

The complete mitochondrial genome analysis of the stonefly, *Flavoperla* sp. (Plecoptera: Perlidae)

Ying Wang, Jinjun Cao, Mengdan Chen and Weihai Li

Department of Plant Protection, Henan Institute of Science and Technology, Xinxiang, P. R. China

ABSTRACT

Flavoperla is a small genus in Acroneuriinae, which was established by Chu but was treated as a synonym for a long time until Uchida and Harper recognized *Flavoperla* as a valid genus. This genus includes 15 species in the world now, including six species from China. Here, we sequenced and annotated the mitochondrial genome of *Flavoperla* sp. under the next-generation sequence technology, the first representative of Genus *Flavoperla*. The complete mitochondrial genome of *Flavoperla* sp. is 15,796 bp in length with an A+T content of 68.3% showed a positive AT-skew (0.037) and a negative GC-skew (−0.262). The gene order and organization of the mitochondrial genome is consistent with other stoneflies. The control region had the highest A+T content. Eleven PCGs started with the typical codon (ATN), the remaining PCGs started with TTG (ND1 and ND5). All PCGs terminated with TAA/TAG, except COII and ND5 used single T. The phylogenetic tree by maximum likelihood (ML) and Bayesian (BI) methods supported that *Flavoperla* sp. was the sister group to *Niponiella limbatella*.

ARTICLE HISTORY

Received 28 September 2019
Accepted 26 October 2019

KEYWORDS

Flavoperla sp.;
mitochondrial genome;
phylogenetic

The subfamily Acroneuriinae of Perlidae contains more than 500 species worldwide (DeWalt et al. 2019). *Flavoperla* is a small genus in Acroneuriinae that was initially established by Chu (1929) but was treated as a synonym of genus *Gibosia* by Wu (1935) for a long time until Uchida (1990) and Harper (1994) recognized *Flavoperla* as a valid genus. Recently, three species were described and reported from Southwestern and Northwestern China. This genus includes 15 species in the world, including six species from China (Chen 2019; DeWalt et al. 2019; Liu et al. 2019). Only five mitochondrial genomes in the Acroneuriinae were sequenced and published to date (Huang et al. 2015; Cao, Li et al. 2019; Cao, Wang, Li et al. 2019; Cao, Wang, Zhang et al. 2019; Li et al. 2019). Here, we sequenced and annotated the mitochondrial genome of *Flavoperla* sp. under the next-generation sequence technology, the first representative of Genus *Flavoperla* and reconstructed the phylogenetic position of *Flavoperla*. The specimen of *Flavoperla* sp. was collected in Huangshan Mountain, Anhui Province, China in 2016 (30.077°N, 118.164°E) by Cao Yuyan. The samples and voucher specimens (No. Voh-0120) were stored in 100% ethanol in the field and then stored at −20°C in Henan institute of Science and Technology (HIST), China. Genomic DNA was extracted from the adult muscle tissues by the Qiagen DNAeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany) stored at −20°C until it was sent to sequencing. The base composition was analyzed by MEGA version 7.0.14 (Kumar et al. 2016). We calculated the base composition by

using the formulas AT and GC skew ($AT\ skew = (A - T) / (A + T)$, $GC\ skew = (G - C) / (G + C)$) (Perna and Kocher 1995).

The complete mitochondrial genome of *Flavoperla* sp. is a double-stranded closed-circular molecule of 15,796 bp in length with the GenBank accession number MN419916. Similar to other published stoneflies, the gene order, and organization of the mitochondrial genome (contains 37 genes and a control region) is consistent with those of putative ancestor of insects (Boore 1999). The mitochondrial genome of *Flavoperla* sp. with an A+T content of 68.3% showed a positive AT-skew (0.037) and a negative GC-skew (−0.262). The control region possessed the highest A+T content (72.7), and the A+T content of the 13 PCGs, 22 tRNAs, 2 rRNAs was 67.1, 70.6, and 70.9%, respectively. Eleven PCGs started with the typical codon (ATN), the remaining two PCGs started with TTG (ND1 and ND5). All PCGs terminated with TAA or TAG, except COII and ND5 used the incomplete T as stop codon.

To better understand the phylogenetic relationship of the *Flavoperla* sp. with other closely related species, we conducted the sequences of PCG and two rRNAs among from eleven Perlidae and two Nemouridae species (as outgroups) by maximum likelihood (ML) and Bayesian (BI) methods to obtain the phylogenetic tree. The phylogenetic tree (Figure 1) in this study was consistent with the proposed and widely accepted view of the internal relationships of the *Flavoperla* sp. was sister clade to *Niponiella limbatella*.

CONTACT Weihai Li  lwh7969@163.com  Department of Plant Protection, Henan Institute of Science and Technology, Xinxiang 453003, P. R. China

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License (<http://creativecommons.org/licenses/by-nc/4.0/>), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

