



Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

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To cite this article: Jing Li, Qing Lv, Hui-lin Han & Ai-bing Zhang (2020) The complete mitochondrial genome of a tussock moth: *Euproctis seitzi* (Lepidoptera: Erebidae, Lymantriinae), Mitochondrial DNA Part B, 5:2, 1319-1320, DOI: [10.1080/23802359.2020.1734493](https://doi.org/10.1080/23802359.2020.1734493)

To link to this article: <https://doi.org/10.1080/23802359.2020.1734493>



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Published online: 04 Mar 2020.



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The complete mitochondrial genome of a tussock moth: *Euproctis seitzi* (Lepidoptera: Erebiidae, Lymantriinae)

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ABSTRACT

We describe the mitogenome sequence of *Euproctis seitzi* collected in the Mt. Luofu, which located in the southeast of China. The assembled mitogenome is 15,276 bp in length and consists of 13 protein-coding genes, 22 transfer-RNA genes, 2 ribosomal-RNA genes, and one A + T rich region. The most common start codon for 13 PCGs is ATT and the most common termination codon is TAA. The overall G + C content was only 18.57% in the heavy strand. The result of the phylogenetic analysis shows that the relationship of *E. seitzi* is close to the species in the same subfamily.

ARTICLE HISTORY

Received 18 January 2020
Accepted 20 February 2020

KEYWORDS

Euproctis seitzi;
mitochondrial genome;
Erebiidae; Lymantriinae;
phylogenetic analysis

Euproctis seitzi Stand, 1910 (Lepidoptera: Erebiidae, Lymantriinae) is a tussock moth mainly distributed in the southern coastal regions of China, which was first described by Strand (1910) from Hongkong. Different with other species in the same genus, such as *E. pseudoconsersa* which is a notorious pest mainly feeding on the leaves of tea trees (Dong et al., 2016), *E. seitzi* is a typically euryphagous insects. It could cause enormous economic loss in economic trees, such as oranges and mulberries (Chao, 1987, 2003). Moreover, the hairy caterpillars of *E. seitzi* might cause outbreaks of irritating cutaneous eruptions due to the venomous spicules on their backs (Bleumink et al. 1982; de Jone et al. 1982). Although previous studies on the genus *Euproctis* have mainly focused on the identification based on morphological characteristics of adults (Chao, 1984, 1986; Wang et al., 2010), there were still challenges in species identification due to the short-term emergence of the adults (mainly in June to August). Other studies of *Euproctis* focused on sex pheromone synthesis (Leonhardt et al. 1991; Wakamura et al. 1994), or the nuclear polyhedrosis virus that infects larvae (Kawamoto et al. 1977; Tang et al. 2009). Molecular information, especially mitogenome which can provide systematically-informative information for identification and phylogenetic analysis, are under development.

We collected the samples of *E. seitzi* in Mt. Luofu, Guangdong Province, China (23°17.5'N and 114°12.3'E) in July 2019. All specimens were preserved in 95% ethanol in the field and stored at 4°C in the laboratory until DNA

extraction. Voucher specimen was deposited at the Entomological Museum of Capital Normal University (No. VLym-19.2016) and the sequence was deposited in GenBank (No. MN916588).

The length of the complete mitochondrial genome of *E. seitzi* is 15,276bp, which contains 37 genes, including 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes, and 1 control region (A + T-rich region) which is 461 bp in length. For the 13 PCGs, the most common start codon is ATT (ATP8, COX2, ND1, ND2, ND3, ND6), then is ATG (ATP6, COX3, Cytb and ND4) and ATA (COX1, ND4L and ND5); the most common termination codon is TAA (13 protein coding genes except ND4L). The mitochondrial base composition is A 39.55%, T 41.88%, G 7.08%, and C 11.49% in the heavy strand, with an obvious (A + T)% > (G + C)%. Similar situation occurred in the non-coding region in which the (A + T) % was more than 90%. The length of the 22 sequenced tRNA genes ranged from 61 to 71 bp. The lrrRNA is 1272 bp long with an A + T content of 84.33% and the srRNA is 811 bp long with an A + T content of 87.54%.

All 13 protein-coding genes were used to reconstruct the phylogenetic tree with the maximum Likelihood approach in RAXML 7.9.6 (Stamatakis 2006). The two *Euproctis* species were clustered into a branch with 100 bootstrap values. Meanwhile, the analysis confirmed the monophyly of the superfamily Noctuoidea (including Noctuidae, Erebiidae and Notodontidae) (Figure 1).

