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The complete linear mitochondrial genome of the hydrozoan jellyfish *Cladonema multiramosum* Zhou et al., 2022(Cnidaria: Hydrozoa: Cladonematidae)

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ABSTRACT

In this study, we sequenced and analyzed the complete mitochondrial genome of *Cladonema multiramosum* Zhou et al., 2022 from Fujian, China. The length of the linear mitochondrial genome is 15164 bp, containing 13 protein-coding genes (*cox2, atp8, atp6, cox3, nad2, nad5, nad6, nad3, nad4L, nad1, nad4, cob, cox1*), two tRNAs (*trnM* and *trnW*) and 2 rRNAs (12S and 16S). The arrangement of mitogenomes show some little differences in different hydrozoan groups. The phylogenetic analysis of 13 protein coding genes (PCGs) in Cnidarians showed that *C. multiramosum* was closely related to *Cladonema pacificum*.

Unlike other hydromedusae, *Cladonema* medusae prefer to stay on substrates with adhesive tentacles, resulting in their absence in conventional zooplankton samples (Schuchert 2006). Although *Cladonema* medusae are easily overlooked in marine ecological investigations, *Cladonema pacificum* and *Cladonema radiatum* have been used as model organisms to research biological development (e.g., branching morphogenesis and eye development), regeneration and evolution (Graziussi et al. 2012; Fujiki et al. 2019; Fujita et al. 2019, 2021). *Cladonema* polyps could be divided into two groups in morphology, one has an aboral whorl of filiform tentacles while the other lacks them (Zhou et al. 2022). According to the phylogenetic tree based on 16S rRNA, *Cladonema* polyps with filiform tentacles form a clade and emerge as a sister group of *C. pacificum* that lacks filiform tentacles (Zhou et al. 2022). Thus, the appearance or disappearance of filiform tentacles in polyps might be related to the phylogeny within the genus *Cladonema*. At present, only the mitochondrial genome of *C. pacificum* has been reported in the genus *Cladonema* (Kayal et al. 2015). Thus, we report the complete mitochondrial genome of *Cladonema multiramosum*, which owns filiform tentacles (Zhou et al. 2022), to provide a robust resource to understand phylogenetic relationship of *Cladonema* species.

The medusae of *C. multiramosum* were collected from an *Oryzias melastigma* aquarium in Dr Chen's lab in the Institute of Oceanography, Minjiang University, Fuzhou, China (26°4′19.24″N, 119°10′46.76″E) in February 2020. The voucher specimens were deposited at Dr. Chen's lab (contact Chen Liang by email: chanleeon@mju.edu.cn) under the voucher number MJU-HYD-1–4. The DNA was extracted from a pool of five medusae using a DNeasy Blood & Tissue Kit (QIAGEN, QIAGEN GmbH, Hilden, Germany) according to the manufacturer's instructions. The sequencing of *C. multiramosum* mitogenome was carried out with an Illumina NovaSeq 6000 platform (paired-end 150 bp reads, 10 Gb in total) at Novogene Co., Ltd. (Beijing, China). The remaining part of the DNA was deposited in Dr. Chen's lab with a unique code (DNA-CM1). *De novo* assembly was conducted using Getorganelle v1.7.1 (Jin et al. 2020). Then, the mitochondrial genome was annotated preliminary in MITOS2 Web Server (http://mitos2.bioinf.uni-leipzig.de/index.py) (Bernt et al. 2013) and tRNAscan-SE v2.0 (Lowe and Eddy 1997). To ensure the accuracy of the annotation, the open reading frames of 13 protein coding genes (PCGs) were check by DNASTAR Lasergenev7.1 (Burland 2000), and then all the annotated genes were confirmed using NCBI-BLAST (http://blast.ncbi.nlm.nih.gov). The annotated mitochondrial genome was deposited in GenBank with the accession number MZ747707. *C. multiramosum* is an invertebrate animal, and is neither endangered or protected species, meeting the needs of ethical approval.

The complete linear mitochondrial genome of *C. multiramosum* was 15164 bp in length and was highly AT-biased (A: 31.0%; T: 40.7%; C: 13.5%; G: 14.8%). The *C. multiramosum* mitogenome contained 13 PCGs (*cox2, atp8, atp6, cox3, nad2, nad5, nad6, nad3, nad4L, nad1, nad4, cob, cox1*), two tRNAs (*trnM* and *trnW*) and two rRNAs (12S and 16S rRNA). The arrangement of mitogenomes show some little differences in different hydrozoan groups (Kayal et al. 2015). But the order

