MITOCHONDRIAL DNA PART B
2022, VOL. 7, NO. 9, 1679–1681
https://doi.org/10.1080/23802359.2022.2122743

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

OPEN ACCESS Check for updates

The complete mitochondrial genome of *Eristalinus viridis* (Coquillett, 1898) (Diptera: Syrphidae) and its phylogenetic implications

Le Zhao[a,b]*, Li Gang[b]*, Yicheng He[a], Hanyue Liu[a] and Keke Huo[a]

[a]School of Biological Science and Engineering, Shaanxi University of Technology, Hanzhong, China; [b]College of Life Sciences, Shaanxi Normal University, Xi'an, China

ABSTRACT

The complete mitochondrial genome of *Eristalinus viridis* (Coquillett, 1898) was obtained for the first time using Next Generation Sequencing (NGS). The mitogenome assembly of E. viridis is 15,640 bp in length and its annotation confirms the presence of 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rRNAs), and one putative control region. The results of the phylogenetic analyses using Maximum Likelihood and Bayesian inference recover a highly supported sister relationship between *E. viridis* and *Mallota bellus*.

ARTICLE HISTORY
Received 14 December 2021
Accepted 5 September 2022

KEYWORDS
Eristalinus viridis; Syrphidae; mitogenome; phylogeny

The family Syrphidae, commonly known as hoverflies, is one of the largest and most diversified Diptera groups, with over 6200 recorded species (Evenhuis and Pape 2021). Members of the genus *Eristalinus* of the subfamily Eristalinae (Diptera, Syrphidae) are important pollinators and are widely distributed in all biogeographic regions (Sonet et al. 2019; Rossi Rotondi et al. 2020). The species *Eristalinus viridis* (Coquillett, 1898) has a black-green body with metallic green reflections, which is the only one without any spotted or striped compound eyes in the genus *Eristalinus* (Huo et al. 2007). Here, we obtained the complete mitogenome data of *E. viridis* and inferred its phylogenetic relationships with other Eristalini members based on mitochondrial genomes.

The specimens of *E. viridis* were collected in the Changqing National Nature Reserve (107°17′E, 33°19′N) and deposited in the Museum of Zoology and Botany, Shaanxi University of Technology, Hanzhong, China (https://www.snut.edu.cn/, L, Zhao, Lezhao@snut.edu.cn) under the accession no. SYY20190217. The whole genomic DNA was isolated from thorax tissue using the DNeasy kit (Qiagen, Hilden, Germany), and sequenced on Illumina Hi-Seq 4000, paired-end 2 × 150bp at Nextomics Bioscience Company (Wuhan, China). The raw sequence data were quality filtered using the fastp (Chen et al. 2018). The complete mitogenome of *E. viridis* was assembled and annotated using MITOZ v2.4 (Meng et al. 2019).

The complete mitogenome of *E viridis* maps as a single circular chromosome and has 15,640 bp in length, with a nucleotide composition rich in T and A (A: 40.9%, T: 37.3%, C: 13.1%, and G: 8.6%). The AT-skew (0.046) was positive and the GC-skew (−0.205) was negative, which is similar to the values reported in other hoverfly mitogenomes (Zhao and Li 2020; Zhou et al. 2021). The typical 37 mitochondrial genes (13 PCGs, 22 tRNAs, and two rRNAs) and one putative D-loop region were found. In addition, ten overlaps and 16 intergenic spacers were found in the mitogenome of *E. viridis*. The start codon is ATN for most PCGs, but there are five genes with ATG (*COX2*, *COX3*, *ND4*, *ND4L*, and *CYTB*), five more genes with ATT (*ATP8*, *ND2*, *ND3*, *ND5*, and *ND6*), and two genes with ATA (*ATP6* and *ND1*), whereas *COX1* gene uses the alternative CAA. Ten PCGs had TAA as the stop codon, two PCGs (*ND1* and *ND3*) presented TAG, and one (*ND5*) used the incomplete stop codon TA.

