Rhynocoris Hahn, 1834 belongs to the family Reduviidae, a large genus with 170 known species (Zhao 2008). Rhynocoris fuscipes (Fabricius 1787) is a common predator in China, distributed in Southeast Asia, and was massively reared in China as a biological control agent. In this study, the complete mitochondrial genome of R. fuscipes was sequenced and described. Adult specimens were collected from Xiongnan, Guangdong, China (25°9'66" N 114°28'45" E) in 18th May 2021 by Mengqing Wang and identified by Mengqing Wang. Specimens were deposited in the Natural Enemy Insects Museum (Accession Number: NI2021-19) of the Institute of Plant Protection, Chinese Academy of Agricultural Sciences (IPPCAAS) (Mengqing Wang, mengqingsw@163.com, Room 307, Plant Protection Building).

The total genomic DNA was extracted from the whole body of the specimen using the QiAamp DNA Blood Mini Kit (Qiagen, Germany) and stored at −20°C until needed. The mitogenome was sequenced in BerryGenomics company used NGS. 1 μg of genomic DNA was used to generate libraries with an average insert size of 350 bp, which were sequenced using the Illumina HiSeq 56000 (San Diego, CA, United States) with 150 bp paired-end reads on one sample per flow-cell lane. A total of 17,635,709 raw paired reads were generated. The quality of all sequences was checked using FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). Clean reads were assembled and annotated using the MitoZ v2.4 pipeline (Meng et al. 2019).

The complete mitogenome of R. fuscipes is 15,542 bp in size (GenBank accession number: MZ440304) including 37 typical insect mitochondrial genes (13 protein-coding genes, 22 transfer RNA genes, and two ribosomal RNA genes) and one control region. Gene arrangement is identical to that of the putative ancestral arrangement of insects. All protein-coding genes initiate with ATN codons and terminate with TAA codons except for COII, ND4, and ND5 use TA or a single T residue as the termination codons. All tRNAs have the clover-leaf structure except for the tRNASer(AGN) and the length of them range from 62 to 70 bp. The phylogenetic result supports the monophyly of Harpactorinae and the sister relationship between R. fuscipes and Rhynocoris incertis.
and the ML tree was constructed by IQ-TREE 2.0.6 (Bui et al. 2020) under the GTR + I + G model estimated by PartitionFinder v1.1.0 (Lanfear et al. 2012). The phylogenetic tree shows Harpactorinae is monophyletic, which is also recovered in previous molecular and morphological analyses (Weirauch et al. 2014; Wu et al. 2020). The sister relationship between R. fuscipes and Rhynocoris incertis is also highly supported. The mitogenomic data of R. fuscipes provides a basic data for future research investigating the unclear relationships within Reduviidae.

Figure 1. Phylogenetic relationship of 51 Reduviidae species inferred from analysis of 13 protein-coding genes and two rRNA genes. Bayesian inference and maximum-likelihood analyses recover the same three topology. Numbers on branches are Bayesian posterior probabilities (left) and bootstrap values (right). The newly sequenced mitochondrial genome was highlighted in red.
Disclosure statement

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

Funding

This research was supported by the National Key Research and Development Plan from the Ministry of Science and Technology of China [2019YFD0300104] and the Major Projects of China National Tobacco Corporation [110202101028 (LS-03), 201941].

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MZ440304. The associated BioProject, SRA, and BioSample numbers are PRJNA740358, SRR14902174, and SAMN19842831, respectively.

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