Characterization of the complete mitochondrial genome of *Drosophila busckii* (Diptera: Drosophilidae)

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**ABSTRACT**

In this study, we sequenced and analyzed the complete mitochondrial genome of *Drosophila busckii* (Diptera: Drosophilidae). The mitogenome was 15,214 bp in length, containing 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes. The gene organization of *D. busckii* is identical to the ancestral gene arrangement found in most insects. All protein-coding genes started with ATN, except for *cox2* and *nad5*, which used noncanonical codon TTG and GTG, respectively.

The fruit fly genus *Drosophila* (Diptera: Drosophilidae) is a diverse insect group with more than 1600 species worldwide (O’Grady and DeSalle 2018). Species of the genus *Drosophila* contain model organisms used in several biological research fields, and economically pests such as *Drosophila suzukii* (Kim et al. 2016). Nine subgenera were divided, including *Dorsilopha, Drosophila, Sophophora,* and so on. *Drosophila busckii* belongs to the subgenus *Dorsilopha,* in which only four species were recorded (O’Grady and DeSalle 2018). In this study, we report the mitochondrial genome of *Drosophila busckii,* representing the first mitogenome of the subgenus *Dorsilopha.*

Adults of *D. busckii* were collected in Nanjing (32.04° N and 118.89° E), Jiangsu province, China. The voucher specimens (DJNS) and its DNA were deposited in the Nanjing Agricultural University, Nanjing, China. Genomic DNA was extracted using Ezup Column Animal Genomic DNA Purification Kit (Sangon Biotech, Shanghai, China) following the manufacturer’s protocols. The DNA concentration was detected by Qubit 3.0 using Q33230 QubitTM 1X dsDNA HS Assay Kit (ThermoFisher, Waltham, MA). The DNA library was sequenced on the Illumina Hi-Seq platform generating 150 bp paired-end reads. The mitogenome was assembled using NOVOPlasty v2.7.2 (Dierckxsens et al. 2017), and annotated via the software MitoZ (Meng et al. 2019).

The complete mitochondrial genomes of *D. busckii* was 15,214 bp in length (GenBank Accession No. MT429169). The mitogenome encodes the whole set of 37 genes (13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes) as observed in most insects. The gene organization of *D. busckii* is identical to that of the ancestral gene arrangement in most insects (Boore 1999).

The typical start codons ATN are assigned to 11 of all protein-coding genes PCGs. The genes *cox1* and *nad5* initiate with TTG and GTG, respectively. For 13 PCGs, four stop codons are found: T (*cox2, nad1*), TA (*nad4, nad5*), TAG (*cytb*) and TAA (other eight PCGs). The predicted secondary structures of all tRNA genes are typical cloverleaf except for *tmnS1* (AGN), lacking the dihydrouridine (DHU) stem. The *nad4l–nad4* overlap was 1 bp in size, and not identical to that of *atp8–atp6* (ATGATAA). The intergenic spacer between *tmnS2* (UCN) and *nad1* was 18 bp in length.

Each PCG was translated into an amino acid sequence, aligned with MAFFT v7.394 (Katoh and Standley 2013), and trimmed using trimAl v1.4.1 (Capella-Gutiérrez et al. 2009). The concatenated dataset of 13 PCGs were generated using FASconCAT-G v1.04 (Kück and Longo 2014). A maximum-likelihood tree (Figure 1) was inferred employing protein mixture model C60 with a bootstrap of 1000 replicates in the IQ-TREE (Nguyen et al. 2015). Three species of Tephritidae were chosen as outgroups. In the ML tree, the position of *D. busckii,* which clustered with *Drosophila albomicans* and *Drosophila unipunctata,* was in the clade of subgenus *Drosophila,* indicating the non-monophyletic subgenus *Dorsilopha*.
Figure 1. Maximum-likelihood phylogenetic tree inferred from 13 protein-coding genes. Bootstrap support values are given on nodes.
Drosophila. The subgenus Sophophora represented by Drosophila melanogaster, Drosophila yakuba and Drosophila suzukii, was clustered with Drosophila formosana. The relationships between subgenus Dorsilopha and other fruit fly species groups need to be further investigated.

Disclosure statement

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

Data availability

The data that support the findings of this study are openly available in figshare at http://10.6084/m9.figshare.12250331.

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