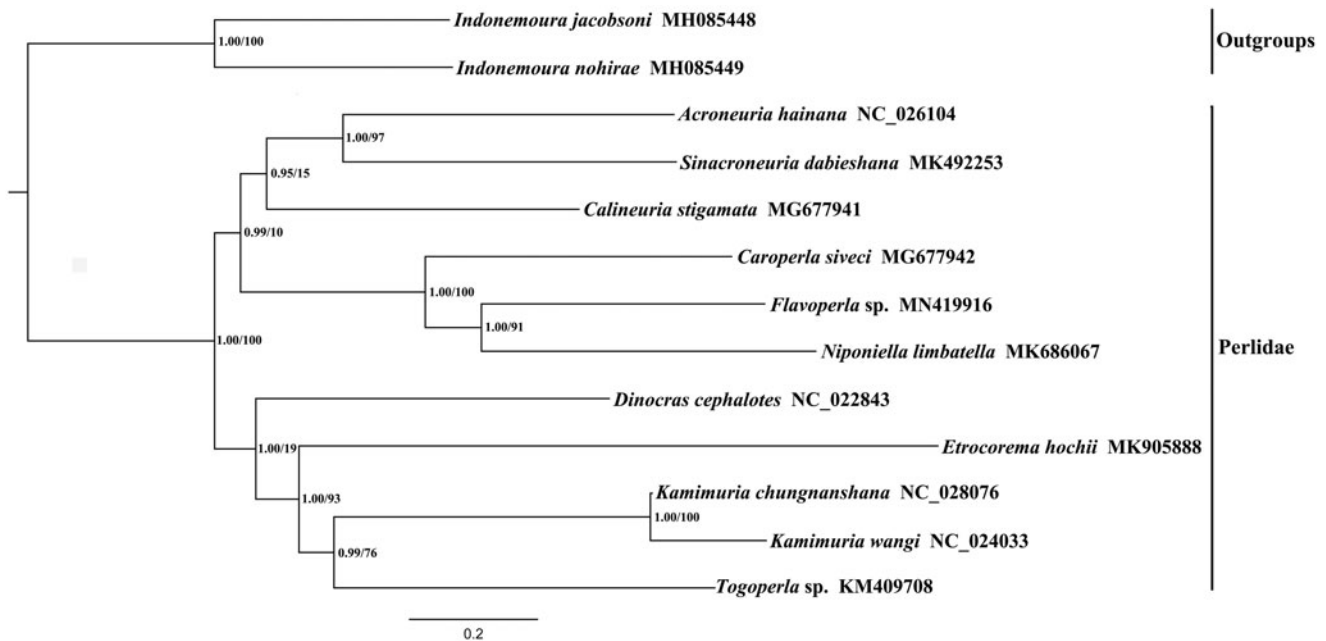


Figure 1. Phylogenetic analyses of *Flavoperla* sp. based on the sequences of PCG and two rRNAs by the maximum likelihood (ML) and Bayesian (BI) methods. The accession number in NCBI of each species is indicated after the scientific name.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the Initial Project of Henan Institute of Science and Technology, grant No. [2015026, No. 2014028] and the National Natural Science Foundation of China, Grant No. [31801999, 31970402].

References

- Boore JL. 1999. Survey and summary: animal mitochondrial genomes. *Nucleic Acids Res.* 27(8):1767–1780.
- Cao JJ, Li WH, Wang Y. 2019. The complete mitochondrial genome of a Chinese endemic stonefly species, *Sinacroneuria dabieshana* (Plecoptera: Perlidae). *Mitochondr DNA B Resour.* 4(1):1327–1328.
- Cao JJ, Wang Y, Li N, Li WH, Chen X. 2019. Characterization of the nearly complete mitochondrial genome of a Chinese endemic stonefly species, *Caroperla siveci* (Plecoptera: Perlidae). *Mitochondr DNA B Resour.* 4(1):553–554.
- Cao JJ, Wang Y, Zhang GQ, Yi SQ, Li WH. 2019. The characterization of the mitochondrial genome of *Calineuria stigmatica* (Plecoptera: Perlidae). *Mitochondr DNA B Resour.* 4(2):2796–2797.
- Chen ZT. 2019. On the identity of the genus *Flavoperla* (Plecoptera: Perlidae), with description of a new species in southwestern China. *Zootaxa.* 4613(1):127–134.
- Chu YT. 1929. Descriptions of four new species and one new genus of stone-flies in the family Perlidae from Hangchow. *China J.* 10:88–92.
- DeWalt RE, Maehr MD, Neu-Becker U, Stueber G. 2019. Plecoptera species file online. [accessed 2019 Sep 19]. <http://Plecoptera.SpeciesFile.org>.
- Harper PP. 1994. Plecoptera. In: Morse JC, Yang L, Tian L, editors. *Aquatic insects of China useful for monitoring water quality*. Nanjing, China: Hohai University Press; p. 176–209.
- Huang MC, Wang YY, Liu XY, Li WH, Kang ZH, Wang K, Li XK, Yang D. 2015. The complete mitochondrial genome and its remarkable secondary structure for a stonefly *Acroneuria hainana* Wu (Insecta: Plecoptera: Perlidae). *Gene.* 557(1):52–60.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol.* 33(7):1870–1874.
- Li JF, Cao JJ, Wang Y, Kong FB. 2019. The mitochondrial genome analysis of a stonefly, *Niponiella limbatella* (Plecoptera: Perlidae). *Mitochondr DNA B Resour.* 4(1):1666–1667.
- Liu H, Yan Y, Li W. 2019. Two new species of *Flavoperla* (Plecoptera: Perlidae) from Shaanxi Province of China. *Zootaxa.* 4614(2):395–400.
- Perna NT, Kocher TD. 1995. Patterns of nucleotide composition at four-fold degenerate sites of animal mitochondrial genomes. *J Mol Evol.* 41(3):353–358.
- Uchida S. 1990. A revision of the Japanese *Perlidae* (Insecta: Plecoptera), with special reference to their phylogeny [unpublished PhD thesis]. Tokyo, Japan: Tokyo Metropolitan University; p. 228.
- Wu CF. 1935. Order IX. *Plecoptera*. Vol. 1. In: Wu CF, editor. *Catalogus insectorum sinensium*. Peiping, China: Fan Memorial Institute of Biology; p. 299–315.