



Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

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To cite this article: Alireza Asem, Hao Lu, Pei-Zheng Wang & Weidong Li (2019) The complete mitochondrial genome of *Sinularia ceramensis* Verseveldt, 1977 (Octocorallia: Alcyonacea) using next-generation sequencing, *Mitochondrial DNA Part B*, 4:1, 815-816, DOI: [10.1080/23802359.2019.1574678](https://doi.org/10.1080/23802359.2019.1574678)

To link to this article: <https://doi.org/10.1080/23802359.2019.1574678>



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Published online: 09 Feb 2019.




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The complete mitochondrial genome of *Sinularia ceramensis* Verseveldt, 1977 (Octocorallia: Alcyonacea) using next-generation sequencing

Alireza Asem^a , Hao Lu^b, Pei-Zheng Wang^a and Weidong Li^a

^aCollege of Life Sciences and Ecology, Hainan Tropical Ocean University, Sanya, China; ^bCollege of Ocean, Hainan University, Haikou, China

ABSTRACT

The complete mitochondrial genome of *Sinularia ceramensis* was completed using next-generation sequencing (NGS) method. The mitochondrial genome is a circular molecule of 18,740 bp in length. The gene arrangements including 14 protein-coding genes (PCGs), 2 rRNAs, and 1 tRNA (tRNA-Met). The base composition is 30.26% A, 16.44% C, 16.35% G, and 33.95% T, with a G + C content of 35.76%. According to the phylogenetic analysis, Alcyonacea family are clustered in different clades.

ARTICLE HISTORY

Received 23 December 2018
Accepted 15 January 2019

KEYWORDS

Mitogenome; soft coral; *Sinularia ceramensis*; protein-coding genes; transfer RNA genes; ribosomal RNA genes

The genus *Sinularia* May, 1898 is one of the most pervasive Indo-Pacific soft corals that has been settled in wide range of habitats (Fabricius and Alderslade 2001). So far, the complete mitogenome of two species of *Sinularia* consisting of *Sinularia peculiaris* (JX023274 and NC_018379) and *Sinularia* cf. *cruciate* (KY462727 and NC_034318) have already been performed. In the present study, the complete mitochondrial genome of *Sinularia ceramensis* Verseveldt, 1977 (GenBank: MK292119) was sequenced using next-generation sequencing.

An individual of *S. ceramensis* was collected from the South China Sea (Sanya, Hainan province, China; 18° 14' 5.93" N, 109° 22' 46.46" E) and stored in Hainan Tropical Ocean University Museum of Zoology. The specimen was identified using PuCAs- *mtMutS* (Benayahu et al. 2018). The genomic DNA was extracted by Rapid Animal Genomic DNA Isolation Kit (Sangon Biotech Co., Ltd., Shanghai, CN; NO. B518221). A genomic library was constructed followed by paired-end (2 × 150 bp) next-generation sequencing, using the Illumina HiSeq X-ten sequencing platform (Tianjin, China). Quality checks for sequencing reads were carried out by FastQC (Andrews 2010) and the sequences were assembled and mapped to the reference *Sinularia* mitochondrial genome (*Sinularia peculiaris*, JX023274) with Spades v3.9.0 (Bankevich et al. 2012) and bowtie v2.2.9 (Langmead and Salzberg 2012). Putative tRNA gene was determined using ARWEN (<http://130.235.46.10/ARWEN/>) online software. All genes were annotated based on gene order on the reference mitochondrial map using BLAST analysis (<https://blast.ncbi.nlm.nih.gov>).

In addition, to annotate PCGs, the position of start and stop codons were re-considered.

The complete mitogenome of *S. ceramensis* was 18,740 bp in length with 14 protein-coding genes (PCGs), 2 ribosomal RNAs (rRNAs), and 1 transfer RNA (tRNA-Met). The overall nucleotide composition of the major strand of the *S. ceramensis* mitogenome was as follows: 30.26% A, 16.44% C, 16.35% G, and 33.95% T, with a total G + C content of 35.76%.

The tRNA-Met and four protein-coding genes (*COX3*, *ATP6*, *ATP8*, and *COX2*) were located on the light strand. All PCGs began with common ATG start codon. Stop codons included TAG (*ND1*, *ND6*, *ND3*, *ND2*, *ND5*, *COX3*, and *COX2*), TAA (*CYTB*, *ND4L*, *mutS*, *ND4*, *ATP6*, and *ATP8*) and non-complete codons T- (*COX1*).

The 12S ribosomal RNA and 16S ribosomal RNA were encoded on the heavy strand from 1583 to 2633 (1051 bp) and 9157 to 11124 (1968 bp), respectively, with 12S having a rather lower A + T content (56.61% vs. 58.49%). The longest gap but a single overlap were determined between *COX2/COX1* (112 bp) and *ND2/ND5* (–13 bp), respectively.

The phylogenetic relationship of *S. ceramensis* among order Alcyonacea was performed from a concatenated dataset consisting of the 14 PCGs and 2 rRNAs using the software MEGA 7.0.26 v. (Kumar et al. 2016) with 1000 bootstrap replicates and GTR model (Figure 1). According to the result, Alcyoniidae was divided into three separated clades while families Gorgoniidae, Briareidae, and Coralliidae were placed between Alcyoniidae clades. A comprehensive taxonomical

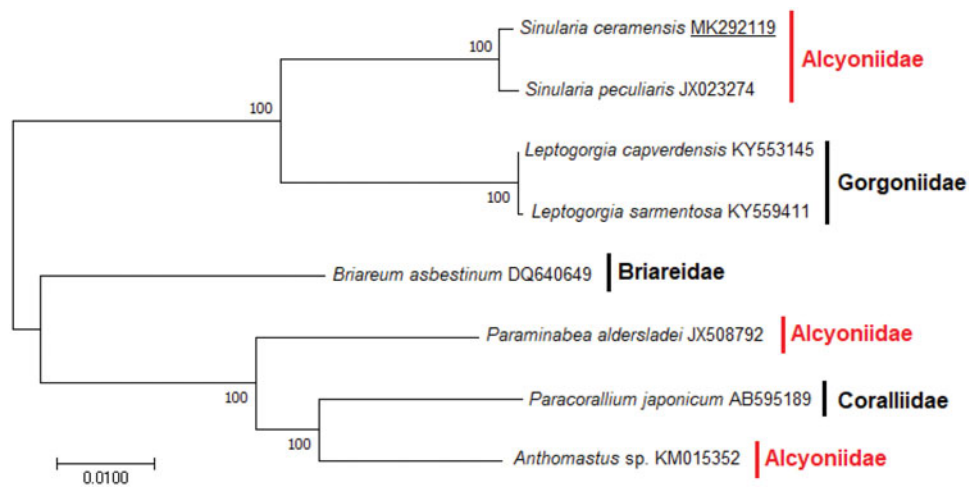


Figure 1. Phylogenetic tree showing the relationship among *S. ceramensis* and other members of order Alcyonacea based on maximum-likelihood (ML) approach. Numbers behind each node denote the bootstrap support values. The GenBank accession numbers are indicated on the right side of species names.

status of Alcyoniidae family needs to revise using whole mitochondrial genome sequences.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the manuscript.

Funding

This project was funded by a cooperative agreement provided by the Science and Technology Major Project of Hainan Province under [Grant ZDKJ2016009-3], Hainan Tropical Ocean University Doctoral Research Funding [RHDXB201628], Science and Technology Cooperation Fund of College and Local Government in SanYa City [2017YD01].

ORCID

Alireza Asem  <http://orcid.org/0000-0002-8991-4903>

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