


## Complete mitochondrial genome of the land snail *Euphaedusa planostriata* (Gastropoda: Stylommatophora: Clausiliidae)

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### ABSTRACT

Clausiliidae snails have been of great interest to conchologists for their unique clausilium structure and rich species diversity. We described the complete mitochondrial genome of *Euphaedusa planostriata* (Heude, 1882). The mitogenome is 15,041bp in length, with a total of 37 genes, including 13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes. It is consistent with the basic characteristics of the known stylommatophoran mitochondrial genome. Phylogenetic analysis using mitogenomes showed that *Euphaedusa planostriata* is clustered with *Albinaria caerulea*, supporting the monophyly of this family. Our study provides valuable information that can be used toward the conservation genetics, taxonomy and evolution of clausiliid snails.

### ARTICLE HISTORY

Received 15 March 2021  
Accepted 3 May 2021

### KEYWORDS

Asia; gene rearrangement;  
land mollusks;  
mitogenome; phylogeny

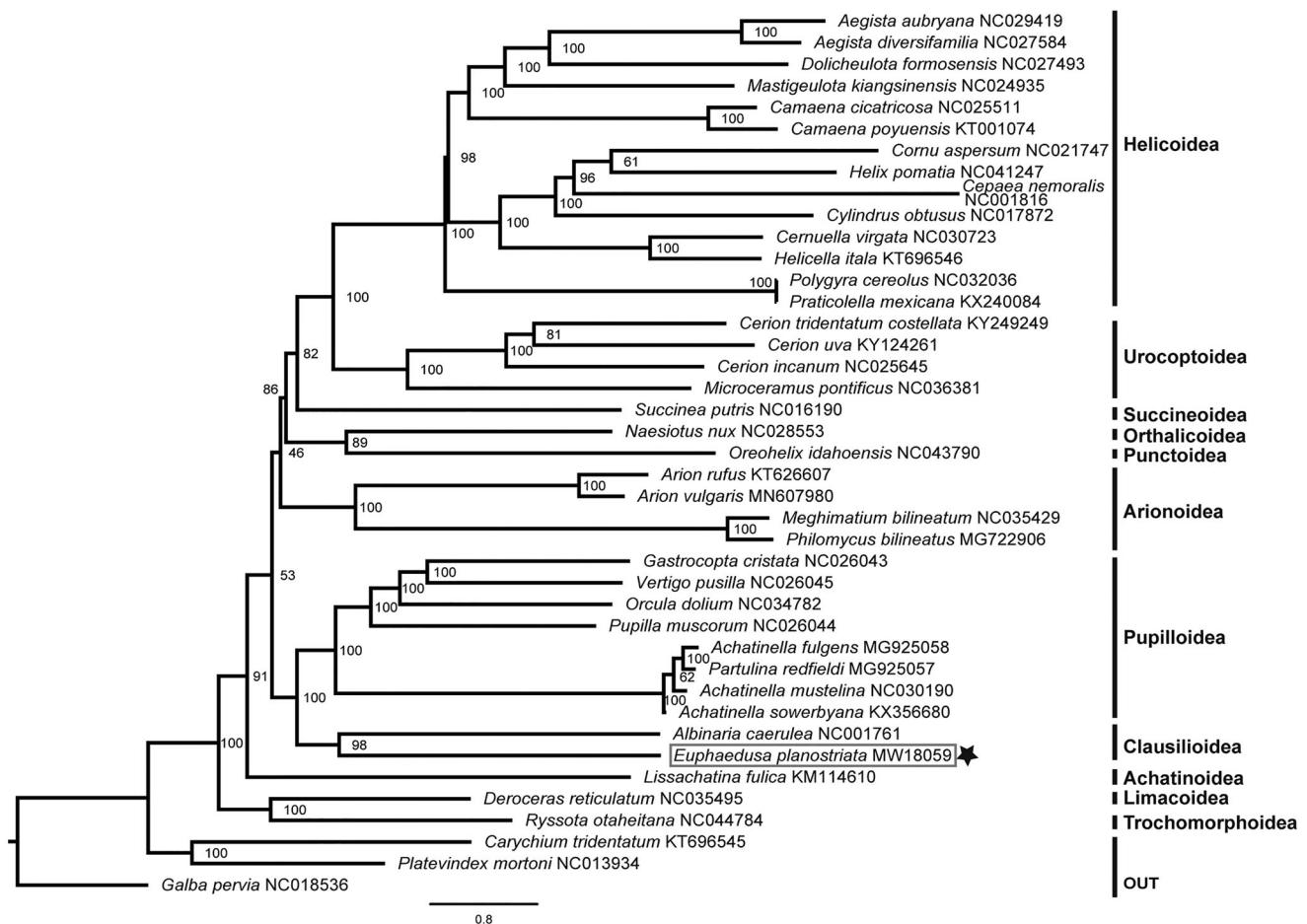
Intrigued by the unique clausilial apparatus and rich species diversity, biologists have been studying terrestrial snails of the family Clausiliidae for taxonomic and evolutionary questions. This speciose family is widely distributed (including Europe, Asia, and South America), and inhabits areas such as damp rocks, walls, and tree trunks (Chen and Zhang 1999). There was a wealth of studies on shell-morphology and anatomy in Clausiliidae (van Moorsel et al. 2000), and Uit de Weerd et al. (2013) provided a phylogenetic framework and discussed the biogeographic scenario of this family. However, researches concerning the molecular phylogeny remain insufficient, especially lacking specimens from Asia. In China there are more than 200 known species belonging to the Clausiliidae, mainly distributed in the Yangtze River Basin (Chen and Zhang 1999). In this study, we characterized the complete mitochondrial genome of *Euphaedusa planostriata* (Heude, 1882) and compared it with the other Clausiliidae species. Our study provides valuable data that can be used in the conservation genetics, taxonomy and evolution of clausiliid snails.