To infer the phylogenetic relationships of *E. viridis*, we reconstructed the phylogeny of the tribe Eristalini using the concatenated sequence data of 13 PCGs from 22 *taxa* and two outgroups. The alignment of the PCGs was done using the software MAFFT with the E-INS-I strategy (Katoh and Standley 2013). The maximum-Likelihood (ML) tree and the Bayesian inference (BI) analyses were obtained using the program IQ-tree (Nguyen et al. 2015) and MrBayes (Ronquist et al. 2012), respectively. The phylogenetic trees obtained from the ML and BI analyses presented identical topologies. As shown in Figure 1, *E. viridis* was resolved as a member of the Eristalini, clustered with *Mallota bellus* Li, 1997 forming a clade with high statistic support. In addition, the monophyly of the tribe Eristalini was well-supported and consistent with previous studies (Moran et al. 2022).

Ethical approval

Ethics approval was not required for this study. All procedures performed in this study involving animals followed the

CONTACT Keke Huo huokk@163.com School of Biological Science and Engineering, Shaanxi University of Technology, Hanzhong, China
*Both authors have contributed equally to this work.

© 2022 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.
This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License (http://creativecommons.org/licenses/by-nc/4.0/), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

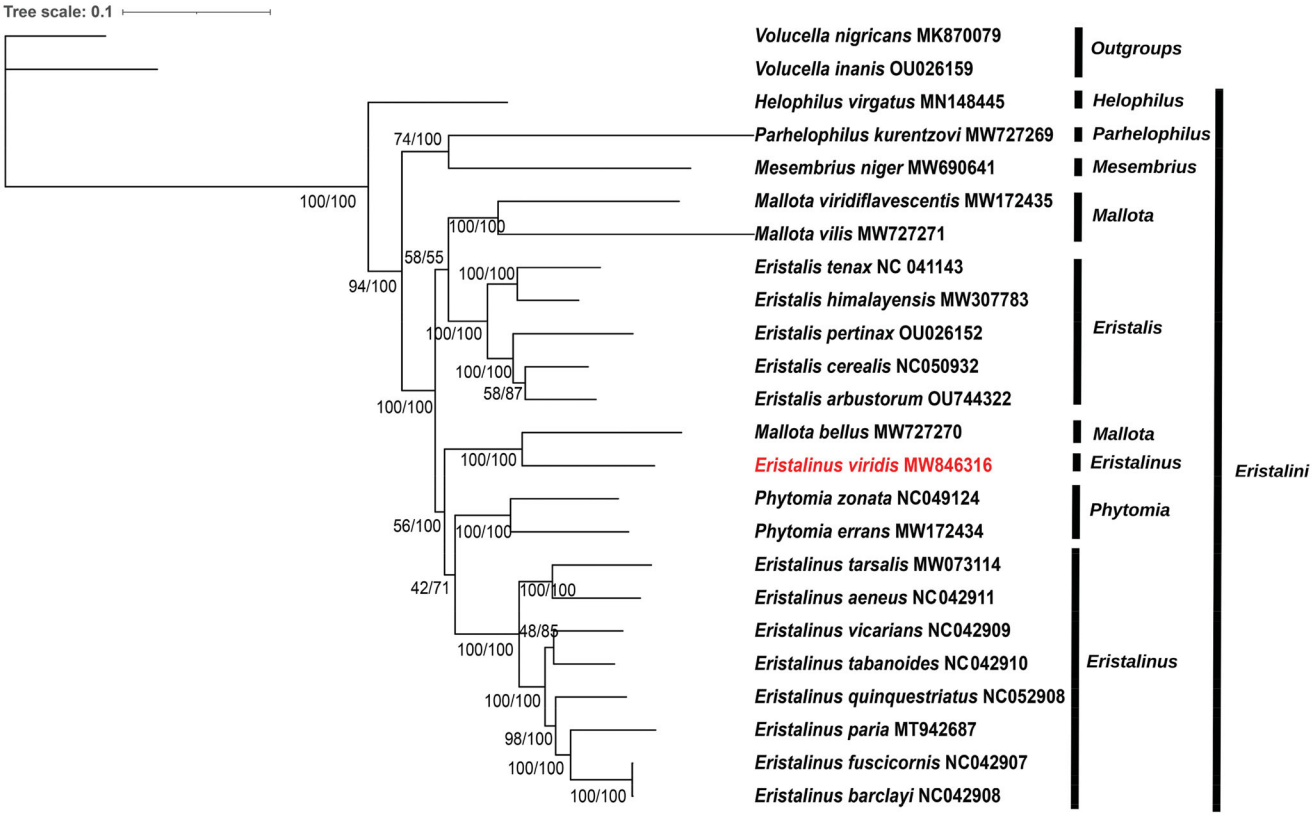

Figure 1. The phylogenetic tree of the tribe Eristalini based on the 13 mitochondrial protein-coding genes using BI and ML methods. Statistical support values (Bootstrap/posterior probability) of ML/BI methods are shown close to each node.

