The complete mitochondrial genome of *Matsumuramata muiri* (Hemiptera: Delphacidae)

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**ABSTRACT**

In this study, we sequenced, annotated, and analyzed the complete mitochondrial genome of *Matsumuramata muiri* (Kirkaldy, 1907) (Hemiptera: Delphacidae). The mitogenome was 16,276 bp in length with high A+T content (76.28%), containing 13 protein-coding genes, 22 tRNA genes, two rRNA genes, and a control region. Gene rearrangement of *M. muiri* was congruent with those of some reported delphacid species. All protein-coding genes initiated with ATN, except for nad5, which used non-canonical start codon GTG. The predicted secondary structures of all tRNA genes were typical cloverleaf except for trnS1 (AGN), lacking the dihydrouridine (DHU) stem.

Many species of Delphacidae (Hemiptera: Fulgoroidea) are economically significant pests of many important crops, such as rice and maize, because of serious crop yield losses caused by direct feeding, and by transmitting plant viral pathogens as disease vectors (Wilson 2005). Delphacidae is a diverse and cosmopolitan planthopper family with ~2100 described species, of which most belong to the subfamily Delphacinae (Urban et al. 2010; Huang et al. 2017). *Matsumuramata* Xing & Chen, 2014, one group of Delphacinae, includes five species: *M. muiri* (Kirkaldy, 1907), *M. sacchari* (Matsumura, 1910), *M. corporaali* (Muir, 1923), *M. parmenio* (Fennah, 1969), and *M. mani* (Asche, 1988) (Bourgoin 2020). Little is known about the mitochondrial genomes of this genus. Here, we sequence and annotate the complete mitogenome of *Matsumuramata muiri* to facilitate a better understanding of the characters of delphacid mitogenomes and the evolutionary history of Delphacidae.

Adults of *M. muiri* were collected in Yingjiang County (N 24.71° and E 97.93°), Yunnan Province, China. The voucher specimen and its DNA were deposited at the Nanjing Institute of Environmental Sciences under the Ministry of Ecology and Environment, Nanjing, China (http://www.nies.org/, Yi Wu, wuyi@nies.org) under the voucher number (F4YN035). Total genomic DNA was extracted using the DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany) following the manufacturer’s protocols. A total of 15 primer pairs were chosen and modified from universal insect mitochondrial primers suggested in Simon et al. (2006) to amplify the whole mitogenome. Purified target PCR products were sequenced directly on an ABI 3730XL DNA Analyzer using BigDye v3.1 (Applied Biosystems, USA). For those that sequence completely with difficulties, such as control region, PCR products were inserted into a pMD 19-T Vector (Takara Biomedical, Dalian, China), and multiple clones were sequenced independently. DNA sequences were edited and assembled into contigs by BioEdit 7.2.6.1 (Hall, 1999). After manually checking the assembly, the whole mitogenome was annotated with MitoZ v2.4-alpha (Meng et al. 2019). The annotation of tRNAs was verified by MITOS Web Server (Bernt et al. 2013). Start and stop codons of some PCGs were corrected according to the alignment of homologous genes in Fulgoroidea.

The complete mitochondrial of *Matsumuramata muiri* (Genbank accession no. MW288929) was 16,276 bp in size, with high A+T content (76.28%). The entire set of 37 genes was encoded, including 13 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes, and a control region, as observed in most insects. Gene rearrangement was detected to be congruent with those of other delphacid species, such as *Sogatella furcifera*, in which two gene clusters trnW-trnC-trnY and trnT-trnP-nad6 undertake conversion to trnC-trnW-trnY and nad6-trnP-trnT, respectively (Zhang et al. 2014).

The typical start codons ATN are used for twelve of all protein-coding genes (PCGs). The exception is nad5, which initiate with GTG. For all PCGs, three stop codons were used: T (atp6, cox1, and cox3), TAG (nad1 and nad3), and TAA (other eight PCGs). All 22 typical tRNA genes were found, ranging from 58 bp (trnS1 (AGN)) to 72 bp (trnK (CUU)). The predicted secondary structures of all tRNA genes are typical cloverleaf except for trnS1 (AGN), lacking the dihydrouridine (DHU) stem.

There were 14 overlaps in the mitogenome of *M. muiri*. The nad4l-nad4 overlap (ATGTTAA) was 7 bp in size, and not identical to that of atp8-atp6 (ATATTTA). A total of 13
non-coding regions were found, including 12 intergenic spacers, and the control region. The intergenic spacer between *trnS2* (*UCN*) and *nad1* was 16 bp in length, which corresponds to the binding sites of a transcription termination peptide. The control region spanned 1,768 bp locating between *rrnS* and *trnI*, and in this AT-rich region, a tandem unit (CATCGATTTTTGAAAAAAATG) was detected to repeat 25 times.

The amino acid sequence of each PCG was aligned individually using MAFFT v7.394 under the L-INS-i strategy (Katoh and Standley 2013). Then each alignment was trimmed and translated back into nucleotide sequence accordingly using trimAl v1.4.1. The nucleotide dataset of 13 PCGs were concatenated using FASconCAT-G v1.04 (Kuck and Longo 2014). The optimal partitioning scheme and the best substitution model for each partition were selected using ModelFinder (Kalyaanamoorthy et al. 2017) implemented in IQ-TREE v1.6.10 (Nguyen et al. 2015). A maximum likelihood (ML) tree (Figure 1) was reconstructed with 1,000 replicates of ultrafast bootstrap in the IQ-TREE v1.6.10 (Nguyen et al. 2015). A maximum likelihood (ML) tree (Figure 1) was reconstructed with 1,000 replicates of ultrafast bootstrap in the IQ-TREE v1.6.10. The Bayesian inference (Figure 1) was performed using MrBayes 3.2.6 (Ronquist et al. 2012) with the best-fitting models found by ModelFinder. *Philaenus spumarius* (Hemiptera: Cercopidae: Aphrophoridae) and one cixiid species *Pentastiridius* sp. were selected as outgroup.

Cixiidae was a sister group to the family Delphacidae in the ML tree. Two clades were well-supported in Delphacidae, the subfamily Asiracinae clade represented by *Ugyops* sp. and the Delphacinae clade. Within Delphacini, *Matsumuramata muiri* and *Peregrinus maidis* were clustered together with strong support, indicating their relatively closed relationships. *Nilaparvata lugens* was sister to *N. muiri* + *N. bakeri*. The genus *Sogatella* seemed closed to both *Unkanodes sapporonus* and *Laodelphax striatellus*.

**Disclosure statement**

The authors report no conflicts of interest.

**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/](https://www.ncbi.nlm.nih.gov/) under the accession no. MW288929.

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**Figure 1.** Maximum likelihood (ML) and Bayesian Inference (BI) phylogenetic tree inferred from nucleotide sequences of 13 protein-coding genes. UFBoot support values (left) and Bayesian posterior probabilities (right) are indicated on nodes. Group names are marked by vertical lines. *Matsumuramata muiri* is marked with an asterisk.
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