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MITOGENOME REPORT

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The first mitogenome report of *Dimorphostylis asiatica* Zimmer 1921 (Malacostraca: Cumacea)

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ABSTRACT

In 1921, Zimmer established the genus *Dimorphostylis* for *Dimorphostylis asiatica* from Japanese waters. This study determined the first complete mitogenome of hooded shrimp sequenced from *Dimorphostylis asiatica* (Cumacea: Diastylidae). *D. asiatica* is a type species of the genus *Dimorphostylis*, distributed in the West Pacific from southern Kuril to Vietnam, including Korean waters. The mitogenome is 14,888 base pairs (bp) long with a high A + T content of 70.9%. Phylogenetic analysis places *Dimorphostylis* within the Superorder Peracarida, providing new insights into the phylogeny and evolution of cumaceans and broader crustacean groups. This report provides a vital reference for further phylogenetic studies of cumaceans and enhances our molecular understanding of crustacean evolution.

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KEYWORDS
Cumacea; *Dimorphostylis asiatica*; phylogeny; complete mitogenome

Introduction

The cumaceans commonly called hooded shrimp, comprise more than 1700 species. Prior to the present study, no complete mitogenome on this group had been reported in the scientific literature, making it challenging to apply molecular data to phylogenetic and evolutionary study. The genus *Dimorphostylis* was established by Zimmer (1921) for *Dimorphostylis asiatica* (Figure 1) from Japanese waters, and 33 species have been described (Lee and Lee 2012; WoRMS 2024). The genus *Dimorphostylis* is only distributed in the Indo-West Pacific and along the coast of Australia (Akiyama 2011; Gerken 2014). Phylogenetic studies of cumaceans using molecular markers were conducted by Haye et al. (2004), Rehm et al. (2020), and Uhlir et al. (2021) based on single-gene analyses and were subsequently expanded to multigene analyses by Gerken et al. (2022). As no complete mitogenome sequence for cumaceans has been reported, this study aimed to provide a valuable reference for further phylogenetic and molecular research by determining the mitochondrial genome of the cumacean species, *D. asiatica*.

Material and methods

Specimens were collected using a light trap (Holmes and O'Connor 1988; Kim 1992) from shallow water at Geojin Port, Geojin-eup, Goseong-gun, Gangwon-do, Korea (38°26′47.7" N 128°27′45.3" E). Specimens were identified using a stereomicroscope (Olympus SZX12, Japan) and light microscope (Olympus BX51, Japan). Genomic DNA extraction and mitochondrial DNA amplification were performed using DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany) and REPLI-g Mitochondrial DNA Kit (Qiagen) with provided primer, respectively. The whole body was used as a material for DNA extraction, owing to the meiofaunal-size. Thus, the specimen collected at the same location and same time was deposited as a voucher specimen (NIBRIV0000881816; National Institute of Biological Resources, Korea; Eun-Jung Nam, ejnam@korea.kr). Mitochondrial genome sequencing was performed using the HiSeq 2000 sequencing system. Assembler and annotation tools, NOVOPlasty (Dierckxsens et al. 2017) and Chlorobox (Tillich et al. 2017), were used, respectively. Illumina sequencing data of *D. asiatica* were mapped onto the *D. asiatica* mitochondrial genome sequence (MZ240751) and the depth of mapped reads was calculated respectively using clc_ref_assemble and clc_mapping_info with default parameters in CLC Assembly Cell package ver. 4.2.1 (Qiagen, Denmark). Phylogenetic analysis was conducted to examine the phylogenetic position of *D. asiatica* using the MEGA 11 software (Tamura et al. 2021). The phylogenetic tree was reconstructed using the maximum likelihood method and GTR+G+I model with a bootstrap of 1000 replicates.