Guidelines of the Shaanxi University of Technology, Hanzhong, China. The field studies did not include vertebrates, regulated invertebrates, and endangered or protected species.

Author contribution

Le Zhao, Keke Huo, and Gang Li conceived and designed the experiments; Yicheng He and Hanyue Liu performed the experiments; Le Zhao and Yicheng He analyzed the data; Le Zhao, Yicheng He, and Gang Li wrote the paper.

Disclosure statement

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

Funding

This research was supported by the National Natural Sciences Foundation of China [31900345], the Natural Science Basic Research Plans in Shaanxi Province of China [2021JQ-757, 2020JM-280, 2019JZ-34], the Scientific Research Program Funded by the Shaanxi Provincial Education Department [21JK0555], the Foundation of Shaanxi University of Technology [SLGRC13], the Opening Foundation of Shaanxi University of Technology [SLGPT2019KF02-02], the Fundamental Research Funds for the Central Universities [GK201902008].

ORCID

Le Zhao http://orcid.org/0000-0003-0505-9936

Data availability statement

The mitogenome sequence data supporting this study's findings are available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under accession no. MW846316. The associated SRA, BioProject, and Bio-Sample numbers are SRR17035427, PRJNA783204, and SAMN23424229, respectively. The specimen was deposited at the Museum of Zoology and Botany, Shaanxi University of Technology, Hanzhong, China (https://www.snut.edu.cn/, Le Zhao, email: Lezhao@snut.edu.cn)

References

Chen S, Zhou Y, Chen Y, Gu J. 2018. FASTP: an ultra-fast all-in-one FASTQ pre-processor. Bioinformatics. 34:i884–i890.

Evenhuis NL, Pape T. 2021. Systema Dipterorum. The biosystematics database of world Diptera. Version 3.4. [Last updated 2021 Oct 27]. http://www.diptera.org/

Huo K, Ren G, Zheng Z. 2007. Fauna of Syrphidae from Mt. Qinling-Bashan in China (Insecta: Diptera). Beijing: Chinese Agricultural Science and Technology Press.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Meng G, Li Y, Yang C, Liu S. 2019. MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Res. 47(11):e63–e63.

Moran KM, Skevington JH, Kelso S, Mengual X, Jordaens K, Young AD, Ståhls G, Mutin V, Bot S, van Zuijen M, et al. 2022. A multigene phylogeny of the *Eristaline* flower flies (Diptera: Syrphidae), with emphasis on the subtribe Criorhinina. Zool J Linn Soc. 194:120–135.

Nguyen LT, Schmidt HA, Von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. Mrbayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 61(3):539–542.

Rossi Rotondi BA, Videla M, Beccacece HM, Fenoglio MS. 2020. New records of the exotic band-eyed drone fly, *Eristalinus taeniops* (Wiedemann, 1818) (Diptera, Syrphidae), in Argentina. CheckList. 16(6): 1523–1529.

Sonet G, De Smet Y, Tang M, Virgilio M, Young AD, Skevington JH, Mengual X, Backeljau T, Liu S, Zhou X, et al. 2019. First mitochondrial genomes of five hoverfly species of the genus *Eristalinus* (Diptera: Syrphidae). Genome. 62(10):677–687.

Zhao L, Li G. 2020. The first complete mitochondrial genome of the tribe Rhingiini (Diptera: Syrphidae) and phylogenetic analysis. Mitochondrial DNA Part B Resour. 5(3):3489–3491.

Zhou Z, Liu H, Gang L, Dang L, Zhao L, Huo K. 2021. Characterization and phylogenetic analysis of the complete mitochondrial genome of *Lathyrophthalmus quinquestriatus* (Fabricius, 1794) (Diptera, Syrphidae). Mitochondrial DNA B Resour. 6(3): 1183–1185.