


## The complete mitochondrial genome sequence of *Coenonympha amaryllis* and monophyly of Satyrinae (Lepidoptera: Nymphalidae)

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### ABSTRACT

The complete mitochondrial genome (mitogenome) of a Satirid species *Coenonympha amaryllis* was assembled and annotated. The mitogenome is a DNA molecule of 15125 bp, and consists of 13 protein-coding genes (PCGs), 22 transfer RNAs, 2 rRNAs, and 1 A–T rich region. The nucleotide composition biases toward A and T is 79.4% of the entirety, which is a typical structure of Lepidopterans. All PCGs started with ATN, except *cox1*, which started with CGA, 8 PCGs stop with TAN and 5 genes exhibited incomplete stop codon. Phylogenetic analysis revealed that Satyrinae is a monophyletic group and *Coenonympha* (*C. amaryllis*) as sister of the genus *Triphysa* (*T. phryne*).

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Satyrinae; mitochondrial genome; phylogeny

Satyrinae, one of the 12 subfamilies of Nymphalidae, is highly diverse and distributed worldwide, including ~2500 described species (Peña and Wahlberg 2008). However, the phylogenetic relationships of Satyrinae have no robust hypotheses (Yang and Zhang 2015). Recent works show mitogenome is effective as molecular markers in phylogeny analysis in Lepidopterans (Kim et al. 2014; Timmermans et al. 2016; Yang M. et al. 2019; Yang Z. et al. 2019)

In this study, we collected samples of *Coenonympha amaryllis* from Shaanxi province, China (E109.37, N36.03) in August 2019. Specimen (Voucher No. LE250372) was deposited in the Entomological Museum of Northwest A&F University, Shaanxi province, China. Total genome DNA was extracted from the thorax muscle of a male adult. The complete mitogenome of *C. amaryllis* is a circular molecule of 15125 bp in size (Genbank accession number is MN756798), including 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes, and 1 A–T rich region (Control region). Its gene arrangement and direction are in accordance with other Nymphalid butterflies (Xu et al. 2019). The *C. amaryllis* mitogenome has an A–T content of 79.4% (A 38.1%; T 41.3%; C 12.6%; G 8.0%), which is a typical structure of Lepidopterans mitogenome. Generally, PCGs are started with ATN codon and terminated with TAN, but one gene (*cox1*) is initiated by CGA, five PCGs (*cox1*, *cox2*, *nd1*, *nd4* and *nd5*) are stopped with single-nucleotide (T—), which was

reported in another study (Shi et al. 2019). All tRNA genes are identified by MITOS web server (Bernt et al. 2013). The 16S rRNA gene is 1337 bp in size and is located between tRNA-L1 and tRNA-V; the 12S rRNA gene is 759 bp in length and is located between tRNA-V and A–T-rich region. The control region is 308 bp long, and is located between 12S rRNA and tRNA-M.

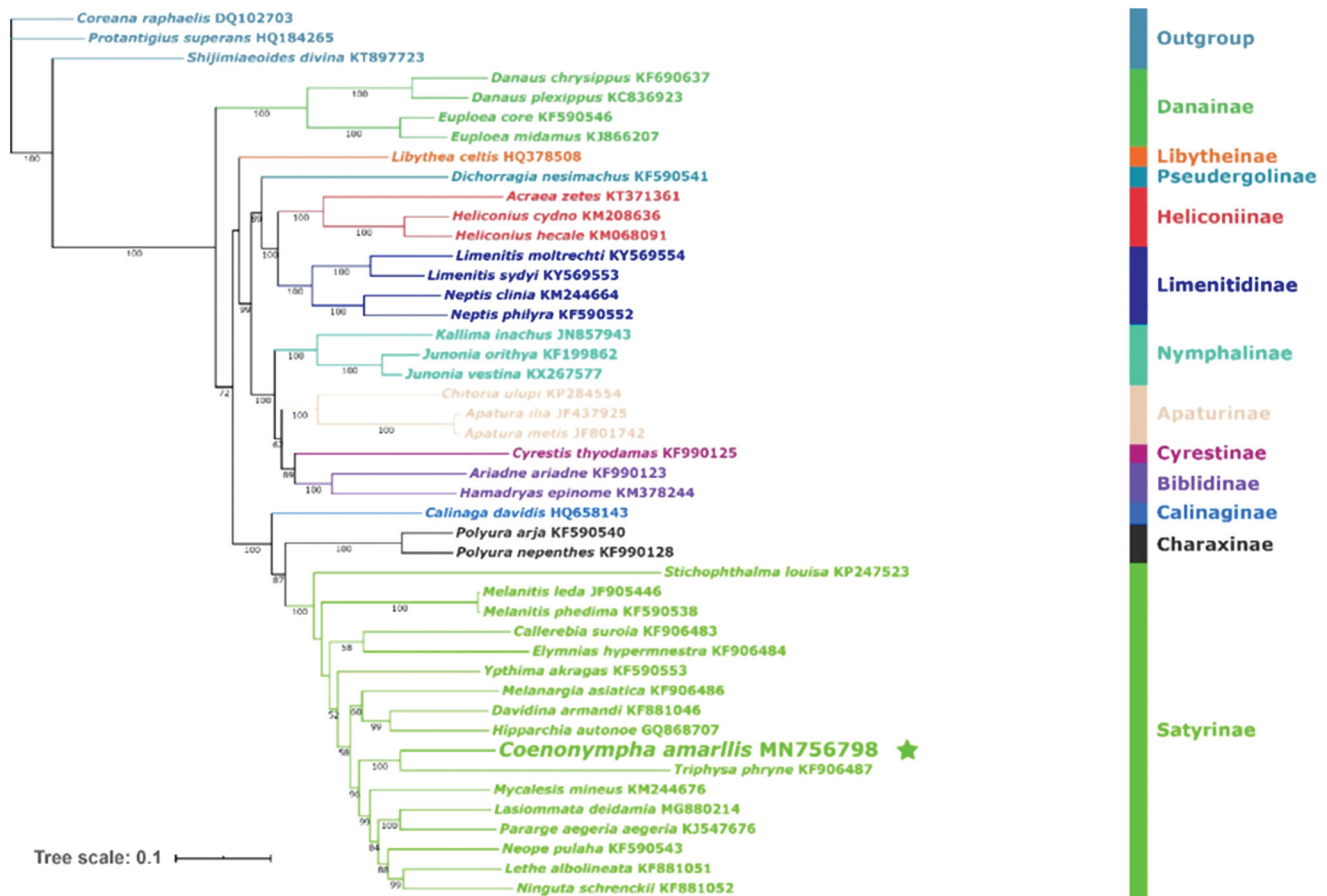
Here, we reconstructed a phylogeny of Nymphalidae using 13 PCGs from *C. amaryllis* and other 41 representatives (Figure 1) from 12 subfamilies of the family and 3 outgroup species (Figure 1) from Lycaenidae. Thirteen concatenated PCG sequences of mitogenomes were analyzed by maximum likelihood (ML) in IQ-tree (Lam-Tung et al. 2015). The phylogenetic tree showed that Satyrinae was a monophyletic group in Nymphalidae and *Coenonympha* (*C. amaryllis*) was sister of the genus *Triphysa* (*T. phryne*).

### Disclosure statement

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

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**Figure 1.** Maximum-Likelihood phylogenetic tree of Nymphalidae based on 11,601 bp of 13 concatenated PCGs. Numbers at nodes are percentage of 1000 bootstrap values (bootstrap values 50> are not shown); star indicates new sequenced data in this study.

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