The complete mitochondrial genome sequence and phylogenetic position of *Xylota coquilletti* Hervé-Bazin, 1914 (Diptera: Syrphidae: Eristalinae: Xylotini)

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**ABSTRACT**

The complete mitochondrial genome sequence of the *Xylota coquilletti* (Diptera: Syrphidae: Eristalinae: Xylotini) was sequenced and reported for the first time. The whole genome was 15,920 bp in length, with 13 protein-coding genes (PCGs), and a control region (CR). Phylogenetic analyses were performed using 13 PCGs and it was found that *Xylota coquilletti* was sister to *Ferdinadea cupera*. All this information could complement the mitochondrial data for a new tribe of Eristalinae.

*Xylota coquilletti* Hervé-Bazin, 1914 belongs to the tribe Xylotini (Diptera: Syrphidae: Eristalinae). Eristalinae includes nine tribes: Brachyopini, Callicerini, Cerioidini, Eristalini, Merodontini, Milesini, Rhingini, Sericomyiini, and Volucellini (Mengual 2015; Young et al. 2016). To date, the number of sequenced and reported complete mitochondrial genomes was only 25, belonging to species of Eristalini, Milesiini, Volucellini, Brachyopini, and Rhingini. In this study, a complete mitogenome from the representative individual named *Xylota coquilletti* belonging to Xylotini was obtained to further identify the phylogenetic relationships in the subfamily.

The sequenced species were collected from Sijihuahai Park, Hefei City, Anhui Province, China (117°16'E, 31°08'N) on 11 June 2021. The voucherer individual was immediately stored in absolute ethanol and was frozen at −20°C in Laboratory 1043, College of Plant Protection, Anhui Agricultural University (voucher number LSH-Sml-Aj13, Zelin Pan, panzelin333@sina.com). The total genomic DNA was extracted from the complete individual except for its genitalia. The mitogenome was sequenced on the MGI T7 platform with 150 bp paired-end reads and yielded 4.30 GB paired raw reads. The quality of the data was checked by FastQC (Andrews 2016). A total of 4.10 GB of clean paired-end reads (Phred scores >20) were quality-trimmed and were assembled using NOVOPlasty4.3.1 (Dierckxsens et al. 2017) with default parameters and the mitochondrial genome of *Xylota sylvarum* (Huo et al. 2018) (GenBank no. LR999962) used as a reference. Gene annotation was carried out by Geneious 8.1.3 (Kearse et al. 2012). PCGs were determined as open reading frames, rRNAs and tRNAs were identified using MITOS (Bernt et al. 2013).

The whole length of the mitochondrial genome from the *Xylota coquilletti* (GenBank no. MZ905457) was 15,920 bp, which included 40.5% A, 39.6% T, 11.7% C, and 8.2% G. In other words, the percentage of A+T (80.1%) was much greater than C+G (19.9%), revealing that the genome exhibited significant A/T bias. The mitochondrial genome was made of 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rRNAs), 13 protein-coding genes (PCGs), and a control region (CR). Most PCGs regarded the ATN putative as the start codon (five ATG, four ATT, and one ATA) except COXI, COXI, and nad5. They were started with CGA, TTG, and GTG, respectively. Besides, most PCGs regarded TAA as the termination codon except nad5, which was stopped with incomplete termination codon T. For tRNA genes, the length of the 22 genes was about 63–72 bp. The secondary structure of tRNA was a typical cloverleaf structure, except trnD and trnS1. In terms of two rRNA genes, the 16S rRNA was 1339 bp, which was placed between trnL1 and trnV. The 12S rRNA was placed between trnV and the CR with a length of 786 bp. The length of CR was 1016 bp and it was placed between 12S rRNA and trnL. According to the whole genome, there was no gene rearrangement.

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This article has been re-published with minor changes. These changes do not impact the academic content of the article.

