The complete mitochondrial genome of the tribe Rhingiini (Diptera:Syrphidae) and phylogenetic analysis

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ABSTRACT

The complete mitochondrial genome of Ferdinandea cuprea was assembled and annotated applying next generation sequencing, which is the first reported mitogenome reference of species from Rhingiini tribe of Syrphidae family. The mitogenome of *F. cuprea* has length of 15,907 base pair and comprises of 37 genes (13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes) and one putative control region. Most protein-coding genes are initiated with ATN or CAA (COX1), and terminate with TAA. The results of phylogenetic tree reconstruction statistically suggested the monophyly of Syrphinae, but that of Eristalinae is not supported, and shows tribe Rhingiini is closer to Milesiini.

Syrphidae is one of the most diverse and species-rich clade in Diptera, comprising over 9,600 described species (Thompson 2008), play an important ecological role in plant pollinators, natural enemies of plant pests and nutrient recycling (Rotheray and Gilbert 2011; Li et al. 2017). While Rhingiini is one of the most important tribe of subfamily Eristalinae (Diptera: Syrphidae) (Thompson and Rotheray 1998), the systemics and taxonomic classification of this tribe is controversial. Following Peck (1988), the tribe Rhingiini were comprised 11 genera, while Thompson (1972) and Shatalkin (1975) classified the tribe Rhingiini into 10 and 8 genera (Peck 1988; Thompson 1972; Shatalkin 1975; Velterop 1986). *Ferdinandea cuprea* (Scopoli, 1763), a very common hoverfly belonging to the tribe Rhingiini of subfamily Eristalinae (Diptera: Syrphidae) has also an ambiguous status (Scopoli 1763; Stuke et al. 2004). The significant morphological characteristics are strong black bristles on thorax and scutellum, and dark spots on wings (Thompson and Rotheray 1998). The adults of *F. cuprea* prefer habitat of natural deciduous forests, while larvae mainly live in sap-runs of generally over-mature trees (Ricarte et al. 2010). Here, we sequenced and assembled the complete mitogenome of species *F. cuprea* to contribute more data for better understanding the phylogenetic relationships within the family Syrphidae.

Specimens of *F. cuprea* were collected from the Changqing National Nature Reserve (107°17'E, 33°19'N) on July 2019 and deposited in the Museum of Zoology and Botany, Shaanxi University of Technology, Hanzhong, China (SUHC), with the accession number of SYY20190077.

Genomic DNA of *F. cuprea* was extracted using the Qiagen DNeasy kit (Qiagen, Hilden, Germany), and 150 bp paired-end library was constructed for sequencing applying Illumina HiSeq 4000 platform. The raw data of whole genome sequencing have been submitted to the Genome Warehouse in National Genomics Data Center (CNB-NGDC) (Zhang et al. 2020) with accession number of CRA003174 (https://bigd.big.ac.cn/gsa/). The software MitoZ (Meng et al. 2019) was used for mitochondrial genome assembly, annotation and visualization. The putative control region was depended on the boundary of tRNAs. The assembled complete mitogenome of *F. cuprea* reported in this paper has been deposited in the sequences database of CNB-NGDC with accession number of GWHAOQX000000000 (https://bigd.big.ac.cn/gwh).

The complete mitogenome of *F. cuprea* is 15,907 bp in length that includes 37 typical insect mitochondrial genes: 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA), and two ribosomal RNA (rRNA), as well one putative control region (D-loop). No rearrangement was detected in this mitogenome and all genes were arranged in the same order as the putative ancestral arrangement of insects (Cameron, 2014). Twenty-three genes were encoded by the majority strand (J-strand) and the other 14 genes were located by the minority strand (N-strand). With the exception of control...
region, 8 overlaps (ranging from 2 to 19 bp) and 20 intergenic spacers (1 and 72 bp) were found as intervals between coding genes in this mitogenome. The overall nucleotide composition of the *F. cuprea* showed a strong AT biased (40.7% of A, 38.9% of T, 8.4% of G, 12.1% of C), a positive AT-skew (0.022) and a negative GC-skew (-0.181) like other Syrphidae mitochondrial genomes (Li et al. 2017). Except gene COX1 started with CAA, the rest of 12 PCGs use ATN as the initiation codon (ATP8, ND2, ND3, ND5 and ND6 used ATT, COX2, COX3, ND4, ND4L and Cytb used ATG, ATP6 and ND1 used ATA). For all PCGs, TAA are used as termination codon.

To determine the phylogenetic position of *F. cuprea*, we reconstructed the phylogenetic tree with other 14 Syrphidae species and three outgroups sequences (available in GenBank database: https://www.ncbi.nlm.nih.gov/). Based on the multiple alignments of 13 PCGs by MAFFT (Katoh and Standley, 2013), the maximum-Likelihood (ML) tree was constructed with IQ-tree (Nguyen et al. 2015) with 1000 bootstrap replications (Figure 1). The tree shows a high support for the monophyly of family Syrphidae which is consistent with the previous published results (Young et al. 2016; Li et al. 2017). The monophyly of Eristalinae was not supported in present analysis. The subfamily Eristaline, including tribes of *Volucellini (V. nigricans*, *E. fuscicornis*, *P. zonata*), *Milesiini* (*K. angustiabdomena*, *H. virgata*, *E. barclayi*, *E. fuscicornis*, *E. tabanoides*, *E. vicarians*, *E. tenax*), *Rhingiini* (*E. barclayi*, *H. virgata*), was not supported as suggested by previous research (Pauli et al. 2018), and tribe Rhingiini is closer to Milesiini.

**Disclosure statement**

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

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**Data availability statement**

The data that support the findings of this study are openly available in CNCB-NGDC at https://bigd.big.ac.cn/gwh, reference number GWHAOQX00000000.

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