Specimens of *E. planostriata* were collected from Nanchang (28°39'39"N, 115°47'20"E), Jiangxi, China. Tissues were preserved at –80 °C, and voucher specimen (number: 20-NCU-SOUY-ZY01; contact Shan Ouyang: [ouys1963@qq.com](mailto:ouys1963@qq.com)) was deposited in the Museum of Biology in Nanchang University. Total genomic DNA was extracted using TIANamp Marine Animals DNA Kit (Tiangen Biotech, Beijing, China) according to the manufacturer's instructions, and subsequently sequenced on the Illumina Novaseq 6000 sequencing platform with PE150 strategy. The whole mitochondrial genome sequence was obtained and annotated according to our previous study (Qin et al. 2019; Xie et al. 2019). We

assembled the mitochondrial genome sequences using *de novo* methods with CLC Genomics Workbench 12.0 (Qiagen). Protein-coding genes (PCGs) and rRNA genes were initially annotated with MITOS web server (Bernt et al. 2013), and manually adjusted by comparing BLAST searches across species. MITOS and ARWEN (Laslett and Canbäck 2008) were used to detect tRNA genes. The best partition schemes and best fit models of substitution were identified using PartitionFinder 2 (Lanfear et al. 2017). Phylogenetic relationships of Stylommatophora were reconstructed under maximum likelihood criteria with 10,000 ultrafast bootstrap replicates in IQ-Tree (Nguyen et al. 2015).

The mitogenome of *E. planostriata* is 15,041 bp in length (GenBank accession number: MW118059). Similar to other stylommatophoran mitogenomes, it contains 13 PCGs, 22 tRNA genes, 2 rRNA genes, and a non-coding control region with 1,555 bp. The entire mitogenome of *E. planostriata* had a high A + T content of 70.10%, in accordance with other land mollusks (Deng et al. 2016; Yang et al. 2016; Xie et al. 2019). The overall nucleotide composition is as follows: A = 31.7%, C = 13.9%, G = 16.0%, and T = 38.4%. Thirteen genes (*trnQ*, *trnL2*, *atp8*, *trnN*, *atp6*, *trnR*, *trnE*, *rns*, *trnG*, *trnM*, *nad3*, *trnS2*, *trnT*) were located on the L strand, while the remains were encoded by the opposite H strand. Compared with the mitogenome of *Albinaria caerulea* (Hatzoglou et al. 1995) from Clausiliidae, *E. planostriata* shares the identical gene order, indicating that mitochondrial gene order is highly conserved at the family level in terrestrial mollusks.

Together with 37 other stylommatophoran species, phylogenetic analysis based on 12 PCGs and 2 rRNA genes showed that Clausiliidae is monophyletic (BS = 98), containing *E. planostriata* and *A. caerulea* (Figure 1). Our tree topology is largely



**Figure 1.** Maximum likelihood tree of 41 terrestrial gastropods based on 12 PCGs and 2 rRNA genes of mitogenomes. *Carychium tridentatum* (Ellobiidae), *Galba pervia* (Lymnaeidae), and *Platevindex mortoni* (Onchidiidae) were used as outgroup taxa.

consistent with previous study, except for the sister relationship of Orthalicoidea and Arionoidea (Doğan et al. 2020). The majority of the tree nodes were well-resolved with high bootstrap values in the present study, showing the effectiveness of mitogenomes for molecular systematics in land mollusks.

## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

## Funding

This work was supported by the National Natural Science Foundation of China [No. 31660619], and the Innovation Fund Designated for Graduate Students of Jiangxi Province [No. YC2020-S018].

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## Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under the accession no MW118059. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA721569, SRR14226860, and SAMN18721254 respectively.

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