

The complete mitochondrial genome of *Silba* sp. (Diptera: Lonchaeidae)

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ABSTRACT

The mitochondrial genome of *Silba* sp. was sequenced and annotated as the first representative of family Lonchaeidae. The complete mitochondrial genome of *Silba* sp. is 16,008 bp totally, consisting of 13 protein-coding genes, two rRNAs, and 22 transfer RNAs, which has a similar gene structure with other published species of Diptera. The nucleotide composition biases toward A and T is 77.2% 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 Diptera species supported the monophyly of superfamily Tephritoidea.

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The Lonchaeidae is a small family with body size from minute to medium (2.0–6.0 mm). Lonchaeids are commonly known as lance flies and found mainly in humid or shaded places (Lemos et al. 2015). They are easily recognized by glossy, dark blue bodies, and hyaline or very pale brown wings. The Lonchaeidae flies have about 500 described species worldwide (Pape et al. 2011). Though larvae of Lonchaeidae are mainly followers of decay in vegetation (McAlpine 1987), some species of genera *Dasiops* and *Neosilba* are important parts of fruit flies and have actual or potential economic importance to the fruit crops or vegetables (Nicácio and Uchôa 2011).

Lonchaeidae is considered to be a family of Tephritoidea. It was thought to be the sister group of the other subgroups of Tephritoidea and distinguished by its unpatterned wings and aerial-swarm mating systems (Sivinski 1999). However, recent molecular studies uncovered that Lonchaeidae and Pallopteridae were sister group (Han and Ro 2005; Han and Ro 2016). The previous phylogenetic researches at high level of Tephritoidea have not been in agreement, and studies about relationships among genera and subfamilies of this family were limited.

Specimens of *Silba* sp. (accession number: WL13) were collected in Gutianshan, Quzhou, Zhejiang, China and identified by Liang Wang. The specimens were deposited in the Entomological Museum of China Agricultural University, Beijing.

The genomic DNA was extracted from adult's whole body using the DNeasy DNA Extraction kit (TIANGEN) and stored at -20°C refrigerator. The library was sequenced on an Illumina HiSeq 2500. The bait sequence COI was amplified by standard PCR reactions and BLAST search was carried out with

BioEdit 7.0.5.3. and the position of all tRNA genes was confirmed using tRNAscanSE 2.0 (Lowe and Chan 2016). The complete mitochondrial genome of *Silba* sp. (MK913844) was 16,008 bp in length and consisted of 13 typical invertebrate PCGs, 22 transfer RNA genes, two rRNA genes (12S and 16S), and a 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), except for tRNA^{Ser(AGN)} gene substituted by another tRNA^{Phe} gene. The mito-genome nucleotide composition of *Silba* sp. was 39.2% of A, 38.0% of T, 9.3% of G, and 13.5% of C, and A + T content was 77.2%. Among the protein-coding genes, six genes took the start codon of ATG and five genes used ATT as start codon while COI gene and ND1 gene got TCG and TTG, respectively. The termination codon of these protein-coding genes had three types (five genes were TAA, three genes use incomplete stop codon TA + tRNA, five genes were T + tRNA).

There are 11 species retrieved from NCBI and one new sequenced data in phylogeny analysis; the genbank accession numbers are listed as follows: *Anopheles oryzalimnetes* NC_030715, *Bactrocera correcta* JX456552.1, *Bactrocera cucurbitae* NC_016056.1, *Ceratitis capitata* NC_000857, *Cestrotus liui* NC_034922, *Drosophila melanogaster* NC_024511, *Drosophila yakuba* NC_001322, *Liriomyza trifolii* NC_014283, *Nemopoda mamaevi* NC_026866, **Silba* sp. MK913844, and *Simulium variegatum* NC_033348. Thirteen protein-coding genes (PCGs) were used to reconstruct phylogenetic relationship with maximum likelihood method. The topology was given and bootstrap support numbers are shown in Figure 1. ML analysis revealed that the outgroups *Anopheles oryzalimnetes* and *Simulium variegatum* were diverged from the rest. Tephritoidea was supported as a monophyletic clade and

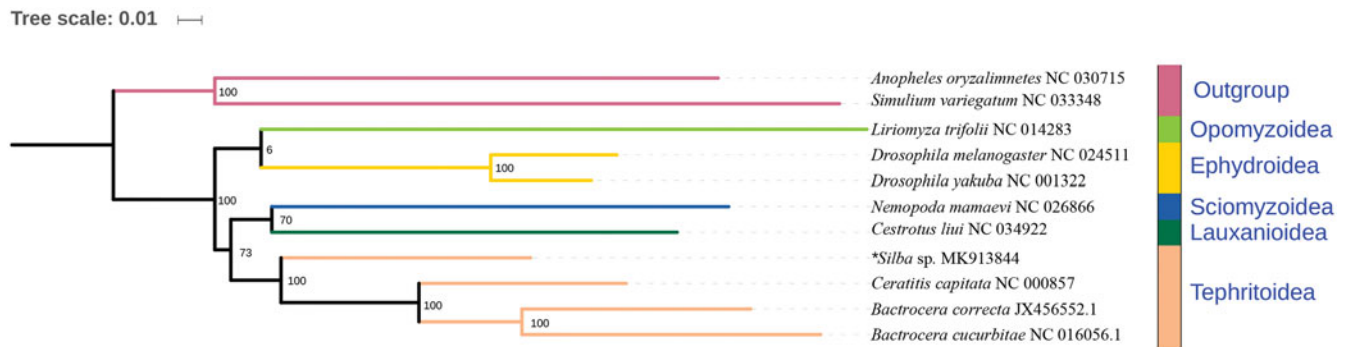


Figure 1. The phylogenetic tree of ML analysis based on 13PCGs; "*" indicated new sequenced data in this study.

assigned to be the sister group of Lauxanioidea + Sciomyzoidea.

The complete mitochondrial genome of *Silba* sp. provides valuable information for future genetic and evolutionary studies of family Lonchaeidae and superfamily Tephritoidea.

Disclosure statement

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

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