

## Characterization and phylogenetic analysis of the complete mitochondrial genome of a tropical sea cucumber, *Holothuria fuscocinerea*

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### ABSTRACT

In this study, the mitochondrial genome (mitogenome) of *Holothuria fuscocinerea* was unraveled to be 15,890 bp in length, containing 13 protein-coding genes (PCGs), 22 tRNA genes, and 2 rRNA genes. The PCGs were initiated by four initiation codons (ATG, TAC, ATC, and ATA). Only one PCG (*nad6*) and five tRNA genes (*tRNA<sup>Ser(UCN)</sup>*, *tRNA<sup>Gln</sup>*, *tRNA<sup>Ala</sup>*, *tRNA<sup>Val</sup>*, and *tRNA<sup>Asp</sup>*) were encoded on the light chain, and the other genes were encoded on the heavy chain. A phylogenetic tree constructed with 16S rRNA sequences showed that *H. fuscocinerea* is most closely related to *H. leucospilota*.

### ARTICLE HISTORY

Received 7 June 2020  
Accepted 20 June 2020

### KEYWORDS

Mitochondrial genome;  
*Holothuria fuscocinerea*;  
Phylogenetic analysis;  
16S rRNA

*Holothuria fuscocinerea* (Echinodermata: Holothuroidea, *H. fuscocinerea*) is naturally distributed near boulders, corals, and seaweed clumps in the West Pacific, East Africa, Australia, and Southeastern China (Liao 1997), and it might play important roles in maintaining a healthy coral reef ecosystem (Birkeland 1989; Schneider et al. 2011).




Compared with whole mitochondrial genes, a fragment of a single mitochondrial gene such as 16S rRNA can provide more information in terms of identification and evolution (Kerr et al. 2005; Byrne et al. 2010; Liu et al. 2016; Zou et al. 2017; Liu et al. 2018). The classification of sea cucumber from the mitochondrial genome (mitogenome) level would be more accurate than the aspect of phenotypic characteristics such as the morphology of the tentacles, the endoskeleton, and the calcareous ring (Liao 1997; Rowe and Richmond 2004).



*Holothuria fuscocinerea* was obtained from Daya Bay (N22°35', E114°31'), Shenzhen, Guangdong, China. The specimen was stored in the Marine Biotechnology and Disease Control Laboratory of the South China Sea at the Chinese Academy of Sciences in Guangzhou, China

(MBDC170711124). Total DNA was extracted and sent to BGI Genomics Co., Ltd., China, for sequencing. After aligning, splicing, correction, and identification of protein-coding genes and tRNA genes, the obtained mitogenome DNA sequence was analyzed by phylogenetic analysis.

The mitogenome of *H. fuscocinerea* (MK391177) show a double-strand molecule of 15,890 bp (33.1% A, 27.3% T, 23.9% C, and 15.7% G), including a set of 22 tRNA genes that varied from 61 bp (*tRNA<sup>Lys</sup>*) to 72 bp (*tRNA<sup>Leu(UUR)</sup>*) in length (the total length of tRNAs was 1,511 bp), 13 protein-coding genes that consisted of 3,690 codons, 2 rRNAs (*16S rRNA*: GC% = 38.07%, *12S rRNA*: GC% = 43.48%), and a putative noncoding control region between *tRNA<sup>Thr</sup>* and *tRNA<sup>Pro</sup>* (GC% = 59.01%).

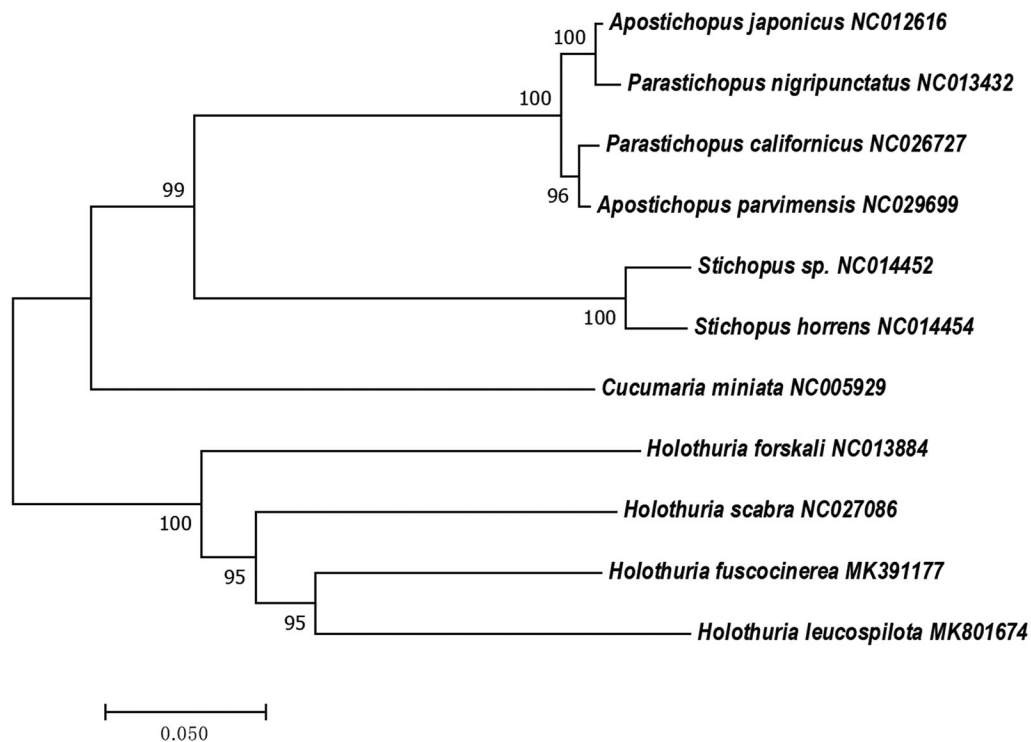
The phylogenetic analyzing demonstrated that *H. fuscocinerea* most closely related to *H. leucospilota* (Figure 1). The phylogenetic tree exhibits consistent topology, indicating that the interspecific relationships among holothuroids are monophyletic (Figure 1). Identifying the taxonomy of organisms from the perspective of mitochondrial genes avoids convergent evolution, which means that distant species can evolve similar phenotypes.

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**Figure 1.** Phylogenetic tree based on the 16S rRNA in the mitochondrial genome of *Holothuria fuscocinerea*.

## Disclosure statement

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

## Funding

This study was supported by the National Key R & D Program of China [2018YFD0901605], the Strategic Priority Research Program of the Chinese Academy of Sciences [XDA13020205], The National Natural Science Foundation of China [41676162], the Guangdong Province Program [2018A030313857, 2017B030314052, 2015A030310120], Guangdong Basic and Applied Basic Research Foundation [2020A1515011115], and the Science & Technology Promoting Projects for Oceanic & Fishery in Guangdong Province [SDYY-2018-01].

## Data availability statement

The data that support the findings of this study are openly available in GenBank at <https://www.ncbi.nlm.nih.gov/genbank/>, reference number MK391177.

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