

Complete mitochondrial genome sequence of *Acromitus flagellatus* and its phylogenetic relationship with related jellyfish species

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ABSTRACT

This study describes the complete mitochondrial genome sequence of the scyphozoan *Acromitus flagellatus* (Maas, 1903), a blooming jellyfish found in the coastal areas of Hainan, China. Its mitochondrial DNA is 16,779 bp in length and has a linear structure, comprising 13 protein-coding genes (PCGs), two rRNAs (s-rRNA and l-rRNA), and two tRNAs (trna-W-TCA and trna-M-CAT). A +T content was 65.39% (A: 29.27%, C: 16.59%, G: 18.03%, and T: 36.12%). ATG was the start codon in 11 PCGs: *COX1*, *COX2*, *ATP8*, *ATP6*, *COX3*, *NAD2*, *NAD6*, *NAD4I*, *NAD1*, *NAD4*, and *COB*. *NAD5* and *NAD3* had GTG as the start codon. TAG was the stop codon for *COX2*, *NAD6*, and *COB*. The other 10 PCGs were terminated by TAA. The neighbor-joining phylogenetic tree of the 15 related jellyfish species showed that *A. flagellatus* is closely related to *Nemopilema nomurai* and *Rhopilema esculentum*.

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In recent decades, jellyfish blooms have frequently appeared in coastal seas worldwide (Condon et al. 2013). Jellyfish blooms cause serious damage to coastal economic development and marine ecosystem, and pose a challenge to human safety (Purcell 2007; Richardson et al. 2009). Extensive studies have examined the mechanisms of jellyfish blooms by focusing on understanding the eco-physiological characteristics of their life cycle stages (Lucas et al. 2012; Purcell 2012; Pitt et al. 2018). However, few studies have focused on the molecular phylogenetic relationships among jellyfish species based on their mitochondrial genomes (Zou et al. 2012; Hwang et al. 2014; Feng et al. 2019). This is important as it may provide insight into the similarity between different species of jellyfish.

The scyphozoan *Acromitus flagellatus* (Maas, 1903) belongs to Catostylidae (Family) under the Suborder Dactyliophorae. In recent years, medusae of *A. flagellatus* appeared in large numbers in the coastal waters of Hainan Province, China, from April to June (Du et al. 2021). To determine the molecular phylogenetic relationships between *A. flagellatus* and other jellyfish, its complete mitochondrial DNA was sequenced. An *A. flagellatus* medusa was collected from the eastern coast of Hainan Province (19.57° N, 110.83° E) and frozen in an ice box containing dry ice. The sample was then transferred to a –80 °C freezer at the Institute of Oceanology, Chinese Academy of Sciences (<http://english.qdio.cas.cn/>, Song Feng: fengsong@qdio.ac.cn) under the voucher ‘A.

flagellatus ①.’ A piece of muscle tissue from *A. flagellatus* medusa was used for extraction of mitochondrial DNA. The extracted DNA was also stored in a –80 °C freezer, as described above, for sequencing (voucher: DNA-A. *flagellatus* ①).

The complete mitochondrial genome of *A. flagellatus* showed a linear molecular structure with a length of 16,779 bp (GenBank accession no. OM457248.1). There were 13 protein-coding genes (PCGs), small and large subunit ribosomal RNAs (s-rRNA and l-rRNA), and methionine and tryptophan transfer RNAs (trna-W-TCA and trna-M-CAT) in the mitochondrial genome. The base composition was 29.27%, 18.03%, 16.59%, and 36.12% for A, G, C, and T, respectively. A +T base composition was less than 70% (65.39%), similar to that in *Nemopilema nomurai* and *Rhopilema esculentum* (Wang and Sun 2017a, 2017b).

Of the 13 PCGs in *A. flagellatus* mitochondrial genome, 11 started with ATG (*COX1*, *COX2*, *ATP8*, *ATP6*, *COX3*, *NAD2*, *NAD6*, *NAD4I*, *NAD1*, *NAD4*, and *COB*). Only *NAD5* and *NAD3* had GTG as the start codon. Complete stop codons were present in all the genes. TAG was the stop codon for *COX2*, *NAD6*, and *COB*. The other 10 PCGs terminated with TAA as the stop codon. The neighbor-joining phylogenetic tree of 15 jellyfish species constructed using the complete mitochondrial genome from NCBI (Figure 1), showed that *A. flagellatus* was closely related to *N. nomurai* (GenBank no. KY454767.1) and *R. esculentum* (GenBank no. NC_035741.1).

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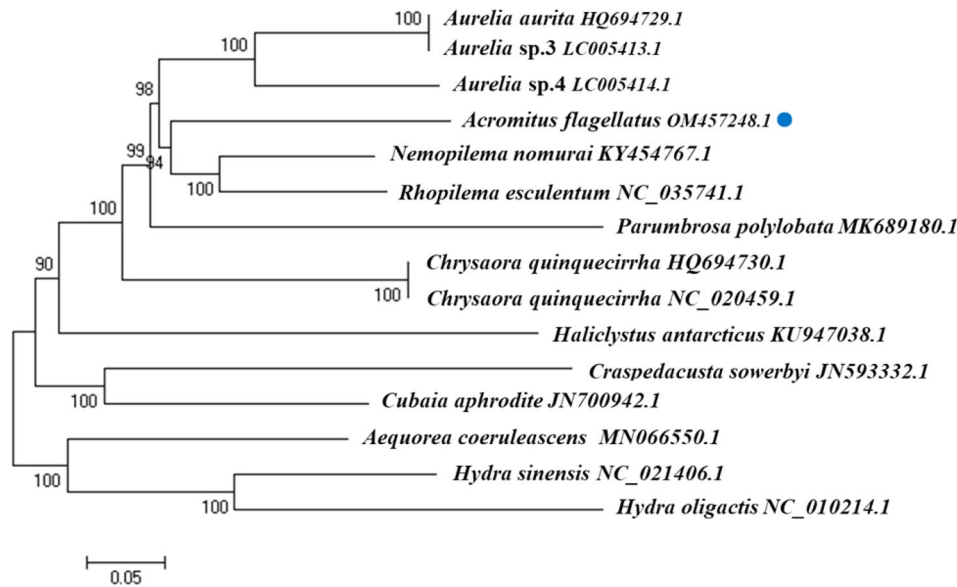


Figure 1. Phylogenetic relationship revealed by neighbor-joining tree.

Ethical approval

The experiments were performed in accordance with the recommendations of the Ethics Committee of the Institute of Oceanology, Chinese Academy of Sciences. These policies were enacted in accordance with the Guide for the Care and Use of Laboratory Animals of the Chinese Association for Laboratory Animal Sciences (No. 2011-2). Permission was granted by the National Natural Science Foundation of China, Natural Science Foundation of Shandong Province, and Fundamental Research Funds of Shandong University.

Author contributions

SF and LW designed the study. QY collected the jellyfish samples and JL conducted the experiments. SF and LW analyzed the data. JL wrote the manuscript with the help of SF and LW.

Disclosure statement

The authors report no conflict of interest.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank (<https://www.ncbi.nlm.nih.gov/>) accession no. OM457248.1. The associated BioProject, SRA, and Bio-Sample numbers were PRJNA817707, SRR18358023, and SAMN26806304, respectively.

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