MITOCHONDRIAL DNA PART B
2022, VOL. 7, NO. 10, 1807–1809
https://doi.org/10.1080/23802359.2022.2131369

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

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.

ARTICLE HISTORY
Received 30 May 2022
Accepted 27 September 2022

KEYWORDS
Chironomids; mitochondrial genome; phylogeny

Axarus 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, Xiao-Long Lin, lin880224@gmail.com) under the voucher number DLC28. 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

CONTACT Ke-Long Jiao jiaokelong@163.com Department of Plant Protection, College of Horticulture and Landscape, Tianjin Agricultural University, Tianjin 300392, China; Xiao-Long Lin lin88024@gmail.com Engineering Research Center of Environmental DNA and Ecological Water Health Assessment, Shanghai Ocean University, Shanghai 201306, China

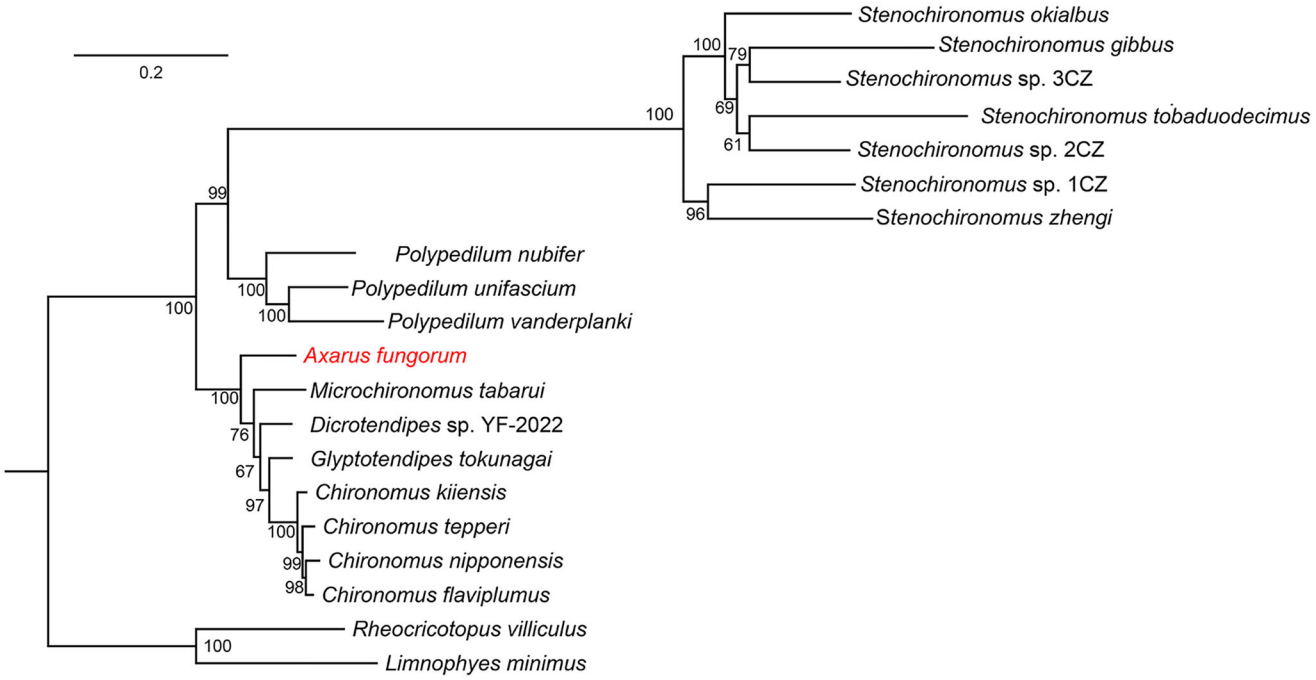

Figure 1. Phylogenetic tree of 20 Chironomidae species based on the concatenated dataset of 13 PCGs using the maximum-likelihood (ML) method. The following sequences were used: *Axarus fungorum* ON099430 (present study), *Chironomus flaviplumus* MW770891 (Park et al. 2021), *Chironomus kiiensis* MZ150770 (Liu et al. 2022), *Chironomus nipponensis* MZ747092 (Shen et al. 2022), *Chironomus tepperi* JN861749 (Beckenbach 2012), *Dicrotendipes* sp. YF-2022 MZ747093 (direct submission), *Glyptotendipes tokunagai* MZ747091 (direct submission), *Limnophyes minimus* MZ041033 (Fang et al. 2022), *Microchironomus tabarui* MZ261913 (Kong et al. 2021), *Rheocricotopus villiculus* MW373526 (Zheng et al. 2021), *Stenochironomus gibbus* OL742440 (Zheng et al. 2022), *Stenochironomus okialbus* OL753645 (Zheng et al. 2022), *Stenochironomus* sp. 1CZ OL753646 (Zheng et al. 2022), *Stenochironomus* sp. 2CZ OL742441 (Zheng et al. 2022), *Stenochironomus* sp. 3CZ OL753647 (Zheng et al. 2022), *Stenochironomus tobaduodecimus* OL753648 (Zheng et al. 2022), *Stenochironomus zhengi* OL753649 (Zheng et al. 2022), *Polypedilum nubifer* MZ747090 (direct submission), *Polypedilum unifascium* MW677959 (Lei et al. 2021), and *Polypedilum vanderplanki* KT251040 (Deviatiiarov et al. 2017).

