The first complete mitochondrial genome of *Notostomus gibbosus* (Caridea, Acanthephyridae)

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**ABSTRACT**

*Notostomus gibbosus* is a deep-sea shrimp, belonging to Caridea, Acanthephyridae. The whole complete mitochondrial genome of *N. gibbosus* was 17,956 bp in length, with 37 genes, containing 13 protein-coding genes, 22 tRNAs, and 2 rRNAs. The GC content of *N. gibbosus* was 39.43%. The genomic structure and gene arrangement were identical to those of Caridea species. The phylogenetic analysis of 13 protein-coding genes showed a close relationship to the genera Acanthephyra.

*Notostomus gibbosus* A. Milne-Edwards, 1881 (Caridea: Acanthephyridae) is a typical deep-sea shrimp ubiquitous in the global ocean (De Grave 2011; WoRMS 2020). This species is famous for its positive buoyancy, using ion replacement to balance body density (Sanders and Childress 1988). *Notostomus gibbosus* has a red soft integument, no cuticular photophores, and small eyes (Chan et al. 2010; Wong et al. 2015). The strengthened carapace and half-serrated mandible of *N. gibbosus* are well adapted to feeding on gelatinous organisms, such as deep-sea fishes (Lunina et al. 2020). *Notostomus gibbosus* contribute significantly to the bathypelagic food web and ecosystem function because of its widespread distribution and large individual biomass (Burghart et al. 2010). More than 52 complete mitochondrial genomes of Caridea have been determined till now (Sun et al. 2020). However, it remains unknown in the genus *Notostomus*. In this study, we reported the first complete mitochondrial genome of *N. gibbosus* and analyzed its phylogenetic relationship among Caridea.

A specimen of *N. gibbosus* was collected in January 2019 from the Indian Ocean (16.96ºS, 89.69ºE). The voucher specimen was stored in Key Laboratory of Science and Engineering for Marine Ecology and Environment, First Institute of Oceanography, MNR (Yuan Chao, yuanchao@fio.org.cn, under the voucher number FIO-ECH-DYS2DQSP02). Genomic DNA was extracted from the muscles using a QIAamp Fast DNA Tissue kit (Qiagen, Germany) according to the manufacturer’s instructions. A genomic library was then constructed. The mitochondrial genome of *N. gibbosus* was sequenced on the Illumina HiSeq 2500 sequencing platform (Illumina, USA) by Novogene Corporation (Beijing, China). The clean data were then assembled using the NOVOPlasty (Dierckxsens et al. 2017). This mitochondrial genome was annotated by MITOS2 and GeSeq (Tillich et al. 2017; Donath et al. 2019). The information of this mitochondrial genome was submitted to Genbank and the accession number is MW479468.

The circular mitochondrial genome of *N. gibbosus* was 17,956 bp in length with 39.43% GC content and contained 37 genes, including 13 protein-coding genes, 2 ribosomal RNA genes, and 22 transfer RNA genes. The composition and arrangement of genes were identical to those of other deep-sea Caridea shrimps. Our 16S rDNA and/or COI sequence were more than 99.5% identical to those of the partial sequence of *N. gibbosus* collected from the Gulf of Mexico (536 bp of 16S rDNA, Genbank accession number of MF197201 and 660 bp of COI, Genbank accession number of MH572548), and Taiwan waters (771 bp of 16S rDNA, Genbank accession number of GQ131894) (Chan et al. 2010).

Phylogenetic relationships between *N. gibbosus* and 12 other Caridea shrimps, as well as one outgroup from the genus *Litopenaeus*, were analyzed using the maximum-likelihood method by IQTREE (Nguyen et al. 2015). Although data from Caridea mitochondrial genome were lacking, phylogenetic analysis established by 13 protein-coding genes resolved a close relationship of *N. gibbosus* to the genera Acanthephyra, together which formed a distinct group to the genera Rimicaris, then to the genera Typhlatya and Cardina in superfamily Atyoidae (Figure 1). This study provided important information for further evolutionary and phylogenetic study of *Notostomus*.
Disclosure statement

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the paper.

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Data availability statement

The raw data that support this study are openly available in SRA of NCBI under accession no. PRJNA728383. The genome sequence data are deposited in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/nuccore under the accession no. MW479468.

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