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

Yang Wang, Xuan Wang & Yang Liu

Published online: 12 Jul 2019.

Submit your article to this journal ⬚

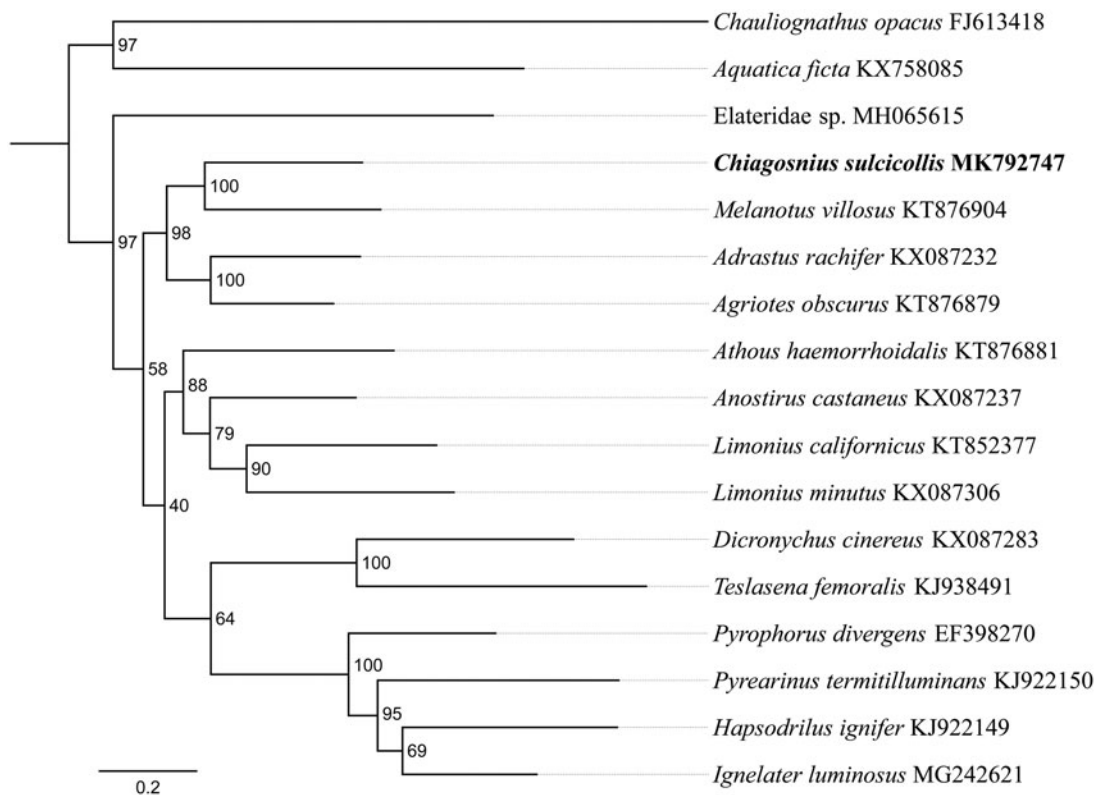Article views: 12

View Crossmark data ⬚

Elateridae commonly known as click beetles due to a unique and well-known startling defence mechanism named 'clicking' contains approximately 10,000 species (Johnson 2002). *Chiagosnius sulcicollis*, with yellowish-brown vertical stripe in the middle of the fore wing, mainly distributed in southern China and Southeast Asia (Jiang and Wang 1999). Here, we determined the complete mitochondrial genome of *C. sulcicollis*, which is the first mitochondrial genome sequenced to date in the genus of *Chiagosnius*.

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. The complete mitochondrial DNA sequence was determined by Illumina HiSeq 2500 Sequencing System (Illumina, San Diego, CA). In total, 5.2 Gb raw reads were obtained, quality-trimmed, and assembled using MITObim v1.7 (Hahn et al. 2013).

The complete mitochondrial genome of *C. sulcicollis* was 15,848 bp in total length and deposited in GenBank database with an accession number MK792747. The overall base composition was 41.6% A, 31.5% T, 16.6% C, and 10.3% G, with an A + T ratio of 73.1%. 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. sulcicollis* is found to be similar to most insect mitochondrial genomes (Wolstenholme 1992). Most PCGs of *C. sulcicollis* have the conventional start codon for invertebrate mitochondrial PCGs (ATN), with the exception of *nad1* (TTG) and *cox1* (AAT), as the asparagine (AAT or AAC) are proposed to be the start codon for *cox1* in suborder Polyphaga (Sheffield et al. 2008). Most of the PCGs terminate with the stop codon TAA or TAG, whereas *cox2*, *cox3* and *nad5* end with the incomplete codon T. Nine protein-coding genes 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 (*rrnL* and *rrnS*) 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 (*rrnL* and *rrnS*) in *C. sulcicollis* are about 1283 and 738 bp, with the A + T contents of 78.1 and 75.9%, respectively. The length of the control region is 1235 bp, with the AT content of this region being ∼81.3%.

The phylogenetic tree was constructed using the maximum-likelihood method through raxmlGUI 1.5 (Silvestro and Michalak 2012). Results showed that the family Elateridae is monophyletic and *C. sulcicollis* is sister to *Melanotus villosus* (Figure 1), which was consistent with the previous studies (Douglas 2011; Lin et al. 2018; Meng et al. 2018). In conclusion, we obtained and described the complete mitochondrial genome of *C. sulcicollis*, which constitute a valuable and useful resource for population genetic study and identification efforts on this species.

CONTACT Yang Liu ✉ liuyangent@nwu.edu.cn 📧 Key Laboratory of Resource Biology and Biotechnology in Western China (Ministry of Education) and College of Life Science, Northwest University, 1 Guoduzhen Xuefu Avenue, Xi'an 710127, China

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

References

Douglas H. 2011. Phylogenetic relationships of Elateridae inferred from adult morphology, with special reference to the position of Cardiophorinae. Zootaxa. 2900:1–45.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads-a baiting and iterative mapping approach. Nucl Acids Res. 41:e129.

Jiang SH, Wang SY. 1999. Economic click beetle faun-na of China (Coleoptera: Elateridae). Beijing (China): China Agriculture Press.

Johnson PJ. 2002. Elateridae. In: Arnett RH, Thomas MC, Skelley PE, Frank JH, editors. American beetles. Vol. 2. Boca Raton (FL): CRC Press LLC; p. 160–173.

Lin A, Zhao X, Song N, Zhao T. 2018. Analysis of the complete mitochondrial genome of click beetle Agriotes hirayamai (Coleoptera: Elateridae). Mitochondrial DNA Part B. 3:290–291.

Meng ZY, Lei CL, Chen XQ, Shi TX, Chen QJ, Jiang SH. 2018. Phylogenetic analysis of click beetles (Coleoptera: Elateridae) based upon 28S rDNA: phylogeny and classification. Entomotaxonomia. 40: 231–252.

Sheffield N, Song H, Cameron S, Whiting M. 2008. A comparative analysis of mitochondrial genomes in Coleoptera (Arthropoda: Insecta) and genome descriptions of six new beetles. Mol Biol Evol. 25: 2499–2509.

Silvestro D, Michalak I. 2012. RaxmlGUI: a graphical front-end for RAxML. Org Divers Evol. 12:335–337.

Wolstenholme DR. 1992. Animal mitochondrial DNA: structure and evolution. Int Rev Cytol. 141:173–216.