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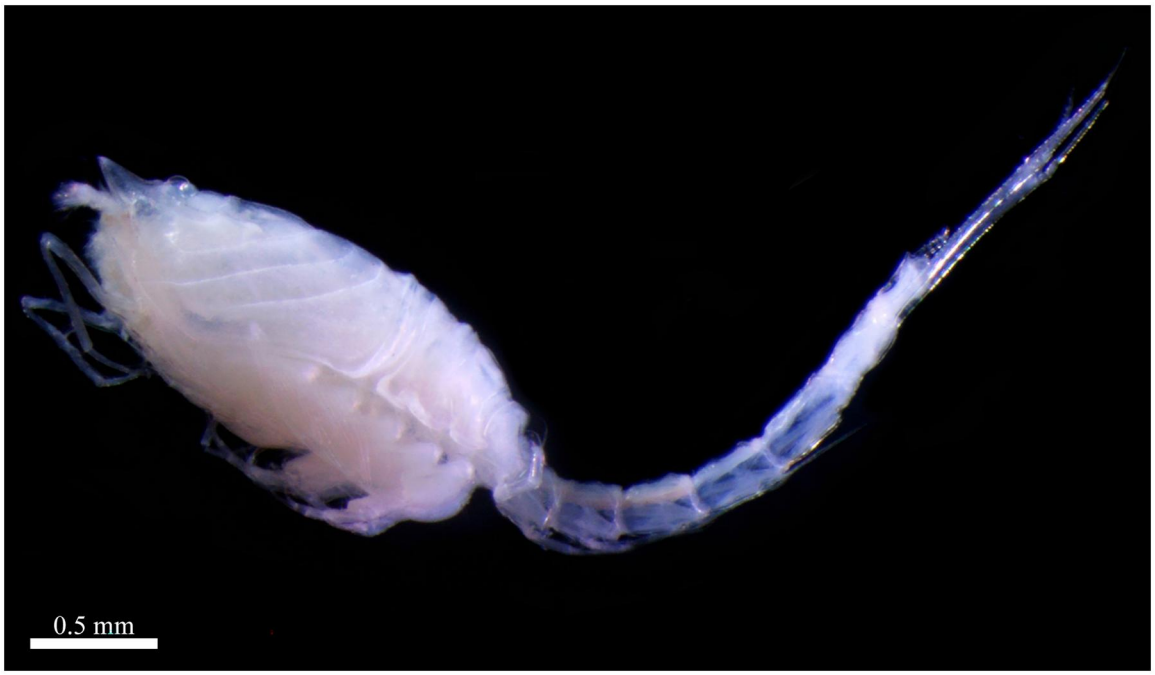


Figure 1. *Dimorphostylis asiatica* Zimmer 1921, adult male, 4.53 mm. The diagnostic characteristics of the adult male *D. asiatica* are as follows: the carapace has a frontal lobe with one transverse ridge, and lateral side of the carapace bears one pair of frontal ridges and three pairs of oblique ridges (anterior, middle, and posterior), with the frontal ridges connecting to the transverse ridge; the telson has 2–4, usually 3, pairs of lateral setae and three terminal setae, with the central seta being slightly longer than the outer pair; the uropod peduncle bears 14–23 setae, and the first to third segments of the uropod endopod each bear 7–12, 3, and 1–3 setae, respectively. The photo was taken by SK, an author this article.

Result and discussion

The complete mitogenome of *D. asiatica* (GenBank accession number MZ240751) is 14,888-bp long and comprises 13 protein-coding genes, two rRNA genes, and 21 tRNA genes (Figure 2). The overall nucleotide composition is 39.7% A, 17.0% C, 12.1% G, and 31.2% T, with high A + T content (70.9%). The average mapping depth was 51.5X coverage (Figure S1). Evolutionary analysis was conducted to understand the position of the present cumacean species within the Superorder Peracarida. The *D. asiatica* sequence was compared with three amphipods, two mysids, three isopods, one tanaidacean species, and one decapod species as an outgroup, using the concatenated sequences of 11 protein-coding genes. According to traditional morphological classification, Peracarida includes Cumacea, Isopoda, Tanaidacea, Mysida, Amphipoda, and other related groups. Our molecular phylogenetic analysis supports the phylogenetic position of Cumacea within Peracarida, consistent with traditional morphological classifications (Figure 3). To our knowledge, this is the first report of the mitochondrial genome of a cumacean species. This report not only provides novel molecular data for *D. asiatica* but also enhances the understanding of the phylogeny and evolution within the Curstacean group.

