

Characterization and phylogenetic analysis of the complete mitochondrial genome of *Lathyrphthalmus quinquestriatus* (Fabricius, 1794)(Diptera, Syrphidae)

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ABSTRACT

In this study, we present the complete mitogenome of *Lathyrphthalmus quinquestriatus* (Fabricius, 1794), which has a total length of 16,198 base pairs and includes 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and one putative control region. Most PCGs started with ATN codons except *COX1* (CAA), and ended with TAA, TAG (*ND3*) or single T(*ND5*). The results of phylogenetic tree reconstruction show that the monophyly of subfamily *Eristalinae* is not supported, and the closer relationship between genus *Lathyrphthalmus* and *Eristalinus*.

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Syrphids, known as hover flies (Diptera: Syrphidae), comprise over 9600 described species (Thompson 2008) and make a diverse and species-rich clade in Diptera. Almost all adult hoverflies visit flowers and play the important ecological role as plant pollinators (Le and Gang 2020). Larvae cover a huge array of ecological niches and present a variety of feeding modes, as zoophagy, phytophagy, coprophagy and saprophagy (Rotheray and Gilbert 1999; Skevington and Yeates 2000). Group *Lathyrphthalmus*, *Eristalodes* and *Eristalinus* (*sensu stricto*) are three monophyletic lineages in Syrphidae, of which the taxonomic status has been argued for long time. Considering the markings on compound eyes shared by all, some researchers suggested these three groups can be combined as subgenera of the genus *Eristalinus* (Pérez-Banón et al. 2003). However, the males of *Eristalinus* (*sensu stricto*) are dichoptic, *Eristalodes* and *Lathyrphthalmus* are holoptic, in addition, *Eristalodes* are different from *Lathyrphthalmus* by the presence of bands, instead of dark spots on compound eyes, these morphological divergence makes some scholars considered the group *Eristalinus* (*sensu stricto*) can be treated as independent genus, but *Eristalodes* and *Lathyrphthalmus* should belong to the genus *Eristalis*, or can be elevated to genus level (Thompson and Rotheray 1998; Pérez-Banón et al. 2003; Huo et al. 2007).

Although the group *Lathyrphthalmus* are widely distributed and highly diverged (75 species have been described) (Thompson 2005), the very limited data restrict the molecular researches to better understand the natural history of this genus. *Lathyrphthalmus quinquestriatus* (Fabricius, 1794), a

particular hoverfly belonging to the tribe Eristalini of subfamily Eristalinae (Diptera: Syrphidae), of which the structure of the male genitalia is similar to that of *Eristalodes* (Kanervo 1938; Pérez-Banón et al. 2003). Here, we sequenced and assembled the complete mitogenome of *L. quinquestriatus* to add new data that can benefit the molecular phylogenetic analyses among hoverflies. The specimen of *L. quinquestriatus* were collected from the Changqing National Nature Reserve (107°17'E, 33°19'N) on 2019, and stored in the Museum of Zoology and Botany, Shaanxi University of Technology, Hanzhong, China (SUHC) (Accession number: SYY20190702). The genomic DNA extraction of *L. quinquestriatus* is applied by the DNeasy kit (Qiagen, Hilden, Germany), and the paired-end libraries were constructed and sequenced (2 × 150 bp) using the Illumina HiSeq 4000 platform by Nextomics Bioscience Company (Wuhan, China). The complete mitogenome of *L. quinquestriatus* was assembled and annotated by MITOZ (Meng et al. 2019).

The complete mitogenome of *L. quinquestriatus* has 16,198bp in length and included 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA), 2 ribosomal RNA (rRNA) and 1 putative AT-rich control region (D-loop). The overall base composition is 41.2% A, 39.4% T, 8.1% G and 11.4% C, like other Syrphidae species had a positive AT-skew (0.022) and a negative GC-skew (−0.167) (Li et al. 2017; Pu et al. 2017; Le and Gang 2020). dAll genes were arranged in the same order as the putative ancestral arrangement of insects (Cameron 2014), 23 genes were encoded by majority strand (J-strand) and the left 14 genes were located by minority strand (N-

