

## The mitochondrial genome analysis of *Flavoperla hatakeyamae* (Plecoptera: Perlidae)

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### ABSTRACT

In this study, we analyzed the entire mitochondrial genome of *Flavoperla hatakeyamae*, which has 15,730 bp in length. This complete mitochondrial genome possessed 13 protein coding genes (PCGs), 2 ribosomal RNA genes, 22 transfer RNA genes, and 1 control region. The nucleotide composition of the complete sequence of mitochondrial genome was accounting for 35.0%, T for 31.3%, C for 21.2%, G for 12.5%, and A + T for 66.3%. Among the 13 protein-coding genes, the starting codon of 12 protein-coding genes was ATN except the starting codon of *COII* was ACC. In addition, 11 of the protein-coding genes used conservative termination codon TAA/TAG, except for *COII* and *ND5* which terminated by a single T. Based on Bayesian (BI) and maximum-likelihood (ML) methods, we found that the genus *Flavoperla* and *Niponiella* were gathered into one branch and the species of Perlinae were clustered in one clade.

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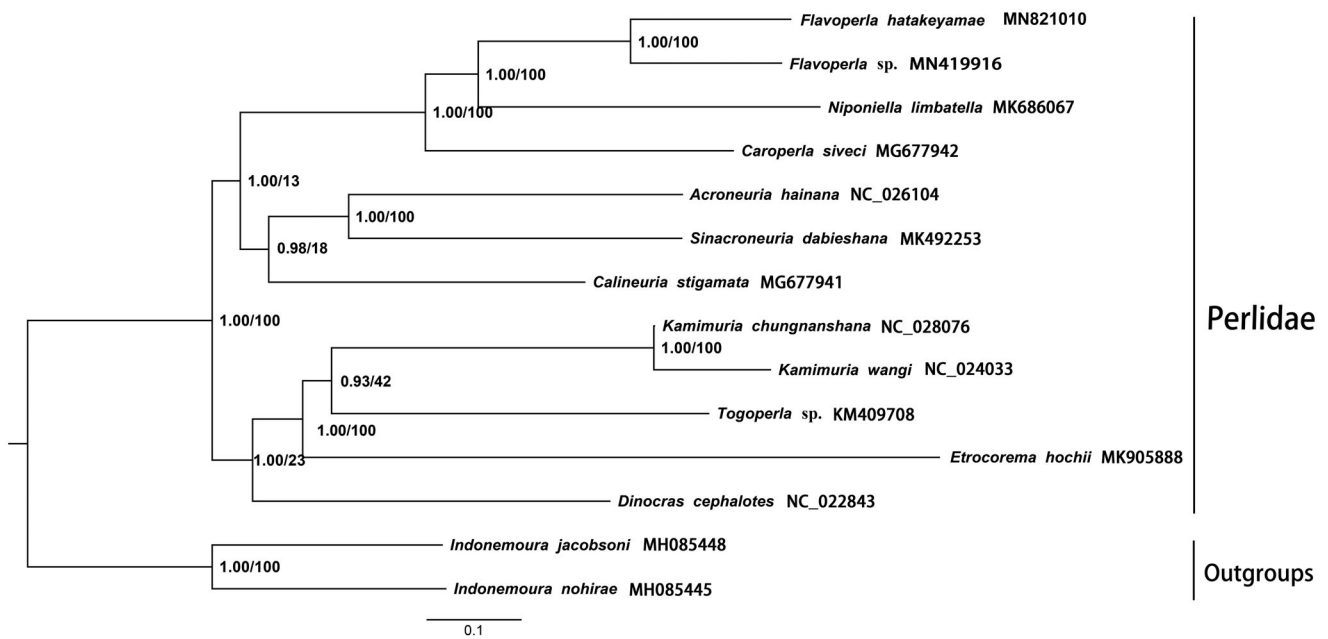
Mitochondrial genome;  
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Over the past two decades, DNA sequencing and analysis have advanced rapidly, and phylogenetic inferences have been made at different levels of classification (Tang et al. 2014; Li et al. 2015; Crampton-Platt et al. 2016; Li et al. 2017; Liu et al. 2018; Ding et al. 2019). As far as we know, 14 mitochondrial genomes of Perlidae have been sequenced and published but only one species of genus *Flavoperla* was included (Huang et al. 2015; Wang et al. 2016; Cao et al. 2019). In this paper, the complete mitochondrial genome of one stonefly *F. hatakeyamae* was sequenced to provide supplementary information for future phylogenetic studies of order Plecoptera. The sample used in this study with an accession number HIST-0028 was collected from Gunma, Nakanoyjo-machi, Japan by Liu Xingyue at June in 2015 (N36°704', E138°801') and is deposited in the insect specimen room of Henan Institute of Science and Technology (HIST), China. Total genetic DNA from the adult's chest of *F. hatakeyamae* was extracted by using the QIAamp DNA Mini Kit (QIAGEN, Germany) and stored at  $-20^{\circ}\text{C}$  till needed.

For the mitochondrial genome of *F. hatakeyamae*, it was deposited in the GenBank with the accession number MN821010, which has a closed circular molecule with 15,730 bp nucleotides in length and composed of 37 code genes and one big non-coding region. The nucleotide composition of *F. hatakeyamae* is inclined to A/T nucleotide, in which the A + T account for 66.3% (A = 35.0%, T = 31.3%, C = 21.2%, G = 12.5%) and the AT Skew and GC Skew of this

genome were 0.056 and  $-0.261$  which is similar to that of other stoneflies. The A + T account of PCGs, tRNAs, and rRNAs were 64.4, 70.4, 70.5%, respectively. All tRNAs had the classical clover secondary structure excepted the *tRNA<sup>Ser(AGN)</sup>* lack the dihydropyridine arm and the length of tRNAs ranged from 64 bp to 72 bp. Among the 13 protein-coding genes, the initial codon of mostly protein-coding genes was ATN while only the *COII* gene started with ACC. In addition, seven protein-coding genes used conservative termination codon TAA and four genes terminated with TAG, except for the *COII* and *ND5* genes ended by the incomplete single T. The length of *srRNA*, *lrRNA*, and the control region were 1338 bp, 830 bp, and 845 bp with the content of A + T were 71.0, 69.8 and 74.2%, and the control region had the highest A + T content among other genes.

Finally, we conducted the sequences of 13 PCGs and 2 rRNAs from 12 Perlidae species and two nemourid species (*Indonemoura jacobsoni* and *Indonemoura nohirae* as out-groups) by using the Bayesian (BI) and maximum likelihood (ML) methods to reconstruct the phylogenetic tree. As shown in Figure 1, both the methods showed the same topology tree, the phylogenetic tree inferred that *F. hatakeyamae* and *Flavoperla* sp. are sister groups, the genus *Flavoperla* and *Niponiella* were gathered into one branch and the species of Perlinae were clustered in one clade which is consistent with the traditional morphological taxonomy (Sivec et al. 1988).



**Figure 1.** Cladograms of relationships resulting from Bayesian inference (BI) and maximum-likelihood (ML) with datasets 13 PCGs and 2 Ribosomal RNAs with *Indonemoura jacobsoni* and *Indonemoura nohirae* (Nemouridae) as outgroups. The scientific name is followed by the NCBI number for each species.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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