First complete mitogenome of *Axarus fungorum* (Albu, 1980) from Guizhou Province, China (Diptera, Chironomidae)

Yan Qi\(^a\), Xin Duan\(^a\), Ke-Long Jiao\(^a\) and Xiao-Long Lin\(^{b,c}\)

\(^a\)Department of Plant Protection, College of Horticulture and Landscape, Tianjin Agricultural University, Tianjin, China; \(^b\)College of Life Sciences, Nankai University, Tianjin, China; \(^c\)Engineering Research Center of Environmental DNA and Ecological Water Health Assessment, Shanghai Ocean University, Shanghai, China

**ABSTRACT**

*Axarus fungorum* (Albu, 1980) exhibits certain adaptations to different aquatic environments, appearing as an important evaluation element for freshwater quality monitoring. In this study, complete mitogenome of *A. fungorum* was provided for the first time to define the systematic and phylogenetic history of this taxon. The whole mitogenome is 15,696 bp long with high A + T content that consists of 13 protein-coding genes, 22 tRNA genes, two rRNA genes, and a noncoding control region. ML analysis showed support for monophyly of Chironominae and close relationship between *A. fungorum* and *Chironomus* generic genera.

*A. fungorum* (Albu, 1980) belongs to Chironominae, a subfamily under the Chironomidae, one of the most abundant invertebrate taxa in freshwater ecosystems with more than 6300 valid species. Chironomid larvae are considered as an excellent indicator for monitoring aquatic environment quality due to their wide distribution, high species diversity, large population, sensitivity, and adaptability (Ferrington 2008). Due to species diversity and variable morphological features within Chironomidae, the traditional morphological identification is inconvenient. In such instances, mitogenomic data can be considered as powerful and convenient material for molecular identification and phylogenetic studies for Diptera (e.g. Yan et al. 2019; Li et al. 2020; Zhang et al. 2022).

However, complete mitogenomes are still scarce for Chironomidae (Beckenbach 2012; Kim et al. 2016; Deviatiiarov et al. 2017; Kong et al. 2021; Lei et al. 2021; Zheng et al. 2021, 2022; Fang et al. 2022). In the present study, we have provided complete mitochondrial genome of *A. fungorum* for the first time.

Fresh and adult male individuals of *A. fungorum* were collected from Meitan, Guizhou, China (27.828857°N, 107.5955098°E) on 8 June 2020. The DNeasy Blood and Tissue kit (QIAGEN Sciences, Valencia, CA) was used to isolate total genomic DNA from the muscle tissues of head and thorax. The DNA and voucher specimen of *A. fungorum* has been deposited in the College of Fisheries and Life Science, Shanghai Ocean University, Shanghai, China (https://www.shou.edu.cn). *COI of A. fungorum* (GenBank accession: MN521232) was used as bait to iterate and assemble the mitogenome of *A. fungorum*. DNA fragments with 350 bp insert size were sequenced by Illumina Nova6000 (PE150, Illumina, San Diego, CA) platform using pair-end strategy at Novogene Co., Ltd. (Cambridge, UK). Four Gb clean data were obtained from the library by trimming using Trimmomatic (Bolger et al. 2014). IDBA-1.1.1 (Peng et al. 2012) software package was employed to assemble the data. The bait sequence of COI (Crampton-Platt et al. 2015) was used in the BLAST program (Altschul et al. 1990) to compare with the mitogenome of *A. fungorum*. The percentage of match rate was found as 100% from the blast result. The mitogenome annotation was conducted as previously described by Zheng et al. (2020).

The double-strand circular mitogenome of *A. fungorum* is 15,696 bp in length (GenBank accession no. ON099430) which encodes for 37 genes (13 protein-coding genes, two rRNA genes, and 22 tRNA genes) and a control region. Nucleotides within the mitogenome were distributed as follows: 41.2% A, 38.3% T, 12.2% C, and 8.3% G. The most frequently observed start codons were ATG for ATP6, COII, COIII, CytB, ND4, ND4L and ATT for ATP8, ND2, ND3, ND6, respectively, while GTG for ND5; TTG for COI and ND1. All of the 13 PCGs were terminated with TAA stop codon. Mitogenome organization, nucleotide composition and codon usage were similar to the previously sequenced Chironomidae mitogenomes with a high AT bias (79.5%).

Eighteen mitogenomes of Chironominae and two of Orthocladiinae were mined from GenBank for the
phylogenetic analysis. Initially, sequences of 13 PCGs were concatenated and then aligned with MAFFT (Katoh and Standley 2013) keeping all the settings in default (Katoh and Standley 2013). Using 1000 bootstraps and PMSF acid substitution model, we conducted phylogenetic analysis by maximum-likelihood (ML) method with IQ-TREE (Nguyen et al. 2015) considering Limnophyes minimus and Rheocricotopus villiculus as outgroups. Topologies from the reconstructed tree strongly supported the monophyly of Chironominae, and the sister relationship between A. fungorum and the Chironomus generic genera (Figure 1).

**Ethics statement**

The collection of specimen conformed to the requirement of international ethics, which did not cause damage to the local environment. The process and purpose of this experimental research were in line with the rules and regulations of our institute. There are no ethical issues and other conflicts of interest in this study.

**Author contributions**

Yan Qi and Xin Duan were involved in the conception and design, analysis, and interpretation of the data; Ke-Long Jiao and Xiao-Long Lin were involved in the drafting of the paper, revising it critically for intellectual content and the final approval of the version to be published; and the authors agreed to be accountable for all aspects of the work. No potential conflict of interest was reported by the authors.

**Disclosure statement**

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

**Funding**

This study was supported by the National Natural Science Foundation of China [31900344] and the China Postdoctoral Science Foundation [2018M640227].

**ORCID**

Ke-Long Jiao [http://orcid.org/0000-0001-7467-9333](http://orcid.org/0000-0001-7467-9333)

Xiao-Long Lin [http://orcid.org/0000-0001-6544-6204](http://orcid.org/0000-0001-6544-6204)

**Data availability statement**

The data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/) under the accession no. ON099430. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA820975, PRJNA820975, and SAMN27029903, respectively.

**References**

Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. J Mol Biol. 215(3):403–410.

Beckenbach AT. 2012. Mitochondrial genome sequences of Nematocera (lower Diptera): evidence of rearrangement following a complete genome duplication in a winter crane fly. Genome Biol Evol. 4(2):89–101.

Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics. 30(15):2114–2120.