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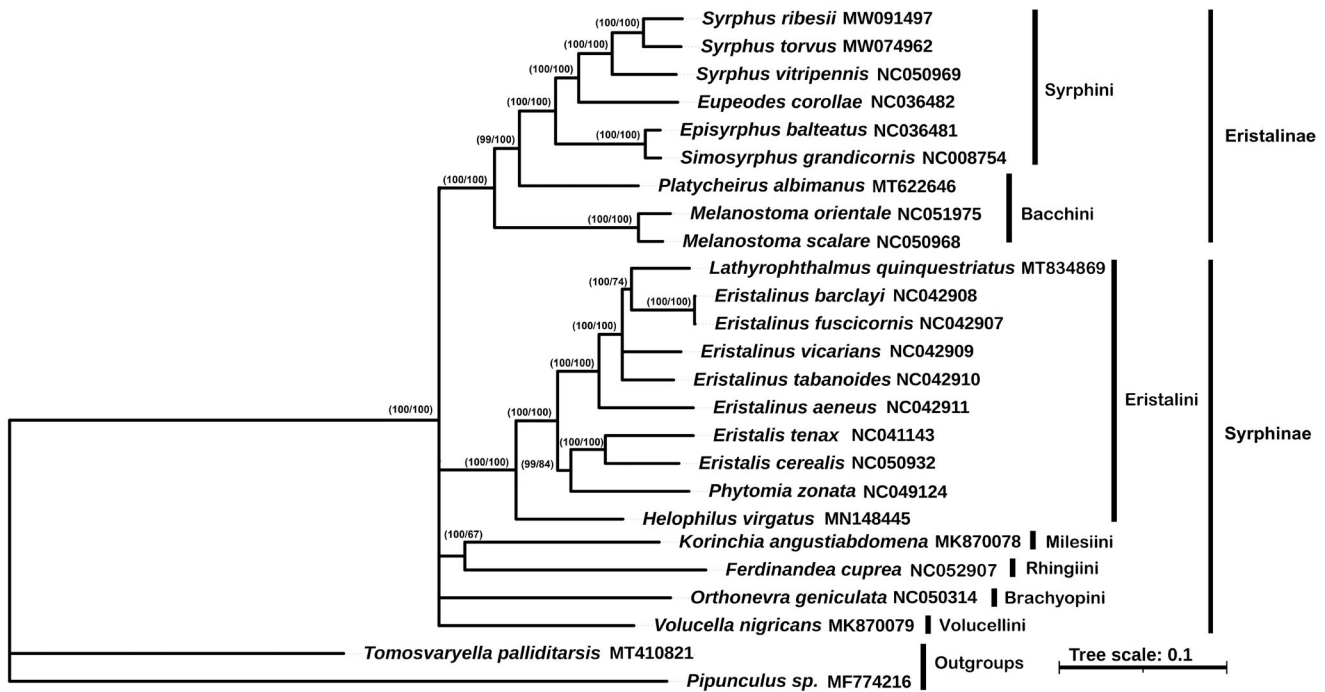


Figure 1. The phylogenetic tree constructed by the sequences of 13PCGs from mitochondrial genome of 22 syrphidae species and two outgroups. The node with low statistic score (<60) are shown in paraphyletic topologies. Statistical support values (posterior probability/Bootstrap) of BI/ML methods are shown above each node.

strand). There were 12 PCGs used ATN as the start codon (*COX2*, *COX3*, *ND4*, *ND4L* and *Cytb* used ATG, *ND3*, *ND5* and *ND6* used ATT, *ATP6* and *ND1* used ATA, *ATP8* and *ND2* used ATC), only *COX1* started with CAA. The most common stop codon was TAA, while TAG and an incomplete stop codon T(AA) was observed in *ND3* and *ND5* genes, respectively.

We reconstructed the phylogenetic tree with other 22 syrphidae species and two outgroups mitogenomic sequences (available in <https://www.ncbi.nlm.nih.gov/>). The multiple sequence alignments of 13 PCGs were preformed using MAFFT v7.429 program with the E-INS-I strategy (Katoh and Standley 2013). The best model and partitioning scheme selection was determined under the AICc criterion by PartitionFinder2 v2.1.1 (Lanfear et al. 2017), the maximum-Likelihood (ML) tree and Bayesian inference (BI) tree were obtained using IQ-tree v2.0.3 (Nguyen et al. 2015) and MrBayes v3.2.7 (Ronquist et al. 2012), respectively (Figure 1). Both BI and ML analysis supported the monophyly of the clade of family Syrphidae and subfamily Syrphinae with high statistic support. The status of Eristalinae was not recovered as monophyletic but paraphyletic, which consisted with the previous published works (Young et al. 2016; Li et al. 2017; Pauli et al. 2018). The topologies of phylogenetic tree constructed by mitogenome data revealed the inset status of *L. quinquestriatus* within the *Eristalinus* genus, that suggested *L. quinquestriatus* need to be reconsidered as a *Eristalinus* species rather than genus *Lathyrophthalmu*. In conclusion, the complete mitogenome of *L. quinquestriatus* will provide a useful genetic resource and help to understand the phylogenetic relationship of the Syrphidae clade, but we still need more mitochondrion sequence of species in this group to

discuss low bootstrapping support values in the Syrphidae phylogenetic tree .

Disclosure statement

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

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Data availability statement

The mitogenome sequence data that support the findings of this study openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under the accession no. MT834869. The associated SRA, BioProject and Bio-Sample numbers are SRR13735676, PRJNA702207 and SAMN17928659, respectively.

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