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 andUCHOA 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
assigned to be the sister group of Lauxanioidea + Sciomyoidea.

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.

**Funding**

This study was supported by National Key Research and Development Plan from the Ministry of Science and Technology of China [2017YFD0201000], the National Natural Science Foundation of China [31772497], and Ministry of Science and Technology of the People’s Republic of China [2005DKA21402].

**ORCID**

Xin Li [http://orcid.org/0000-0003-0773-6232](http://orcid.org/0000-0003-0773-6232)

**References**

Han HY, Ro KE. 2005. Molecular phylogeny of the superfamily Tephritoidea (Insecta: Diptera): new evidence from the mitochondrial 12S, 16S, and COII genes. Mol Phyl Evol. 34:416–430.

Han HY, Ro KE. 2016. Molecular phylogeny of the superfamily Tephritoidea (Insecta: Diptera) reanalysed based on expanded taxon sampling and sequence data. J Zool Syst Evol Res. 54:276–288.

Lemos L, Adidas E, Costa-Neto S, Deus E, Jesus-Barros C, Striks P. 2015. New findings on Lonchaeidae (Diptera: Tephritoidea) in the Brazilian Amazon. Fla Ent. 98:1227–1238.

Li X, Wang Y, Su S, Yang D. 2016. The complete mitochondrial genomes of *Musca domestica* and *Scathophaga stercoraria* (Diptera: Muscoidea: Muscidae and Scathophagidae). Mitochondrial DNA A. 27:1435–1436.

Lowe T, Chan P. 2016. trRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. Nucleic Acids Res. 44:W54–W57.

McAlpine J. 1987. Lonchaeidae. In: McAlpine J, editor. Manual of nearctic Diptera, Vol. 2. Ottawa: Biosystematics Research Institute; p. 791–797.

Nicacio J, Uchoa M. 2011. Diversity of frugivorous flies (Diptera: Tephritidae and Lonchaeidae) and their relationship with host plants (Angiospermae) in environments of South Pantanal Region. Brazil Fla Ent. 94:443–466.

Pape T, Blagoderov V, Mostovskiy M. 2011. Order Diptera Linnaeus, 1758. Zootaxa. 3148:222–229.

Qilemoge Gao S, Tang C, Wang N, Yang D. 2018. The mitochondrial genome of *Dioscoccus lamellatus* (Diptera: Dolichopodidae). Mitochondrial DNA B. 3:346–347.

Ren J, Yang Q, Gao S, Pan Z, Chang W, Yang D. 2019. The mitochondrial genome of *Limonia phragmitidis* (Diptera Limoniidae). Mitochondrial DNA B. 4:719–720.

Sivinski J. 1999. Breeding habits and sex in families closely related to the tephritidae: opportunities for comparative studies of the evolution of fruit fly behavior. In: Aluja M, Norrbom A, editors. Fruit flies (Tephritidae): phylogeny and evolution of behavior. Boca Raton: CRC Press; p. 23–37.

Zhou Q, Ding S, Li X, Zhang T, Yang D. 2017. Complete mitochondrial genome of *Allognosta vagans* (Diptera, Stratiomyidae). Mitochondrial DNA B. 2:461–462.