

The complete mitochondrial genome of soft coral *Sinularia penghuensis* Ofwegen and Benayahu, 2012 (Octocorallia: Alcyonacea): the analysis of mitogenome organization and phylogeny

Chun-Yang Shen^a, Pei-Zheng Wang^b, Wei Xue^c, Zhao-Hui Liu^a, Jing-Yi Zhao^d, Xiao-Bo Tong^e, Chunwei Liu^b, Xiao-Fang Wu^b, Xiaonan Mao^a, Sihang Tian^a and Chunzheng Fu^f

^aDepartment of Biology, Chengde Medical University, Hebei Province, Chengde, PR China; ^bCollege of Ecology and Environment, Hainan Tropical Ocean University, Sanya, PR China; ^cDepartment of Chemical Engineering, Chengde Petroleum College, Chengde, PR China; ^dDepartment of Functional Center, Chengde Medical University, Hebei Province, Chengde, PR China; ^eHemorheology Center, Chengde Medical University, Hebei Province, Chengde, PR China; ^fInstitute of Sericulture, Chengde Medical University, Hebei Province, Chengde, PR China

ABSTRACT

The complete mitochondrial genome of *Sinularia penghuensis* was sequenced and analyzed using next-generation sequencing. The present mitochondrial genome was 18730 bp in length, containing 14 protein-coding genes (PCGs) (*cox1-cox3.nad1-nad6, nad4L, atp6, atp8, cytb, and MutS*), two ribosomal RNA genes (*rRNAs*) (*12S* and *16S*), and one transfer RNA gene (*Met-tRNA*). The phylogenetic analysis of family Alcyoniidae revealed that *S. penghuensis* and *Sinularia maxima* cluster together. Five species in *Sinularia* reveals high identity in mitogenome sequences that the lowest variable sites (SNPs) were found between *S. penghuensis* and *S. maxima*.

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Coral ecosystem is not only the largest ecosystem in the ocean, but it is the most complex aquatic ecosystem. Coral reefs provide the highest biodiversity in all marine ecosystems (Baums 2008; Keller et al. 2017). Genus *Sinularia* is the largest genus of the family Alcyoniidae with approximately 170 species. *Sinularia* contain compounds with unique structure and bioactivity, which makes it an important natural resource (Lakshmi and Kumar 2009). *Sinularia penghuensis* is usually in greenish brown or turquoise gray color, grows on the reef platform or slope with a depth of 3–15 m, and it also distributed in the sea area with slightly turbid water quality.

In this study, the complete mitochondrial genome (mitogenome) of *S. penghuensis* Ofwegen and Benayahu, 2012 (GenBank: MW256412) was sequenced using next-generation sequencing. The specimen of *S. penghuensis* was collected from the coral reef in West Island (Sanya, Hainan province, China; 18° 14' 5.93" N, 109° 22' 46.46" E), and deposited at Hainan Tropical Ocean University Museum of Zoology (www.hntou.edu.cn, Pei-Zheng Wang, condywpz@126.com) under the voucher number NO. 0007-Sp). The identification of the specimen was performed using PuCAs-mtMutS and PuCAs-28S. The total genomic DNA was extracted and used for sequencing on Illumina HiSeq 4000 platform (Novogene: Tianjin, China).

10G raw data was obtained followed by *de novo* assembling and mapping to the reference *Sinularia* mitochondrial genome (*Sinularia ceramensis*, NC_044122) with Spades version 3.9.0 (Bankevich et al. 2012) and bowtie version 2.2.9 (Langmead and Salzberg 2012). Protein-coding genes (PCGs) and ribosomal RNA genes (rRNAs) were annotated using alignment with a large number of Alcyonacea mitogenome available in genbank and the online gene detection server NCBI ORF Finder (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>). Position and secondary structure of transfer RNA gene (*tRNA*) was performed by online server tRNAscan-SE2.0 (<http://lowelab.ucsc.edu/tRNAscan-SE/>).

The complete mitogenome of *S. penghuensis* was 18,730 bp in size, with a base composition of 30.19% A, 34.00% T, 19.34% G, and 16.47% C. The base composition of the complete mitogenome reveals strong AT bias, the AT content of whole mitogenome was 64.19%, and AT content of PCGs, tRNA, and rRNAs were 65.50%, 54.93%, and 56.95%, respectively.

