


Complete sequence of mitochondrial DNA of a deep-sea holothurian species of the genus *Synallactes* (Synallactida: Synallactidae)

Meijie Liao^{a,b} , Bin Li^{a,b}, Ning Xiao^{c,d,e}, Miao Kong^{a,b}, Yingeng Wang^{a,b}, Jinjin Wang^{a,b}, Xiaojun Rong^{a,b}, Zheng Zhang^{a,b} and Yongxiang Yu^{a,b}

^aYellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Qingdao, China; ^bQingdao National Laboratory for Marine Science and Technology, Laboratory for Marine Fisheries Science and Food Production Processes, Qingdao, China; ^cInstitute of Oceanology, Chinese Academy of Sciences, Qingdao, China; ^dLaboratory for Marine Biology and Biotechnology, Qingdao National Laboratory for Marine Science and Technology, Qingdao, China; ^eCenter for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao, China

ABSTRACT

One complete mitochondrial genome (mitogenome) was determined for a deep-sea holothurian species of the genus *Synallactes* (Synallactida: Synallactidae). The mitochondrial genome size of the sea cucumber was 15,920 bp. The sequence contains 2 ribosomal RNA genes (12S and 16S), 22 transfer RNA genes, and 13 protein-coding genes, as found in most previously determined holothurian mitogenomes. The A+T content of the complete mitochondrial genome sequence was 64.45%. The base composition showed a tendency of AT. The resulted maximum likelihood (ML) tree of Holothuroidea supported that *Synallactes* sp. is a species of Synallactida.

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In recent years, with the development of navigation technology, the resources of deep-sea species of Echinodermata have been discovered continuously, which proves that the Echinodermata are important dominant species in the deep-sea, and indicates that deep-sea echinoderms contain important anti-stress gene resources (Solís-Marín 2005; Xiao et al. 2018). Therefore, it is of great significance to explore the germplasm resources of Echinodermata, especially sea cucumbers (Holothuroidea), for the industrialization of sea cucumbers. Extant holothuroids fall into two main clades: Apodida and Actinopoda. Within the latter taxon, Pneumonophora and Elaspodida are recognized, as well as a series of smaller clades within Pneumonophora: Holothuriida and Neoholothuriida (containing Molpadida, Persiculida, Synallactida, and Dendrochirotida) (Miller et al. 2017). The recently named order Synallactida (Miller et al. 2017) includes the family Synallactidae Ludwig, 1894, which is one of the least studied groups of sea cucumbers (Gebbruk et al. 2012). Here, we sequenced the mitochondrial genomes (mitogenomes) of a deep-sea sea cucumber sample of the genus *Synallactes*. In order to provide theoretical basis and scientific guidance for the utilization and development of echinoderm resources in the deep sea, mitochondrial gene composition, biological evolution, and molecular identification were studied.

The sample of this experiment was collected by the 'KEXUE' marine scientific research vessel in 2014, which was built by the Institute of Oceanology, Chinese Academy of Sciences. The collection location was the western Pacific

Ocean (137°48'E, 8°54'N) with a water depth of 1062 m. The sample was deposited at the Marine Biological Museum (MBM), Institute of Oceanology of the Chinese Academy of Sciences (IOCAS), in Qingdao. The voucher number is MBM286683. Total DNA was extracted by using OMEGA Mollusk DNA Kit. The genome was sequenced by BGISEQ-500 method. The type of sequencing was PE100 and the length of the inserted fragment was 250 bp. The remaining reads were assembled using NOVOplasty. ORF Finder (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>) and BLASTx were used to determine the protein-coding genes (PCGs) using the invertebrate mitochondrial genetic code. The positions of transfer RNA (tRNA) genes were localized by ARWEN (Laslett and Canbäck 2008) and DOGMA (Wyman et al. 2004) using the invertebrate mitochondrial genetic code and the default search mode.

The complete mitogenome sequence was 15,913 bp in length submitted in GenBank (accession no. MT559281). The complete mitogenome contained 2 ribosomal RNA genes (12S and 16S), 22 tRNA genes, and 13 PCGs. The A+T content of the complete mitochondrial genome sequence was 64.45%. The base composition showed a tendency of high AT, which was similar with *Apostichopus japonicus* tested by Shen et al. (2009).