Author contributions

Jiseon Park analyzed the mitogenome sequence and writing draft. Sung-Hyun Kim conducted collecting the specimen, species identification, and writing draft. Taeseo Park conducted collecting the specimen and revising manuscript. Jongwoo Jung contributed conception, designing this study, and revising manuscript.

Ethical approval

The material of this paper does not involve ethical conflicts. *Dimorphostylis asiatica* is neither endangred on the CITES catalog nor collected from a natural reserve.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank (National Center for Biotechnology Information) at https://www.ncbi.nlm.nih.gov, accession no. MZ240751. The associated BioProject, SRA, and BioSample numbers are PRJNA732591, SRR14695635, and SAMN19459914, respectively. The data that support the findings of this study are openly available in Mendeley (https://doi.org/10.17632/wgydvkcw2v.1).

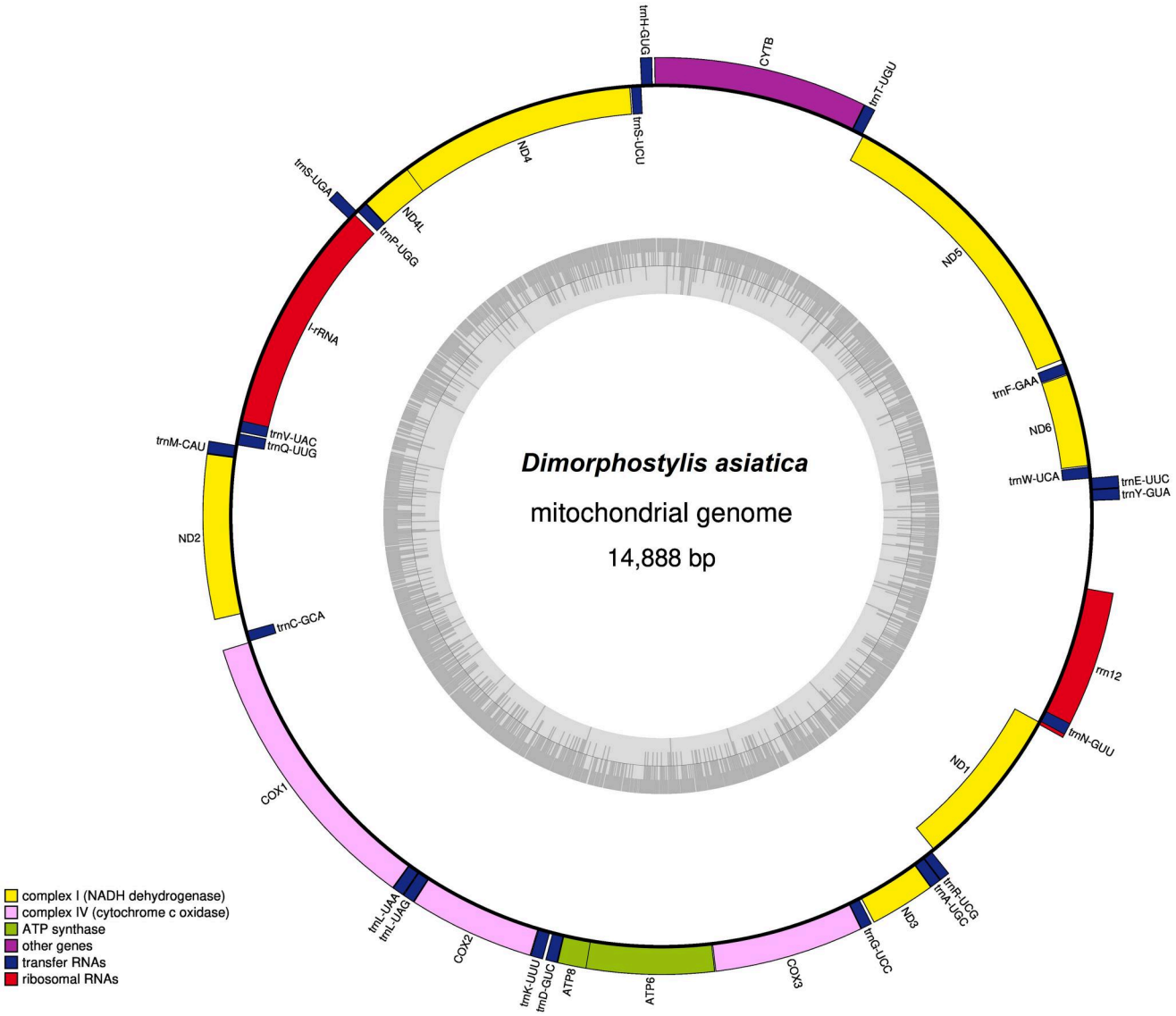


Figure 2. Schematic map of overall features of the *Dimorphostylis asitica* mitochondrial genome.

