

The mitochondrial genome of *Prosthiochaeta* sp. (Diptera: Platystomatidae)

Xin Li^a , Jiale Zhou^a, Liang Wang^a, Peng Hou^b and Ding Yang^a

^aCollege of Plant Protection, China Agricultural University, Beijing, China; ^bCollege of Life Science and Bioengineering, Shenyang University, Shenyang, China

ABSTRACT

The mitochondrial genome of *Prosthiochaeta* sp. was sequenced and annotated as a new representative of family Platystomatidae. The nearly complete mitochondrial genome of *Prosthiochaeta* sp. is 16,169 bp totally, consisting of 13 protein-coding genes, 2 rRNAs, and 22 transfer RNAs, which gene frame is similar with other dipteran mitogenomes. The nucleotide composition biases toward A and T is 70.8% of the entirety. IQ-tree analysis revealed that Tephritoidea including *Prosthiochaeta* sp. was monophyletic as a sister group to Opomyzoidea and Syrphoidea. Tephritoidea as well as Syrphoidea and Opomyzoidea were nested in Ephydroidea, while Lauxanioidea and Sciomyzoidea were assigned to be sister groups. Platypezoidea was monophyletic as a basal clade of phylogenetic tree.

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Species of Platystomatidae are small to medium-sized (body length 2.5–20.0 mm) and generally have the metallic color (Wendt 2016). They are characterized by the transverse section of CuA₂ not indented, cell cup not produced into an acute posterodistal lobe, costal break at subcostal position absent, and incurved lower orbital bristles also absent (McAlpine 1998). They are almost distributed worldwide with over 1200 known species (McAlpine 1998, 2001).



Specimens of *Prosthiochaeta* sp. (CAU-WL-2019511) were collected in Shengshuige, Emei Mountain, Sichuan province, China (E103.416784, N29.570113) and identified by Liang Wang. The specimens were deposited in the Entomological Museum of China Agricultural University (CAU), Beijing.

The genomic DNA was extracted from an adult's whole body except head and wings using the DNeasy DNA Extraction kit (TIANGEN) and stored at –20 °C refrigerator. After NGS sequencing, the sequenced reads were assembled by NOVOPlasty 3.7.2. The mitochondrial genome of *Prosthiochaeta* sp. contains 22 transfer RNA genes, 13 protein-coding genes, and 2 ribosomal RNA genes, which are close to other flies reported before (Kang et al. 2016; Li et al. 2017; Zhou et al. 2017; Yang et al. 2019; Hou et al. 2020). The mitochondrial genome nucleotide composition of *Prosthiochaeta* sp. is 39.8% of A, 31.0% of T, 11.1% of G, 18.0% of C, and A + T content is 70.8%. The genes ATP6, COX2, COX3, CYTB, NAD3, NAD4 and NAD4L started with codon ATG; the start codon ATT was shared with genes NAD1, NAD2, NAD5 and NAD6; only ATP8 was started with ATC codon. There were 9 genes (ATP6, ATP8, COX1, COX3, NAD2, NAD3, NAD4, NAD4L and NAD6) terminated with TAA stop codon; CYTB ended with TAG codon; COX2 and NAD5 stopped with single T; and NAD1 terminated with TA.