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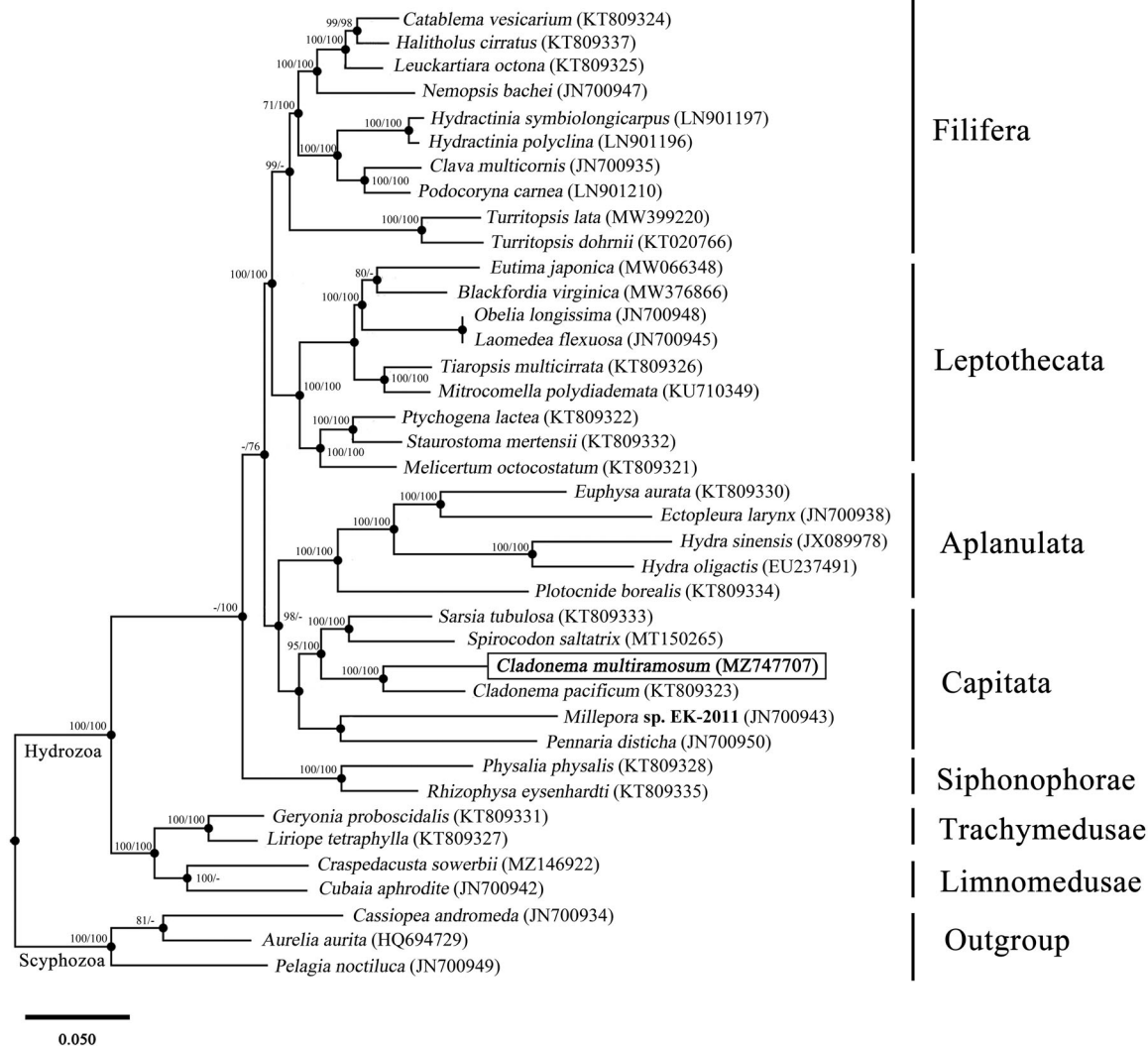
Figure 1. Maximum-likelihood phylogeny of 36 hydrozoans including *Cladonema multiramosum* and three scyphozoans (outgroup) based on the tandem nucleotide sequences of 13 mitochondrial protein-coding genes. Bootstrap values of 1000 pseudoreplicates higher than 70% were shown above the branches as node-support values. The first number at nodes refers to the maximum likelihood bootstrap values, while the second one refers to the neighbour-joining bootstrap values. The black rectangle indicates the species analyzed in this study.

of the 13 PCGs of *C. multiramosum* was the same as other known hydrozoan mitochondrial genomes (Seo et al. 2021).

The tandem sequences of 13 mitochondrial PCGs of 36 hydrozoan species and three scyphozoan species (outgroup) were used to infer the phylogenetic trees using maximum-likelihood (ML, based on GTR + G + I model) in PhyML 3.0 (Guindon et al. 2010) and neighbour-joining (NJ, based on the K2P model) in MEGA X (Tamura et al. 2011) with 1,000 bootstrap replicates. The ML topology showed that the *C. multiramosum* formed a sister relationship with *C. pacificum* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the author(s).

Author contributions

All the authors agreed to be listed and approved the submitted version of this manuscript. Xinyu Fang completed the analysis and manuscript, Konglin Zhou conducted experiments and revised the manuscript, Jianming Chen provided the funds and resource for this research.

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/nuccore/MZ747707 under the accession no.MZ747707. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA803599, SRX14160122, and SAMN25658255, respectively.

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