

The mitochondrial genome of *Paralimna (Paralimna) concors* (Diptera: Ephydriidae)

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ABSTRACT

The mitogenome of *Paralimna (Paralimna) concors* was sequenced. The mitogenome was 16,155 bp totally, consisting of 13 protein-coding genes (PCGs), two rRNAs, and 22 transfer RNAs. The nucleotide composition biases toward A and T is 78.6% of the entirety. All PCGs start with ATN codons except COI and ND1, and end with TAA or incomplete stop codon. Phylogenetic analyses based on 11 dipteran species supported the monophyly of Ephydroidea and the relationship of Opomyzoidea + (Ephydroidea + (Lauxanioidea + (Sphaeroceroidea + (Sciomyzoidea + Tephritoidea))).

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Introduction

Adults of *Ephydriidae* are often dull and dark colored, but unusually diverse in body structure, vestiture, and ornamentation (Mathis and Zatwarnicki 1998). The ephydrid flies with about 2000 described species from the world are placed in superfamily Ephydroidea (Pape et al. 2011). The genus *Paralimna* Loew, 1862 is one of the richest in species genera in the tribe Dryxini. The attention of many dipterologists was attracted to this group of Diptera because the largest and remarkable specimens were discovered in the field (Krivosheina and Ozerov 2020). Species of *Paralimna* regularly occur in grassy habitats (Foote 1995).

The adult specimens of *Paralimna (Paralimna) concors* (Voucher number: CAU-YDEPHY-Para-1) used for this study were collected from 2W Hown District (19.8976°N, 101.1438°E, 1278 m), Pak Beng, Laos, on 25 Jun 2015. The specimens were identified by Liang Wang and deposited in the Entomological Museum of China Agricultural University (CAU).

The genomic DNA was extracted from adult's whole body using the DNeasy DNA Extraction kit (TIANGEN) and stored at -20°C refrigerator. DNA samples were pooled for next-generation sequencing library construction following the method of Gillett et al. (2014). All quantified DNA extracts were included in a single pool at equimolar concentration, aiming for 50 ng/ul of dsDNA per sample, resulting in a DNA pool of approximately 5 ug. The library was sequenced on an Illumina HiSeq 2500 by BIONONA CO., LTD. Rough read data were trimmed and cropped in Trimmomatic version 0.30 (Bolger et al. 2014) with the default setting. Four Gigabytes

of high-quality reads were used to assemble mitogenomes with the *de novo* assembler IDBA_UD (Peng et al. 2012). The bait sequence COI was amplified by standard PCR reactions and BLAST search was carried out with BioEdit version 7.0.5.3 and the position of all tRNA genes was confirmed using tRNAscanSE version 2.0 (Lowe and Chan 2016). The nearly complete mitogenome of *Paralimna (Paralimna) concors* (MT938921) was 16,154 bp in length and consisted of 13 typical invertebrate PCGs, 22 transfer RNA genes, two rRNA genes (12S and 16S), and part control region, which were similar to other Diptera flies reported before (Li et al. 2016; Zhou et al. 2017; Qilemoge et al. 2018; Ren et al. 2019). The nucleotide composition of the mitogenome was biased toward A and T, with 78.6% of A+T content (A=39.2%, T=39.4%, C=12.6%, and G=8.9%). Among the protein-coding genes (PCGs), six genes took the start codon of ATG, five genes used ATT as start codon, while COI gene and ND1 gene got ACG and TTG, respectively. The termination codon of these PCGs had three types (seven genes used TAA, CYTB gene used TAG, five genes used T+tRNA).

There are 10 species retrieved from NCBI and one new sequenced datum used in phylogenetic analysis. The genbank accession numbers are listed as follows: *Anopheles oryzalimnetes* NC_030715, *Bactrocera cucurbitae* NC_016056.1, *Ceratitis capitata* NC_000857, *Drosophila melanogaster* NC_024511, *Drosophila yakuba* NC_001322, *Ilythea japonica* MT_527723, *Liriomyza trifolii* NC_014283, *Nemopoda mamaevi* NC_026866, **Paralimna (Paralimna) concors* MT938921, *Simosyrphus grandicornis* NC_008754.1, *Suillia* sp. MN026917. Thirteen PCGs were used to reconstruct phylogenetic relationship with the maximum likelihood method using IQTREE

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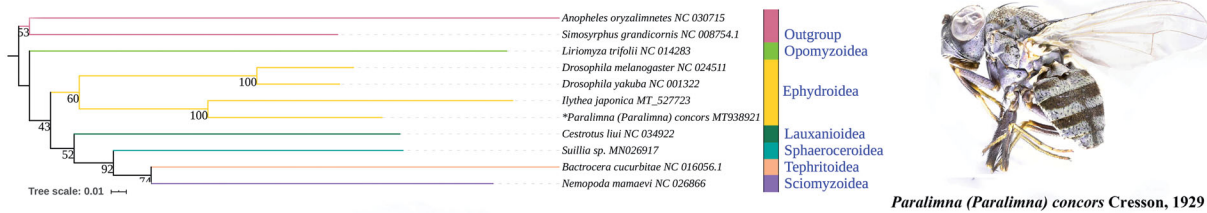


Figure 1. The phylogenetic tree of ML analysis based on 13PCGs and adult of *Parolimna (Parolimna) concors* Cresson, 1929. “*” Indicated new sequenced data in this study.

Web Server (<http://iqtree.cibiv.univie.ac.at/>) (Jana et al. 2016). The topology was given and bootstrap support numbers are shown in Figure 1. ML analysis revealed that *Ephydridae* was monophyletic. The higher-level relationship of Opomyzoidea + (Ephydroidea + (Lauxanioidea + (Sphaeroceroidea + (Sciomyzoidea + Tephritoidea)))) was supported.

The complete mitochondrial genome of *Parolimna (Parolimna) concors* provides valuable information for future genetic and evolutionary studies of family *Ephydridae* and superfamily Ephydroidea.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in [NCBI] at [<https://www.ncbi.nlm.nih.gov/>], reference number [MT938921].

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