

The complete mitochondrial genome of click beetle *Chiagosnius vittiger* (Coleoptera: Elateridae) and phylogenetic analysis

Yaling Zhao^{a*}, Yang Wang^{a,b*} and Yang Liu^{a,c}

^aKey Laboratory of Resource Biology and Biotechnology in Western China (Ministry of Education), Shaanxi Key Laboratory for Animal Conservation, College of Life Science, Northwest University, Xi'an, PR China; ^bCollege of Biology Pharmacy and Food Engineering, Shangluo University, Shangluo, PR China; ^cKey Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, PR China;

ABSTRACT

In this study, we determined the complete mitochondrial genome sequence of click beetle *Chiagosnius vittiger* (Heyden, 1887) (GenBank accession no. MN306531) using next-generation sequencing (NGS) method. The mitogenome is 15,842 bp in length, consisting of 13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNAs), 22 transfer RNA genes (tRNAs), and one non-coding control region. The overall nucleotide composition was 41.6% A, 31.1% T, 16.9% C, and 10.4% G, with 72.7% AT, respectively. The gene arrangement is consistent with the typical insect mitochondrial genome. Phylogenetic analysis revealed that *C. vittiger* clustered into a clade with *Chiagosnius sulcicollis* with high bootstrap support.

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Insecta; molecular phylogeny; mitochondrial DNA; genetic diversity

Elateridae commonly known as click beetles and contains approximately 10,000 species (Johnson 2002). *Chiagosnius vittiger*, with dark brown oval marking in the middle of pronotum, mainly distributed in southern China and East Asia (Jiang and Wang 1999). Here, we determined the complete mitochondrial genome of *C. vittiger*, which is the second mitochondrial genome sequenced to date in the genus of *Chiagosnius* Fleutiaux, and the first one is *Chiagosnius sulcicollis* (Wang et al. 2019).

The sampled specimen was collected from Jianfengling National Nature Reserve, Hainan, China (18°44'N, 108°54'E) in May, 2018. The specimen was stored in the Entomological specimen room of Shangluo University (voucher no. CO-2018229). The complete mitochondrial DNA sequence was determined by Illumina HiSeq 2500 Sequencing System (Illumina, San Diego, CA, USA). In total, 5.6 G raw reads were obtained, quality-trimmed, and assembled using MITObim version 1.7 (<https://github.com/chrisshah/MITObim>) (Hahn et al. 2013).

The complete mitochondrial genome of *C. vittiger* was 15,842 bp in total length and deposited in GenBank database with an accession number MN306531. The overall base composition was 41.6% A, 31.1% T, 16.9% C, and 10.4% G, with an A + T ratio of 72.7%. The full mitochondrial genome contains 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), two ribosomal RNAs (rRNAs) and a putative control region (CR). The gene arrangement of *C. vittiger* is found to be similar to most insect mitochondrial genomes (Wolstenholme 1992). Most

PCGs of *C. vittiger* have the conventional start codon for invertebrate mitochondrial PCGs (ATN), with the exception of *nad1* (TTG) and the start codon of *cox1* not determined. Most of the PCGs terminate with the stop codon TAA or TAG, whereas *cox2*, *cox3*, and *nad5* end with the incomplete codon T. nine PCGs are encoded on the majority strand (J-strand) and four (*nad5*, *nad4*, *nad4L*, and *nad1*) on the minority strand (N-strand). All 22 tRNA genes can be folded into the typical cloverleaf structure except for *trnS1*, in which the dihydrouridine (DHU) arm cannot form a stable stem-loop structure but a simple loop. Two rRNA genes (*rnl* and *rns*) locate at *trnL1/trnV* and *trnV/control* regions, respectively, and both rRNA genes are encoded on the N-strand. The lengths of the two rRNA genes (*rnl* and *rns*) in *C. vittiger* are about 1283 and 736 bp, with the A + T contents of 78.7% and 75.9%, respectively. The length of control region is 1230 bp, with the AT content of this region is up to 81.9%.