There is datum of 20 species retrieved from NCBI and 1 new sequenced data used in phylogenetic analysis. Genbank accession numbers are listed as follows: *Ceratitis capitata* NC_000857, *Zeugodacus cucurbitae* NC_016056, *Procecidochares utilis* NC_020463, *Anastrepha fraterculus* NC_034912, *Dacus bivittatus* NC_046468, *Bactrocera ruiiensis* NC_046952, *Tephritis femoralis* NC_047184, *Pipunculus* sp. MF774216, *Trypetoptera punctulata* MK644823, *Nemopoda mamaevi* NC_026866, *Lonchoptera multisetata* MF774215, *Platypeza* sp. MF774217, *Liriomyza trifolii* NC_014283, *Liriomyza bryoniae* NC_016713, *Cestrotus liui* NC_034922, *Spaniocelyphus pilosus* NC_034924, *Drosophila yakuba* NC_001322, *Drosophila melanogaster* NC_024511, *Anopheles oryzalimnetes* NC_030715, *Simulium variegatum* NC_033348, *Euprosopia* sp. MK640609 and *Prosthiochaeta* sp. MT528242. Thirteen protein-coding genes (PCGs) were used to reconstruct the phylogenetic relationship with IQ-tree (Nguyen et al. 2015; Hoang et al. 2018) in Phylsuite software (Zhang et al. 2020). The topology was given and bootstrap support numbers are shown in Figure 1. IQ-tree analysis revealed that the outgroups *Anopheles oryzalimnetes* and *Simulium variegatum* diverged from the rest. The Tephritoidea including *Prosthiochaeta* sp. was monophyletic as a sister group to Ephydroidea + (Opomyzoidea + Syrphoidea). All the four superfamilies are paraphyletic with Lauxanioidea and Sciomyzoidea, which were assigned to be sister groups. Platypezoidea was monophyletic as a basal clade of phylogenetic tree.

Disclosure statement

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

CONTACT Ding Yang  dyangcau@126.com  College of Plant Protection, China Agricultural University, Beijing, China

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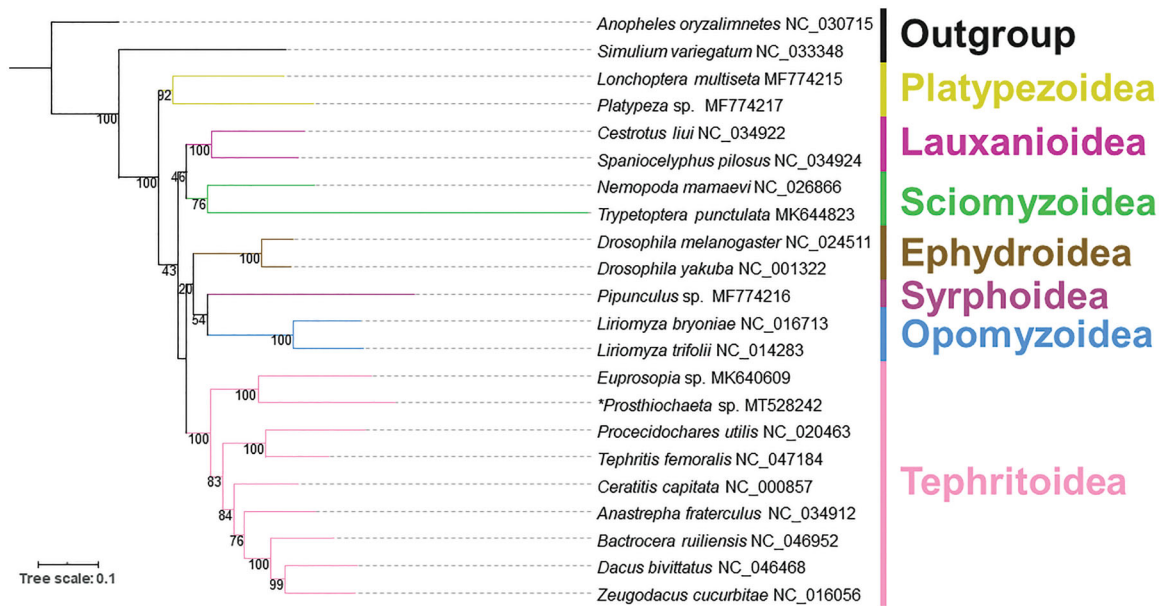


Figure 1. The phylogenetic tree of IQ-tree analysis based on 13PCGs. '*' indicated newly sequenced data in this study.

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ORCID

Xin Li  <http://orcid.org/0000-0003-0773-6232>

Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov>), accession number is MT528242.

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