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In order to estimate the phylogenetic position of *X. coquillettii*, the mitochondrial DNA sequences of the other 28 Syrphidae species (25 Eristalinae as ingroup and three Syrphinae as outgroup) were selected from the GenBank database to further define the relationship within Eristalinae. All the PCGs of the 29 species data were aligned by multiple alignments using MAFFT 7 plugin in PhyloSuite 1.2.2 (Zhang et al. 2020). The gaps and the ambiguous sites were removed using the Gblocks plugin in PhyloSuite 1.2.2 (Zhang et al. 2020). The aligned PCGs data of the different species were concatenated using concatenate sequence plugin in PhyloSuite 1.2.2 (Zhang et al. 2020) and the best-fit substitution model for phylogenetic analyses was determined using PartitionFinder 2.7 plugin in PhyloSuite 1.2.2 (Zhang et al. 2020). The maximum-likelihood tree was established by MEGA X (Kumar et al. 2018) based on 13 PCGs (Figure 1). It showed that Eristalinae could be divided into six major clades: Eristalini, Milesiini, Volucellini, Chrysogasterini, Cheilosiiini, and Xylotini. Eristalinae was monophyletic, which was consistent with the previous report (2003). Besides, each tribe was also monophyletic. It is revealed in Figure 1 that *X. coquillettii* (Xylotini) should be regarded as a sister to *Ferdinadea cupera* (Rhingiini). In this research, essential fundamental data to understand the phylogenetic relationships among major lineages of the subfamily was provided.

**Ethics statement**

All animal-related experiments were performed according to the protocols approved by the Institutional Animal Care and Use Committee of Anhui Agricultural University (Grant number AHAU2021038).

**Author contributions**

Conceptualization, S.L. and Q.T.; data curation, Z.P. and X.C.; formal analysis, Z.P. and X.C.; funding acquisition, S.L. and Q.T.; investigation, Z.P. and R.Z.; methodology, Z.P.; project administration, S.L. and Q.T.; supervision, S.L. and Q.T.; validation, Z.P. and R.Z.; visualization, S.L., Q.T., and R.Z.; writing-original draft, Z.P.; writing-review and editing, S.L., Q.F., and R.Z. All authors contributed to the final version of the paper. All authors have read and agreed to the published version of the manuscript.

**Disclosure statement**

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

**Funding**

This research was supported by the Key Project of the Natural Science Foundation of Anhui Provincial Department of Education [KJ2020A0100], Grants from Anhui Agricultural University [2020zd28] and the Talent Research Project of Anhui Agricultural University [rc342009].
Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under the accession no. MZ905457. The associated BioProject, BioSample numbers, and SRA are PRJNA757554, SAMN21018174, and SRS9990438, respectively.

References

Andrews S. 2016. FASTQC; [accessed 2021 Feb 2]. http://www.bioinformatics.babraham.ac.uk/projects/fastqc.
Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 313–319.
Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):18.
Hervé-Bazin.1914. Syrphides recueillis au Japon par M. Edme Gallois (Diptera). Annales de la Société Entomologique de France. 83, 398–416.
Huo KK, Li H, Lan F. 2018. Investigation on syrphidae in anzihe nature reserve of Sichuan. J Shaanxi Univ Technol. 34(2):72–78.
Kearse MD, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12): 1647–1649.
Kumar S, Stecher G, Michael L, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549.
Mengual X. 2015. The systematic position and phylogenetic relationships of Asiobaccha Violovitsh (Diptera, Syrphidae). J Asia Pac Entomol. 18(3):397–408.
Young AD, Lemmon AR, Skevington JH, Mengual X, Stahls G, Reemer M, Jordaens K, Kelso S, Lemmon EM, Hauser M, et al. 2016. Anchored enrichment dataset for true flies (order Diptera) reveals insights into the phylogeny of flower flies (family Syrphidae). BMC Evol Biol. 16(1):243.
Zheng R, Gao FL, Jakovlic I, Zou H, Zhang J, Li WX, Wang GT. 2020. PhylSoUtis: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Mol Ecol Resour. 20(1):348–355.