The phylogenetic tree was constructed using the maximum-likelihood method through RaxMLGUI version 1.5 (<http://sourceforge.net/projects/raxmlgui/>) (Silvestro and Michalak 2012). Results showed that the family Elateridae is monophyletic and the genus *Chiagosnius* Fleutiaux is sister to *Melanotus* Eschscholtz (Figure 1), which was consistent with the previous studies (Lin et al. 2018; Meng et al. 2018; Wang et al. 2019). As a conclusion, we obtained and described the complete mitochondrial genome of *C. vittiger*, which constitute a valuable and useful resource for population genetic study and identification efforts on this species.

CONTACT Yang Liu  liuyagent@nwu.edu.cn  Key Laboratory of Resource Biology and Biotechnology in Western China (Ministry of Education), Shaanxi Key Laboratory for Animal Conservation, College of Life Science, Northwest University, Xi'an, Shaanxi Province, PR China; Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, PR China

*These authors contributed equally to this work.

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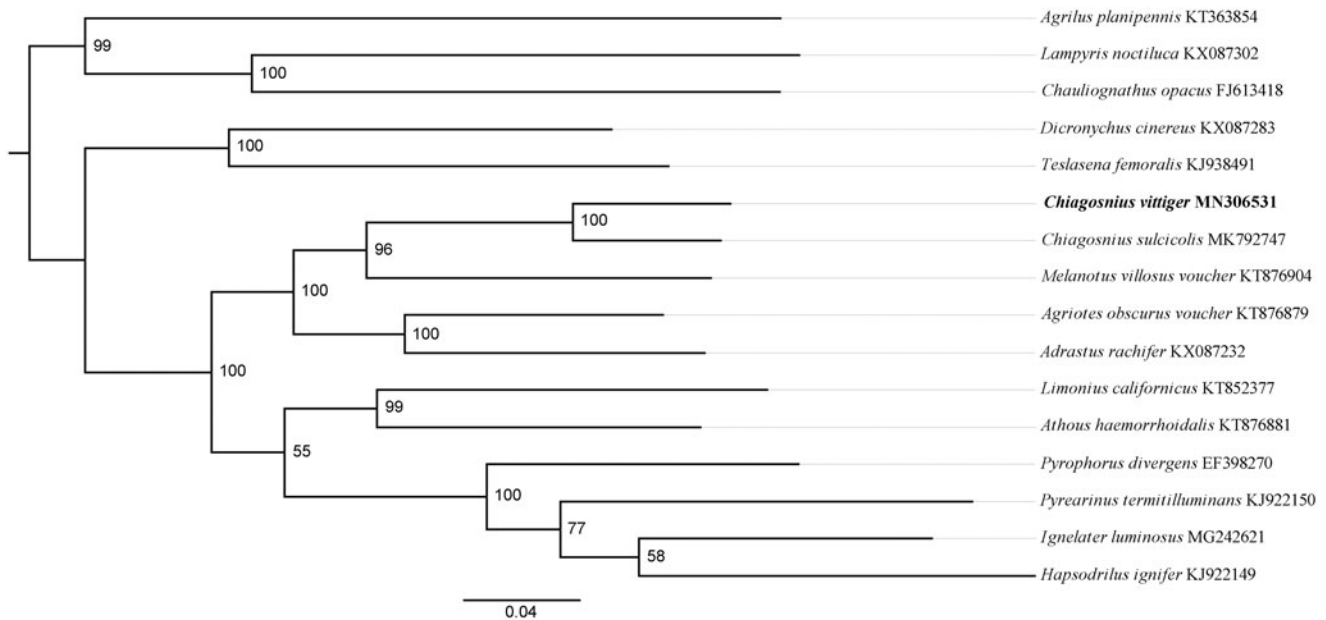


Figure 1. Phylogenetic relationships based on the 13 mitochondrial protein-coding genes sequences inferred from RaxML. Numbers on branches are bootstrap values (BV).

Disclosure statement

All authors have read and approved the final manuscript. No conflict of interest was reported by the authors.

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