


## The complete mitochondrial genome of *Metasepia tullbergi* (Cephalopoda: Sepiidae)

Hung-Tai Lee<sup>a</sup>, Cheng-Hsin Liao<sup>a</sup>, Chang-Wen Huang<sup>b</sup>, Chia-Huan Ma<sup>b</sup> and Te-Hua Hsu<sup>b,c</sup> 

<sup>a</sup>Department of Environmental Biology and Fisheries Science, National Taiwan Ocean University, Keelung, ROC; <sup>b</sup>Department of Aquaculture, National Taiwan Ocean University, Keelung, ROC; <sup>c</sup>Center of Excellence for the Oceans, National Taiwan Ocean University, Keelung, ROC

### ABSTRACT

The first complete mitochondrial genome of *Metasepia tullbergi* has been characterized in this study. The circular mitogenome is 16182 bp in length and comprises 13 protein-coding genes (PCGs), 22 transfer RNA genes, and two ribosomal RNA genes. The organization of these genes is highly consistent with that of other Sepiidae. The overall base composition of mitogenome is 39.20% A, 36.07% T, 8.98% G, and 15.75% C, with 75.27% AT. Phylogenetic analysis further suggests that *M. tullbergi* is placed within the Sepiidae and is closely related to *Sepia latimanus* and *S. apama*.

### ARTICLE HISTORY

Received 9 October 2020  
Accepted 8 March 2021

### KEYWORDS

Cuttlefish; phylogenetic analysis; mitogenome; next-generation sequencing

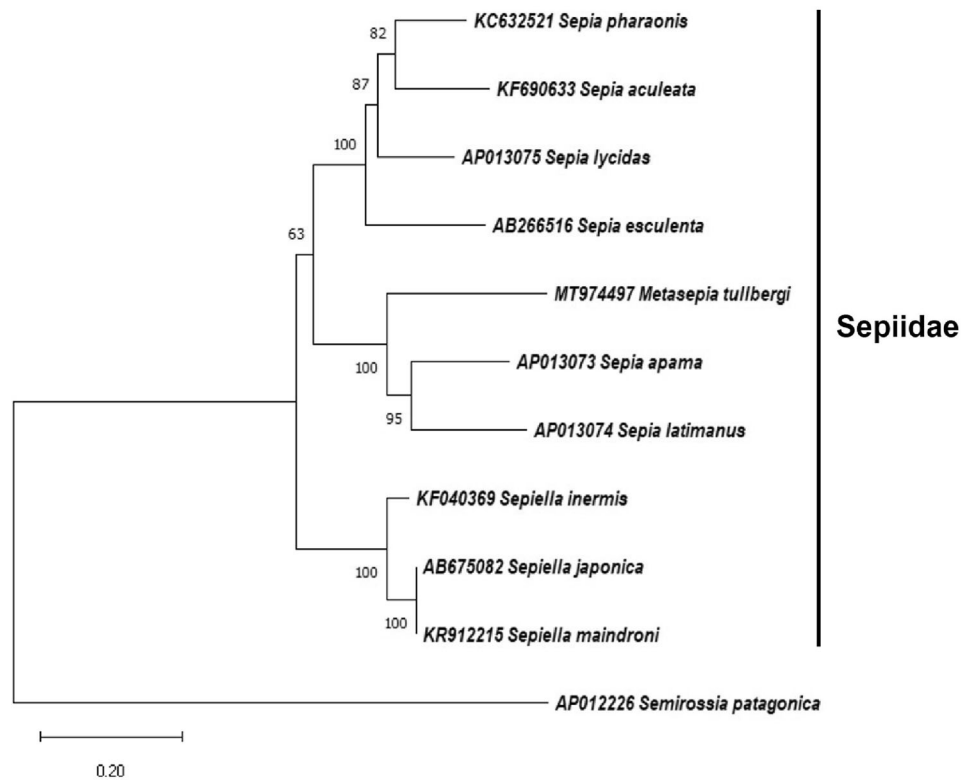
The paintpot cuttlefish (*Metasepia tullbergi*) is a small cuttlefish belonging to the Sepiidae family. It is a neritic demersal species that inhabits the sandy and muddy continental shelf with a water depth of 20–100 m. *M. tullbergi* commonly appears in the Indo-Pacific region, including Japan, Korea, China, Hong Kong, Taiwan, the Philippines, and the Gulf of Thailand (Reid et al. 2005). As a member of the *Metasepia* genus, *M. tullbergi* has a small and thick, diamond-shaped cuttlebone and exhibits a unique body coloration (Thomas and MacDonald 2016). In this study, we aim to report the first complete mitochondrial genome of *M. tullbergi* and further analyze its phylogenetic relationship within the family Sepiidae.

The specimen of *M. tullbergi* was collected from the coastal water off northeastern Taiwan (121.9°E, 25.1°N) in May of 2020 and stored at National Taiwan Ocean University with a specimen number (NTOU-MT-01-2020). The total genomic DNA was prepared and then followed by the pair-end sequencing (2 × 150 bp) with Novaseq (Illumina, San Diego, CA). The *de novo* assembly of the complete mitochondrial genome of *M. tullbergi* was performed using Geneious Prime 2020.2 (Kearse et al. 2012). The identification and annotation of protein-coding genes (PCGs) were conducted using ORFfinder (<https://www.ncbi.nlm.nih.gov/orfnder>). Additionally, the transfer RNA (*tRNA*) and ribosomal RNA (*rRNA*) genes were

identified and annotated using MITOS Web Server (Bernt et al. 2013).

The complete mitochondrial genome of *M. tullbergi* was a closed-circular molecule with 16,182 bp in length (GenBank accession number: MT974497). It contains 13 PCGs, 22 transfer RNA genes (*tRNAs*), two ribosomal RNA genes (12S rRNA and 16S rRNA). The overall base composition of mitochondrial genome is biased toward A + T content at 75.27% (A = 39.20%, T = 36.07%, G = 8.98%, and C = 15.75%). The length of 13 PCGs ranges from 156 to 1749 bp. All PCGs initiate with ATG. 9 PCGs terminate with TAA while 4 PCGs (ATP6, NAD1, CYTB, and NAD6) terminate with TAG. The length of the 22 *tRNA* genes ranges from 60 to 73 bp. All *tRNA* genes possess a typical cloverleaf-shaped secondary structure. The 16S rRNA with a length of 1061 bp is located between *trnL* and *trnV*. The 12S rRNA with a length of 891 bp is located between *trnV* and *trnC*.

The phylogenetic position of *M. tullbergi* was further examined based on a maximum-likelihood phylogenetic tree constructed by 13 PCGs in the complete mitochondrial genomes of *M. tullbergi* and other closely related species using MEGA X (Kumar et al. 2018). The result indicated that *M. tullbergi* clustered within the Sepiidae and was closely related to *Sepia latimanus* and *S. apama* (Figure 1).



**Figure 1.** Maximum-likelihood phylogenetic tree constructed by 13 PCGs in the mitochondrial genome of *Metasepia tullbergi* and the other nine Sepiidae species. *Semiossia patagonica* is used as the outgroup. Numbers beside each node represent percentages of 1000 bootstrap values.

## Disclosure statement

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

## Funding

This study was supported by Taiwan Ocean Conservation and Fisheries Sustainability Foundation [109toffrest001].

## ORCID

Te-Hua Hsu  <http://orcid.org/0000-0001-7819-4122>

## Data availability statement

The data that support the findings of this study are publicly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>, Accession number: MT974497. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA679401, SRX9530327, SAMN16832771.

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