A maximum likelihood phylogenetic tree of nine species in the class Holothuroidea and the two-outgroup species was constructed based on the concatenated nucleic acid of 13 PCGs in Holothuroidea (Figure 1). The result supported that all the species of Synallactida formed a monophyletic clade

CONTACT Meijie Liao  liaomj@ysfri.ac.cn; Yingeng Wang  wangyg@ysfri.ac.cn  Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Qingdao, China

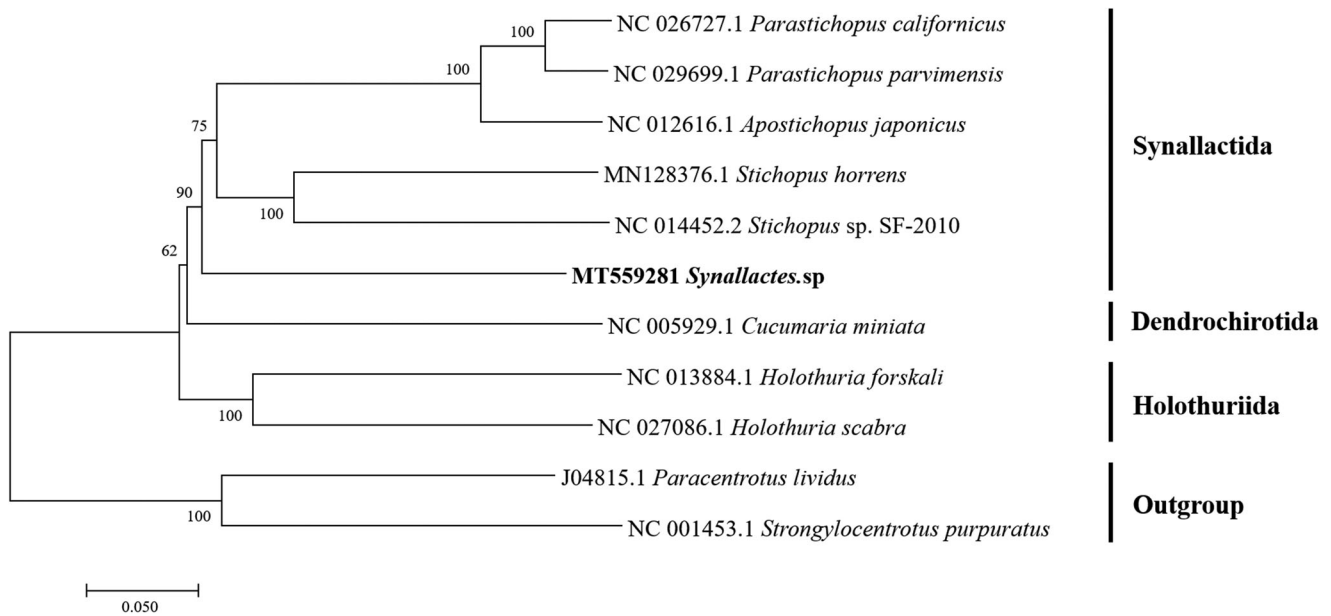


Figure 1. Phylogenetic trees based on the concatenated nucleic acid of 13 protein-coding genes. The branch lengths are determined with ML analysis.

and outgroup has a distant relationship with Synallactida, Dendrochirotida, and Holothuriida.

Disclosure statement

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

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ORCID

Meijie Liao  <http://orcid.org/0000-0002-9478-359X>

Data availability statement

The data that support the findings of this study are openly available in NCBI GenBank (<https://www.ncbi.nlm.nih.gov/>) with reference number [MT559281].

References

- Gebruk AV, Solis-Marín FA, Billett DSM, Rogacheva AV, Tyler PA. 2012. Review of the genus *Zygothuria* Perrier, 1898 and the Atlantic group of species of the genus *Mesothuria* Ludwig, 1894 (Synallactidae: Holothuroidea) with description of the new species *Mesothuria milleri* sp. nov. *J Nat Hist.* 46(5–6):265–348.
- Laslett D, Canbäck B. 2008. ARWEN: a program to detect tRNA genes in metazoan mitochondrial nucleotide sequences. *Bioinformatics.* 24(2): 172–175.
- Miller AK, Kerr AM, Paulay G, Reich M, Wilson NG, Carvajal JI, Rouse GW. 2017. Molecular phylogeny of extant Holothuroidea (Echinodermata). *Mol Phylogenet Evol.* 111:110–131.
- Shen X, Tian M, Liu Z, Cheng H, Tan J, Meng X, Ren J. 2009. Complete mitochondrial genome of the sea cucumber *Apostichopus japonicus* (Echinodermata: Holothuroidea): the first representative from the sub-class Aspidochirota with the echinoderm ground pattern. *Gene.* 439(1–2):79–86.
- Solis-Marín FA. 2005. *Synallactes laguardai*, a new species of sea cucumber from South Africa (Echinodermata: Holothuroidea: Synallactidae). *Proc Biol Soc Washington.* 118(3):570–575.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics.* 20(17):3252–3255.
- Xiao N, Li XM, Sha ZL. 2018. *Psychropotid holothurians* (Echinodermata: Holothuroidea: Elaspodida) of the tropical Western Pacific collected by the KEXUE expedition with description of one new species. *Mar Biol Res.* 14(8):816–826.