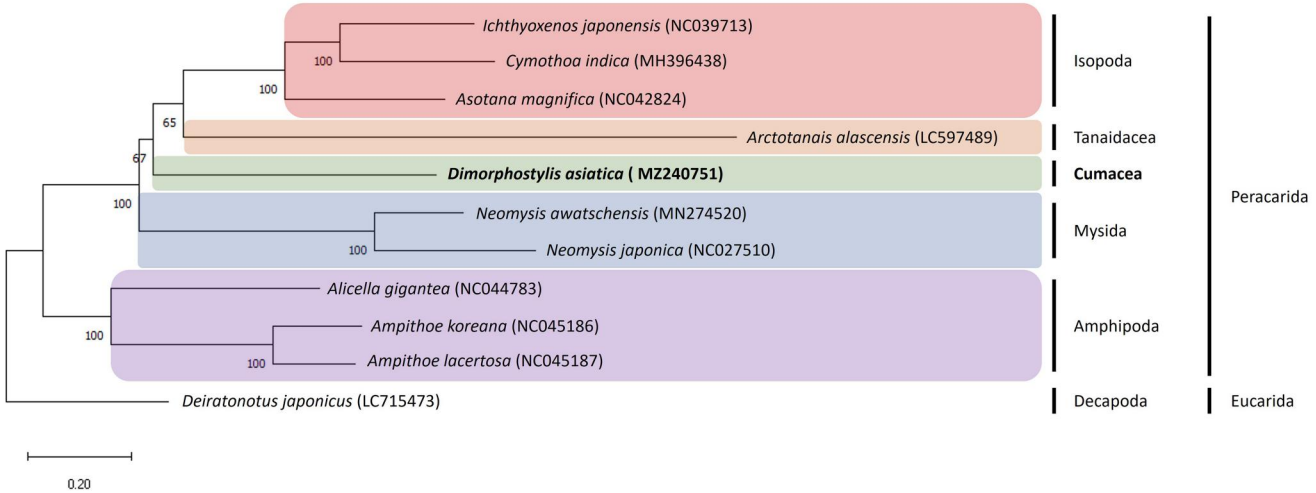


Figure 3. Maximum likelihood (ML) tree reconstructed using concatenated data set of 13 protein-coding genes based on 11 mitogenome sequences including *Dimorphostylis asiatica* from the present study. The GenBank accession number of each species is enclosed in parentheses after the species name. The following sequences were used: *Dimorphostylis asiatica* MZ240751 (Unpublished, this study), *Ichthyoxenos japonensis* NC039713 (Unpublished), *Cymothoa indica* MH396438 (Unpublished), *Asotana magnifica* NC042824 (Unpublished), *Arctotanais alascensis* LC597489 (Kakui and Kano 2021), *Neomysis awatschensis* MN274520 (Choi et al. 2019), *Neomysis japonica* NC027510 (Song et al. 2016), *Alicella gigantea* NC044783 (Li et al. 2019), *Ampithoe koreana* NC045186 (Lee et al. 2019b), *Ampithoe lacertosa* NC045187 (Lee et al. 2019a), and *Deiratonotus japonicus* LC715473 (Kobayashi et al. 2023).

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