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
Xiao-Long Lin 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/ 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.

Crampton-Platt A, Timmermans MJ, Gimmel ML, Kutty SN, Cockerill TD, Vun Khen C, Vogler AP. 2015. Soup to tree: the phylogeny of beetles inferred by mitochondrial metagenomics of a Bornean rainforest sample. Mol Biol Evol. 32(9):2302–2316.

Deviatiiarov R, Kikawada T, Gusev O. 2017. The complete mitochondrial genome of an anhydrobiotic midge *Polypedilum vanderplanki* (Chironomidae, Diptera). Mitochondrial DNA A DNA Mapp Seq Anal. 28(2):218–220.

Fang XL, Li X, Lu T, Fu J, Shen M, Xiao YL, Fu Y. 2022. Complete mitochondrial genome of *Limnophyes minimus* (Diptera: Chironomidae). Mitochondrial DNA Part B. 7(1):280–282.

Ferrington LC. 2008. Global diversity of non-biting midges (Chironomidae; Insecta-Diptera) in freshwater. Hydrobiologia. 595(1): 447–455.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kim S, Kim H, Shin SC. 2016. Complete mitochondrial genome of the Antarctic midge *Parochlus steinenii* (Diptera: Chironomidae). Mitochondrial DNA Part A. 27(5):3475–3476.

Kong FQ, Zhao YC, Chen JL, Lin XL. 2021. First report of the complete mitogenome of *Microchironomus tabarui* Sasa, 1987 (Diptera, Chironomidae) from Hebei Province, China. Mitochondrial DNA B Resour. 6(10):2845–2846.

Lei T, Song C, Zhu XD, Xu BY, Qi X. 2021. The complete mitochondrial genome of a non-biting midge *Polypedilum unifascium* (Tokunaga, 1938) (Diptera: Chironomidae). Mitochondrial DNA Part B. 6(8): 2212–2213.

Li XY, Yan LP, Pape T, Gao YY, Zhang D. 2020. Evolutionary insights into bot flies (Insecta: Diptera: Oestridae) from comparative analysis of the mitochondrial genomes. Int J Biol Macromol. 149:371–380.

Liu C, Xu G, Lei T, Qi X. 2022. The complete mitochondrial genome of a tropical midge *Chironomus kiiensis* Tokunaga, 1936 (Diptera: Chironomidae). Mitochondrial DNA Part B. 7(1):211–212.

Nguyen LT, Schmidt HA, Haeseler AV, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Park K, Kim WS, Park JW, Kwak IS. 2021. Complete mitochondrial genome of *Chironomus flaviplumus* (Diptera: Chironomidae) collected in Korea. Mitochondrial DNA Part B. 6(10):2843–2844.

Peng Y, Leung H, Yiu S, Chin F. 2012. IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. Bioinformatics. 28(11):1420–1428.

Shen M, Li Y, Yao Y, Fu Y. 2022. Complete mitochondrial genome of *Chironomus nipponensis*, new record from China (Diptera: Chironomidae). Mitochondrial DNA Part B. 7(6):1163–1164.

Yan L, Pape T, Elgar MA, Gao Y, Zhang D. 2019. Evolutionary history of stomach bot flies in the light of mitogenomics. Syst Entomol. 44(4): 797–809.

Zhang X, Yang D, Kang Z. 2022. New data on the mitochondrial genome of Nematocera (lower Diptera): features, structures and phylogenetic implications. Zool J Linn Soc. zlac012.

Zheng CG, Liu Z, Zhao YM, Wang Y, Bu WJ, Wang XH, Lin XL. 2022. First report on mitochondrial gene rearrangement in non-biting midges, revealing a synapomorphy in *Stenochironomus* Kieffer (Diptera: Chironomidae). Insects. 13(2):115.

Zheng CG, Ye Z, Zhu XX, Zhang HG, Dong X, Chen P, Bu WJ. 2020. Integrative taxonomy uncovers hidden species diversity in the rheophilic genus *Potamometra* (Hemiptera: Gerridae). Zool Scr. 49(2): 174–186.

Zheng CG, Zhu XX, Yan LP, Yao Y, Bu WJ, Wang XH, Lin XL. 2021. First complete mitogenomes of Diamesinae, Orthocladiinae, Prodiamesinae, Tanypodinae (Diptera: Chironomidae) and their implication in phylogenetics. PeerJ. 9:e11294.