The complete mitochondrial genome sequence and phylogenetic analysis of *Lycocerus asperipennis* (Coleoptera, Cantharidae)

Ping Wang, Li-Lan Yuan, Xue-Ying Ge, Hao-Yu Liu and Yu-Xia Yang

**College of Agriculture, Yangtze University, Jingzhou, Hubei Province, China; Laboratory of Zoological Systematics and Application, College of Life Sciences, Hebei University, Baoding, Hebei Province, China**

**CONTACT**
Hao-Yu Liu liuhy@aliyun.com; Yu-Xia Yang yxyang@hbu.edu.cn The Key Laboratory of Zoological Systematics and Application, College of Life Sciences, Hebei University, Baoding 071002, Hebei Province, China

**ARTICLE HISTORY**
Received 17 August 2019 Accepted 13 October 2019

**KEYWORDS** Mitochondrial genome; Cantharidae; Cantharinae; *Lycocerus asperipennis*

**ABSTRACT**
The complete mitochondrial genome of a common Chinese soldier beetle was sequenced, *Lycocerus asperipennis* (Coleoptera, Cantharidae, Cantharinae). The mitogenome is a double-stranded circular molecule, and the obtained sequence with 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA subunits, and an AT-rich region, as in other insects. Total length of this mitogenome is 16162 bp and the composition of each base is A (41.5%), T (37.7%), C (12.4%), G (8.4%), respectively. The phylogenetic tree analysis using 16 species of Elateroidea shows that *L. asperipennis* is closest to *Chauliognathus opacus*, which belongs to the subfamily Chauliognathinae of Cantharidae.

*Lycocerus asperipennis* (Fairmaire, 1891) is a species of the family Cantharidae. The species could be easily recognized by the middle-sized body and the body colouration, about 10–12 mm in length, elytra black, legs mixed black with yellow, pronotum reddish-brown, with a large inverse-triangular black marking on anterior part, head reddish-brown, black on posterior part of dorsum. The female and male could be distinguished by the pro- and meso-outer claws each with a tooth at base or not, and the middle antennae present with smooth impressions or not.

*Lycocerus asperipennis* is a common cantharid species in China. It is widely distributed from the southernmost to the northern part, including Yunnan, Sichuan, Hubei, Gansu, Shaanxi, Shanxi, Henan (Yang et al. 2013). The adult mostly occurs in large groups from April to June and could be trapped by the light.

The specimens used in this study were collected from Wenshui Forestry, 31°34′27″N, 110°20′03″E, Shennongjia, Hubei Province, China, and stored in the Museum of Hebei University, Baoding, China (MHBU, accession number CAN0007). Genomic DNA was extracted by DNeasy Blood & Tissue kit (QIAGEN, Germany). Illumina TruSeq libraries were prepared using genomic DNA with an average insert size of 450 bp and were sequenced on the Illumina Hiseq2500 platform with 250 bp paired-end reads at BerryGenomics (Beijing, China). The sequence reads were first filtered by the programmes following Zhou et al. (2013) and then the remaining high-quality reads were assembled using IDBA-UD (Yu and Henry 2012). In order to study the accuracy of assembly, Geneious 2019.2 was used to map clean reading onto the mt genome sequence. The annotations of genes were done by Geneious 2019.2 software and tRNAscan-SE 1.21 (Schattner et al. 2005). Annotated sequence was registered in GenBank with accession number MN255352.1.

The complete mitochondrial genome (mitogenome) of *Lycocerus asperipennis* is a double-stranded circular molecule of 16,162 bp in length, which contains 22 tRNA genes, 13 protein-coding genes (PCGs), 2 rRNA subunits and an AT-rich region, as in other insects. The composition of each base was calculated as A (41.5%), T (37.7%), C (12.4%), G (8.4%), respectively. The phylogenetic inference was done based on 13PCGs. Trans Align methods were used to align all protein-coding genes (Bininda-Emonds 2005). The aligned data from 13PCGs were concatenated with Sequence Matrix v.1.7.8 (Vaidya et al. 2011). Data were partitioned according to loci of 13 PCGs. The bootstrap showed sufficient value at all nodes. It was found that *Lycocerus asperipennis* was closer to *Chauliognathus opacus*.
The two species both belong to Cantharidae and placed in the subfamilies Cantharinae and Chauliognathinae, respectively (Brancucci 1980).

