTC CTTTC

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(B)

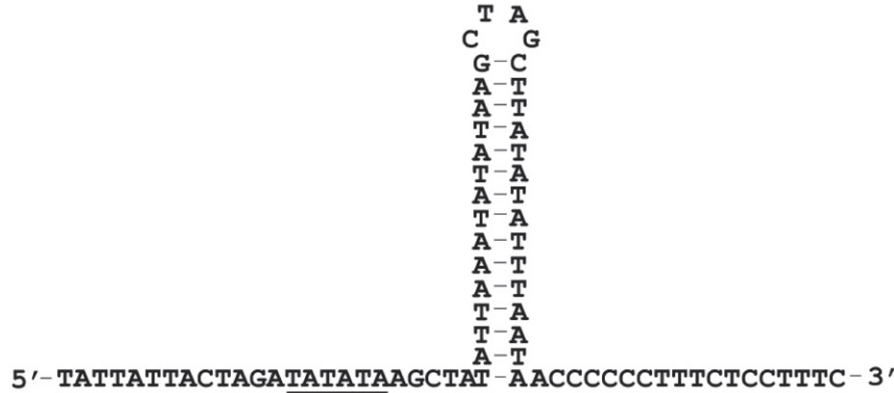


Figure 1. Inverse-repeated sequence blocks on both ends of the control region in the mitochondrial genome of *Paraglypturus tonganus*. (A) Sequences of the control region (1035 bp) and position of the inverse-repeated regions (bold), and (B) putative secondary structure from base positions 14,440 to 14,515 on the heavy strand. Underline indicates a “TATA-box”.

relationships, mitogenome evolution, and biogeography of Axiidea.

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 grants from the R&D project titled “Exploration of seafloor hydrothermal deposits in Tongan waters (PM57063)” funded by the Ministry of Oceans and Fisheries of Korea, and the Basic Research Program of the Korea Polar Research Institute (PE14020).

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