


The complete mitochondrial genome of *Sinularia maxima* Verseveldt, 1971 (Octocorallia: Alcyonacea) using next-generation sequencing

You Chen^a, Ya-Ting Dan^b, Hao Lu^c, Pei-Zheng Wang^a, Alireza Asem^b  and Weidong Li^b

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

ABSTRACT

The mitochondrial genome of *Sinularia maxima* was completed using next-generation sequencing (NGS) method. The mitochondrial genome is a circular molecule of 18,730 bp in length. The gene arrangements include 14 protein-coding genes (PCGs), 2 ribosomal RNA genes, and 1 tRNA (*tRNA-Met*). The base composition is 30.18% A, 16.47% C, 19.35% G, and 33.99% T, with an A+T content of 64.18%. With regard to the phylogenetic analysis, members of genus *Sinularia* were clustered in different clades.

ARTICLE HISTORY

Received 20 September 2019
Accepted 25 September 2019

KEYWORDS

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

The genus *Sinularia* May, 1898 is one of the most widespread Octocorallia soft corals has been distributed in a wide range of habitats (Fabricius and Alderslade 2001). To date, the complete mitogenome of three species of *Sinularia* including *Sinularia ceramensis* (MK292119), *Sinularia* cf. *cruciata* (NC_034318) and *Sinularia peculiaris* (NC_018379) have been sequenced. In the present study, the complete mitochondrial genome of *Sinularia maxima* Verseveldt, 1971 (GenBank: MN485891) was analyzed using next-generation sequencing.

A specimen of *S. maxima* was collected from the South China Sea (West Island, Sanya, Hainan province, China; 18°14' 8.75"N, 109° 22'39.10" E) and stored in Hainan Tropical Ocean University Museum of Zoology (NO.0001-Sm). Taxonomical status of the specimen was identified by PuCAs-*mtMutS* (Benayahu et al. 2018) and PuCAs-28S (Quattrini et al. 2019). The whole DNA was extracted using Rapid Animal Genomic DNA Isolation Kit (Sangon Biotech Co., Ltd., Shanghai, CN; NO. B518221). A genomic library was made by paired-end (2 × 150 bp) next-generation sequencing, using the Illumina HiSeq X-ten sequencing platform (Asem et al. 2019). FastQC programme was utilized to check quality of sequencing reads (Andrews 2010) and the sequences were annotated and assembled to the *Sinularia* mitochondrial genome (*Sinularia ceramensis*, MK292119) with Spades v3.9.0 (Bankevich et al. 2012) and bowtie v2.2.9 (Langmead and Salzberg 2012). Putative tRNA gene was established 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>).

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

The complete mitogenome of *S. maxima* was 18,730 bp in length, with 14 protein-coding genes (PCGs), two ribosomal RNAs (rRNAs) and one transfer RNA (*tRNA-Met*). We found that *tRNA-Met* can be folded into typical clover-leaf secondary structures with 46.6% of GC content. The overall nucleotide composition of the major strand of the *S. maxima* mitogenome was as follows: 30.18% A, 16.47% C, 19.35% G, and 33.99% T, with a total A+T content of 64.18%.

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

The 12S ribosomal RNA and 16S ribosomal RNA were encoded on H strand from 1583 to 2633 (1051 bp) and 9147 to 11115 (1969 bp), respectively, with 12S having a rather higher G+C content (43.58% vs. 41.24%). A single overlap and the longest gap were found between and *ND2/ND5* (−13 bp) and *COX2/COX1* (112 bp), respectively.

A phylogenetic analysis of four completed *Sinularia* mitogenomes was established based on and an outgroup (*Leptogorgia capverdensis*, KY553145). The concatenated dataset for nucleotides contained 14 PCGs and two ribosomal RNAs. The maximum-likelihood (ML) phylogenetic analysis was performed using the software MEGA X (Kumar et al. 2018). Regarding phylogenetic tree, *Sinularia* is divided into

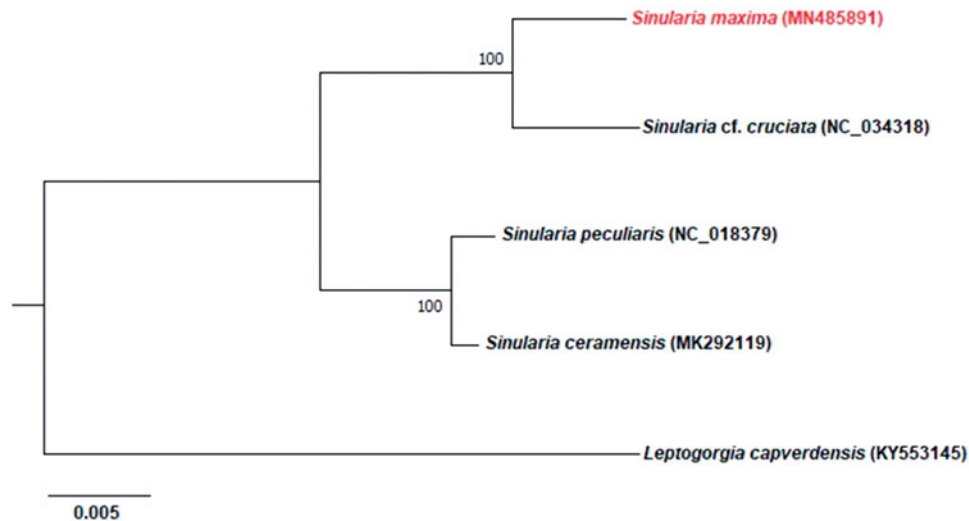


Figure 1. Phylogenetic tree showing the relationship among *S. maxima* and other members of order genus *Sinularia* based on maximum-likelihood (ML) approach. Numbers behind each node denote the bootstrap support values. The GenBank accession numbers are indicated on the right side of species names.

two clads including *Sinularia cf. cruciata* + *Sinularia maxima* and *Sinularia peculiaris* + *Sinularia ceramensis* (Figure 1).

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 Hainan Province Science and Technology Department Key Research and Development Programme [ZDYF2019154], and the Science and Technology Major Project of Hainan Province under [ZDKJ2016009-3].

ORCID

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

References

- Andrews S. 2010. FastQC: A quality control tool for high throughput sequence data [accessed 2018 Oct 4]. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>.
- Asem A, Lu H, Wang P, Li W. 2019. The complete mitochondrial genome of *Sinularia ceramensis* Verseveldt, 1977 (octocorallia: Alcyonacea) using next-generation sequencing. *Mitochondr DNA B*. 4: 815–816.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol*. 19:455–477.
- Benayahu Y, van Ofwegen LP, Dai C-F, Jeng MS, Soong K, Shlagman A, Du SW, Hong P, Imam NH, Chung A, et al. 2018. The octocorals of Dongsha Atoll (South China Sea): an iterative approach to species identification using classical taxonomy and molecular barcodes. *Zool Stud*. 57:50.
- Fabricsius K, Alderslade P. 2001. Soft corals and sea fans: a comprehensive guide to the tropical shallow-water genera of the Central-West Pacific, the Indian Ocean and the Red Sea. Townsville: Australian Institute of Marine Science.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol*. 35:1547–1549.
- Langmead B, Salzberg S. 2012. Fast gapped-read alignment with Bowtie 2. *Nat Methods*. 9:357–359.
- Quattrini AM, Wu T, Soong K, Jeng M-S, Benayahu Y, McFadden CS. 2019. A next generation approach to species delimitation reveals the role of hybridization in a cryptic species complex of corals. *BMC Evol Biol*. 19:116.