Disclosure statement
The authors report no conflict of interest. The authors alone are responsible for the content and writing of the article.

Funding
This work was supported by the National Natural Science Foundation of China [Nos. 31772507 and 41401064], the Knowledge Innovation of Chinese Academy of Sciences [No. KSCX2-EW-Z-8], Natural Science Foundation of Hebei Province [No. C201720112] and a foundation for young talents of colleges and universities in Hebei Province [No. BJ2017030].

References
Amaral DT, Mitani Y, Ohmiya Y, Viviani VR. 2016. Organization and comparative analysis of the mitochondrial genomes of bioluminescent Elateroidea (Coleoptera: Polyphaga). Gene. 586(2):254–262.
Bininda-Emonds O. 2005. Trans Align: using amino acids to facilitate the multiple alignment of protein-coding DNA sequences. BMC Bioinf. 6(1):156.
Brancucci M. 1980. Morphologie comparée, évolution et systématique des Cantharidae (Insecta: Coleoptera). Ent Basil. 5:215–388.
Gerritsen AT, New DD, Robison BD, Rashed A, Hohenlohe P, Forney L, Rashidi M, Wilson CM, Settles ML. 2016. Full mitochondrial genome sequence of the sugar beet wireworm, Limonius californicus (Coleoptera: Elateridae), a common agricultural pest. Genome Announc. 4(1):e01628–15.
Jiao HW, Ding M-H, Zhao HB. 2013. Sequence and organization of complete mitochondrial genome of the firefly, Aquatica leii (Coleoptera: Lampyridae). Mitochondr DNA. 26(5):775–776.
Hong MY, Jeong HC, Kim MJ, Jeong HU, Lee SH, Kim I. 2009. Complete mitogenome sequence of the jewel beetle, Chrysochroa fulgidissima (Coleoptera: Buprestidae). Mitochondr DNA. 20(2–3):46–60.
Li XY, Ogoh K, Ohba N, Liang XC, Ohmiya Y. 2007. Mitochondrial genomes of two luminous beetles, Rhagophthalmus fulgensensis and R. ohbai (Arthropoda, Insecta, Coleoptera). Gene. 392(1–2):196–205.
Linard B, Arribas P, Andújar C, Crampton-Platt A, Vogler AP. 2016. Lessons from genome skimming of arthropod-preserving ethanol. Mol Ecol Resour. 16(6):1365–1377.
Linard B, Crampton-Platt A, Moriniere J, Timmermans M, Andújar C, Arribas P, Miller KE, Lipecki J, Favreau E, Hunter A, et al. 2018. The contribution of mitochondrial metagenomics to large-scale data mining and phylogenetic analysis of Coleoptera. Mol Phylogen Evol. 128:1–11.
Sheffield NC, Song H, Cameron SL, Whiting MF. 2009. Nonstationary evolution and compositional heterogeneity in beetle mitochondrial phylogenomics. Syst Biol. 58(4):381–394.
Schattner P, Brooks AN, Lowe TM. 2005. The trnA scan-SE, snoscan and sngos web servers for the detection of tRNAs and snoRNAs. Nucleic Acids Res. 33:686–689.
Uribe JE, Gutiérrez-Rodríguez J. 2016. The complete mitogenome of the trilobite beetle Plateterodrilus sp. (Elateroidea: Lycidae). Mitochondr. DNA. 1(1):658–659.
Vaidya G, Lohman DJ, Meier R. 2011. Sequence Matrix: concatenation software for the fast assembly of multi-genome datasets with character set and codon information. Cladistics. 27(2):171–180.
Yang YX, Kopetz A, Yang X. 2013. Taxonomic and nomenclatural notes on the genera Themus Motschulsky and Lycocerus Gorham (Coleoptera, Cantharidae). Zookeys. 340:1–19.
Yu P, Henry C. 2012. IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. Bioinformatics. 28:1420–1428.
Zhou X, Li YY, Liu SL, Yang Q, Su X, Zhou LL, Tang M, Fu RB, Li JG, Huang QF. 2013. Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. GigaSci. 2(1):4.