

## The complete mitochondrial genome of *Hemisphaerius rufovarius* Walker, 1858

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### ABSTRACT

In this study, we have sequenced and annotated the complete mitochondrial genome (mitogenome) of *Hemisphaerius rufovarius* (Hemiptera: Fulgoroidea: Issidae) for the first time, the mitogenome is 15,955 bp (GenBankNo. MT210096), includes 13 PCGs, 2 rRNAs, 22 tRNAs and one putative control region (D-loop). The AT content of this mitogenome is 78.3% (A 47.7%, T 30.6%, C 13.3%, and G 8.4%). Most the PCGs started with ATN or TTG(nad5), and ended with TAN or single T. The result of Phylogenetic tree showed a close relationship among the families Issidae, Flatidae and Ricaniidae.

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### KEYWORDS



*Hemisphaerius rufovarius*;  
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The Family Issidae 1839 is composed of 1,068 species with a broad distribution in word (Bourgoin 2020), is harmful for the host plant that includes woody and herbaceous plants. However, only the complete mitochondrial genome (mitogenome) of the species *Dentatissus damnosus* had been sequenced in last ten years (Nan Song et al. 2010). *Hemisphaerius rufovarius* (Hemiptera: Fulgoroidea: Issidae) is a ubiquitous species of Issidae in south of China, Malaysia (Borneo), Myanmar (ex Burma), Thailand, and Vietnam (Bourgoin 2020), is a serious pest of Lauraceae tree. In this study, the mitogenome sequences of *H. rufovarius* are sequenced to help to understand the phylogenetic relationship of Fulgoroidea and the evolution of Issidae. The total genome DNA extracted from the male samples which was captured from Mengla County, Yunnan province, China (101°21'E, 21°96'N, H 626 m) in 12 June 2019. The specimen (Accession number: GUGC2019/06/12-43 YLJ XTL 2males) and voucher specimen's genome DNA (YLJ M 2019/9/18-10) were deposited in The Institute of Entomology, Guizhou University, Guiyang, China (GUGC). The mitogenome sequences of *H. rufovarius* were sequenced by next-generation sequencing method (illumine HiSeq X 10) ([http://hannonlab.cshl.edu/fastx\\_toolkit/index.html](http://hannonlab.cshl.edu/fastx_toolkit/index.html)), and assembled using Geneious 10.2.2 (<http://www.geneious.com>) (Kearse et al. 2012), annotated and conducted using MITOZ (Meng et al. 2019). The complete chloroplast genome sequence of *H. rufovarius* has been deposited in GenBank with the accession number MT210096 (The NCBI genbank accession link: <https://www.ncbi.nlm.nih.gov/nucleotide/MT210096>).

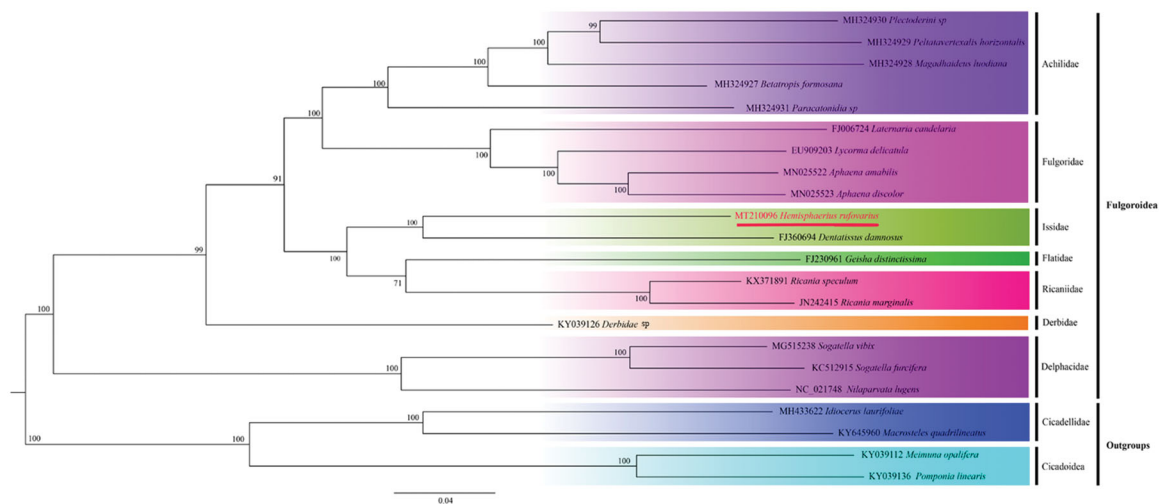
The complete mitogenome of *H. rufovarius* is 15,955 bp in length (GenBankNo: MT210096), consists of 13 protein-coding

genes (PCGs), 2 ribosomal RNA genes (rRNAs) and 22 transfer RNA genes (tRNAs) and one large non-coding region (D-loop: [A + T]-rich region). D-loop is 1707 bp, exists between 12S rRNA and *trnI*. The overall bases composition complete mitogenome are 47.7% A, 30.6% T, 13.3% C and 8.4% G, with AT content rich (78.3%). AT skew ((A - T)/(A + T)) and GC skew ((G - C)/(G + C)) are 0.219, -0.227, respectively. All the 13 PCGs started with ATN, excepted nad5 (TTG), ended with TAN or single T residue. All tRNAs presented the typical cloverleaf structures, excepted *tRNA<sup>Ser(AGN)</sup>*, which DHU arm is not a typical neck ring structure. The mitogenome of *H. rufovarius* includes 19 intergenic spacers, totals 230 bp, ranges in size from 1 to 33 bp, the longest one located between *trnY* and *trnW*, and includes 9 gene overlaps, totals 47 bp, fluctuates in size from 1 to 13 bp. All PCGs of *H. rufovarius* is 10,708 bp totally, the shortest one and the longest one are *atp8* (158 bp) and *nad5* (1,746 bp), respectively.

MEGA7.00 (Kumar et al. 2016) was used to construct the maximum likelihood (ML) tree based on complete mitogenome sequences of *H. rufovarius* and another 17 related species which belonged to differently family of the Fulgoroidea. The phylogenetic tree confirmed that the Fulgoroidea was a monophyly with high node values (BS  $\geq$  91). As the topologies tree showed, two species (*H. rufovarius* and *D. damnosus*) of Issidae were clustered together; Issidae was placed near the middle and included in a clade with Flatidae and Ricaniidae in the following relationship (BS = 100): (Issidae + (Flatidae + Ricaniidae)), that were consistent with Xu et al. (2019) (Figure 1).

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**Figure 1.** The maximum likelihood tree based on 22 the complete mitochondrial genome sequences. 18 in-group (Fulgoroidea) and 4 out-group (2 Cicadellidae and 2 Cicadoidea), respectively.

## Disclosure statement

All referred data of this MitoGenome Announcements is published by NCBI (National Center for Biotechnology Information Search database). No potential conflict of interest was reported by the authors. The mitogenome of *H. rufovarius* (the registered numbers of GenBank: MT210096) is published in the NCBI and the link is as follows: <https://www.ncbi.nlm.nih.gov/nuccore/MT210096.1/>.

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