Totally 17 genes were detected on the mitogenome, including 14 PCGs, two rRNAs, and one tRNA. Four PCGs (*cox2, cox3, atp6, and atp8*) and the only tRNA gene (*tRNA-Met*) were located on the light strand and other genes (*cox1, cytb, nad1, nad2, nad3, nad4, nad4L, nad5, nad6, mutS, 12S, and 16S*) were encoded on the heavy strand. This species has

CONTACT Chun-Yang Shen  scyshenchunyang@yeah.net  condywpz@126.com

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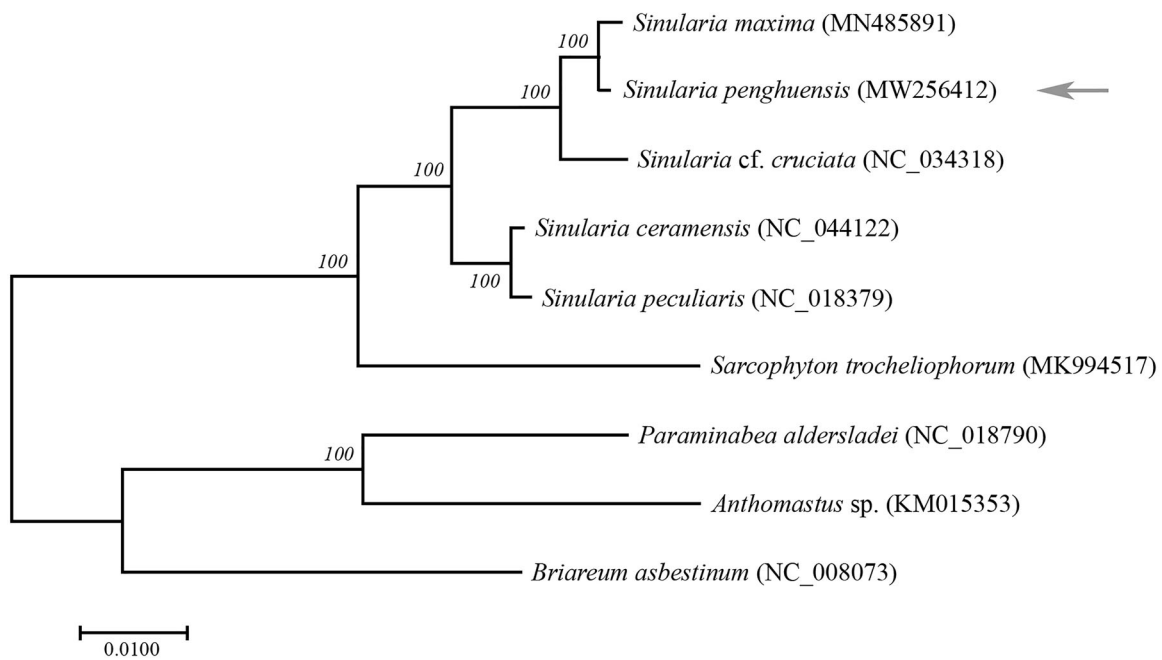


Figure 1. Phylogenetic tree showing the relationship among species of Alcyoniidae based on maximum-likelihood (ML) approach. Numbers behind each node denote the bootstrap support values. The arrow shows position of *S. penghuensis* in phylogenetic tree.

identical gene order with the other published mitogenome in *Sinularia*.

ATG was the only selected start codon among all PCGs. Eight genes (*nad1*, *cytb*, *nad6*, *nad3*, *nad2*, *nad5*, *cox3*, and *cox2*) were stopped by TAG, and five genes (*nad4L*, *mutS*, *nad4*, *atp6*, and *atp8*) use TAA as stop codon. *Cox1* was stopped by premature stop codon T, which was presumably to form TAA codon *via* posttranscriptional polyadenylation (Boore JL 2001). Only one tRNA, *tRNA-Met*, was detected that can be folded into typical clover-leaf secondary structures. Totally 15 intergenic regions were existed, which range from 4 to 112 nucleotides.

The new present mitogenome and all sequences mitogenomes in Alcyoniidae were used in phylogenetic analysis (Brockman and Mcfadden 2012; Kayal et al. 2013; Figueroa and Baco 2015; Shimpi et al. 2017; Asem et al. 2019; Chen et al. 2019; Shen et al. 2019), and *Briareum asbestinum* (Medina et al. 2006) was set for the outgroup. The concatenated dataset for nucleotides including all 14 PCGs and two rRNAs were performed to draw phylogenetic tree using the maximum-likelihood method (ML). The generate phylogenetic tree topology revealed that the species of genus *Sinularia* cluster together and divided with the *Sarcophyton*, and *S. penghuensis* has the most closed relationship with *Sinularia maxima* (Figure 1). The clade of (*S. penghuensis*+ *S. maxima*) + *Sinularia cf. cruciata* was sister with the other two *Sinularia* species (*Sinularia peculiaris* + *Sinularia ceramensis*). The sequences of mitogenomes in *Sinularia* species exhibited a high degree of consistency. The variable sites (SNPs) between *S. penghuensis* and other *Sinularia* species (*S. maxima*, *S. cruciata*, *S. ceramensis*, and *S. peculiaris*) were 53, 189, 381, and 391, respectively. It could be considered that *S. penghuensis* and *S. maxima* are the most closed species, which was consistent with the result of phylogenetic analysis.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>, reference number MW256412.

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