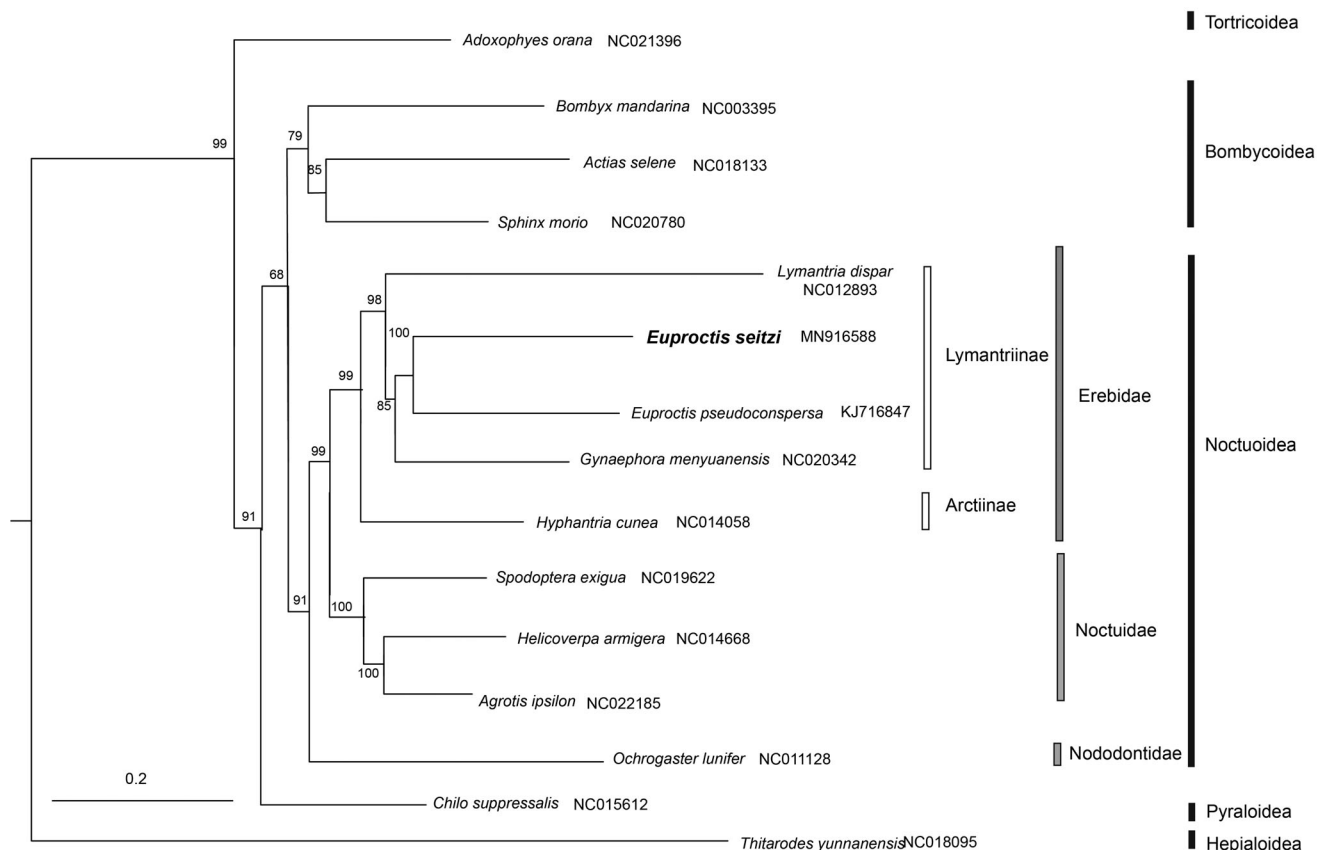


Figure 1. Phylogenetic relationship of 15 species in Lepidoptera based on the concatenated data set of 13 protein-coding genes. Number above/under each node indicates the ML bootstrap support values. Alphanumeric terms indicate the GenBank accession numbers.

Disclosure statement

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

Funding

This work was sponsored by the Natural Science Foundation of China [Grant/Award Number: 31772501 and 31400191], China National Funds for Distinguished Young Scientists [Grant/Award Number: 31425023], Program of Ministry of Science and Technology of China [Grant/Award Number: 2018FY100403], Academy for Multidisciplinary Studies, Capital Normal University, and also supported by Program for Changjiang Scholars and Innovative Research Team in University [IRT_17R75], Joint Fund of the Natural Science Foundation of Beijing Municipality and Beijing Municipal Education Commission [Grant/Award Number: KZ 201810028046], Natural Science Foundation of Beijing Municipality [Grant/Award Number: 5172005].

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