

Mitochondrial genome of a medicinal beetle *Blaps rhynchopetera* (Coleoptera, Tenebrionidae) and phylogenetic analysis

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ABSTRACT

Blaps rhynchopetera is a species of folk medicinal beetle that has been used for a long time in Southwest China. The complete mitogenome of the beetle (GenBank accession number MK854717) is 16,149 bp in size, including 13 protein-coding, 22 transfer RNAs, two ribosomal RNAs genes, and a non-coding D-loop region. The D-loop of 1255 bp length is located between rRNA-S and tRNA^{Ile}. The overall base composition of *B. rhynchopetera* is 41.58% for A, 10.31% for G, 31.77% for T, and 16.34% for C, with a high AT bias of 73.35%. The present data could contribute to detailed phylogeographic analysis of this valuable medicinal insect.

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Blaps rhynchopetera (Coleoptera, Tenebrionidae) is a species of folk medicinal insect. It is mainly distributed in Yunnan, Sichuan and Guizhou Province of China (Zhao et al. 2007). This beetle is popular as medicine of anti-inflammatory and analgesia in local, especially among the minority Yi people. Elucidating the structure and function of *B. rhynchopetera* mitogenome is important for understanding its diversity, genetics and evolution.

The specimen of *B. rhynchopetera* was obtained from Kunming, Yunnan, China (N 25°02', E 102°42') and deposited in the Insect Collection of Research Institute of Resource Insects with an accession number RIRI-w-20190418. Sequencing work of the complete mitogenome of *B. rhynchopetera* was performed by Illumina Nextseq500 in Beijing Microread Genetics Co., Ltd., with a total data volume 4G (150 bp Reads), and high-quality reads were assembled from

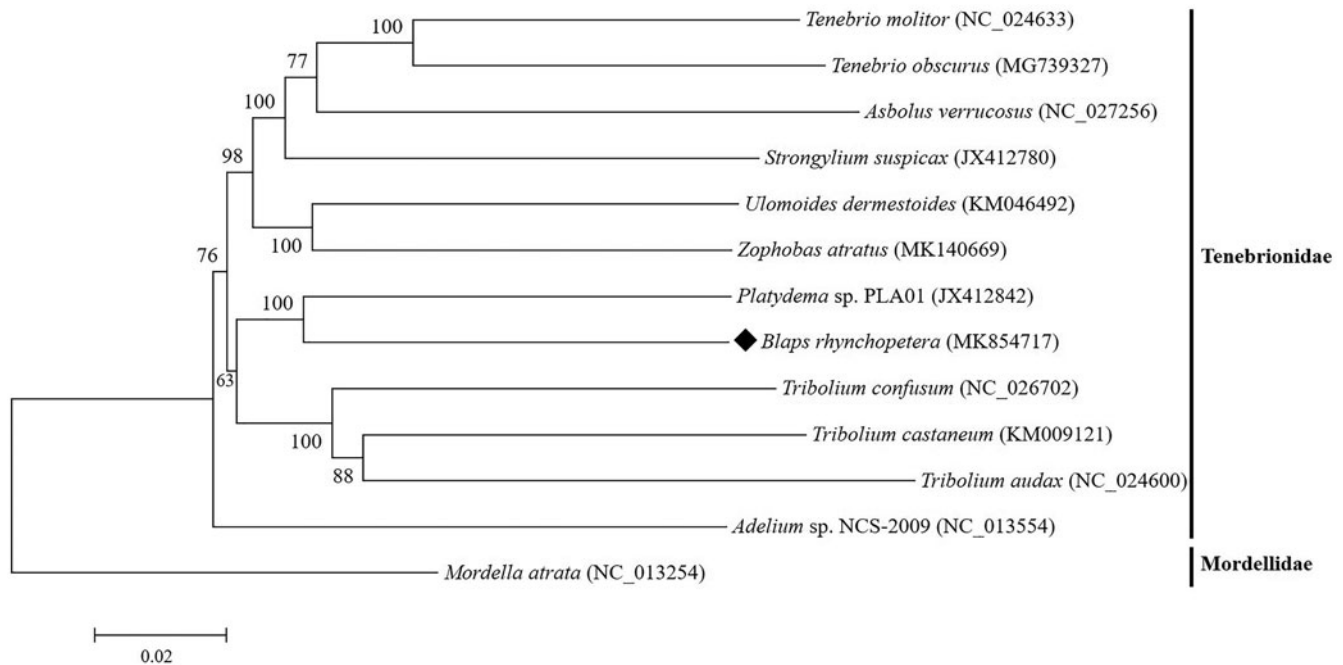


Figure 1. Phylogenetic tree showing the relationship between *B. rhynchopetera* and 11 other Tenebrionidae beetles based on neighbor-joining method. *Mordella atrata* (Mordellidae) was used as an outgroup. GenBank accession numbers of each species were listed in the tree.

scratch using IDBA-UD and SPAdes (Gurevich et al., 2013). Protein-coding genes (PCGs) of the *B. rhynchopetera* mitogenome were identified using BLAST search in NCBI, and tRNA genes were identified using the tRNAscan-SE search server (Schattner et al. 2005).

The gene order and orientation of *B. rhynchopetera* mitogenome are identical to the most common type of Coleoptera insects (Wang et al. 2016; Bai et al. 2018). It was 16,149 bp in size (GenBank accession number MK854717), including 13 typical invertebrate PCGs, 22 transfer RNA genes, two ribosomal RNA genes, and a noncoding control region (D-loop). The A + T content of the whole *B. rhynchopetera* mitogenome is 73.35%, showing an obvious AT mutation bias (Eyre-Walker 1997). The D-loop region exhibits the highest A + T content (78.59%) in the *B. rhynchopetera* mitogenome.

All PCGs use standard ATN as a start codon. As for the stop codon, 11 PCGs had the common stop codon TAA, while *COX3*, *ND4* terminated with incomplete stop codon T. Similar cases could be found in other insect mitogenomes (Yin et al. 2012). All the tRNAs except *tRNA^{Ser}* (AGN) could be folded into the typical cloverleaf secondary structures. The unusual *tRNA^{Ser}* (AGN) lacks dihydrouridine (DHU) arm.

Based on the concatenated 13 mitochondrial PCGs sequences of 12 species from Tenebrionidae, the neighbour-joining method was used to construct the phylogenetic relationship of *B. rhynchopetera* with 11 other Tenebrionidae beetles (Figure 1). *Blaps rhynchopetera* was clustered with *Platydema* sp. PLA01, indicating a close relationship between *Platydema* and *Blaps*. This mitogenome data might be also useful for further phylogeography analyses in Tenebrionidae.

Disclosure statement

The authors declare no competing materials in the preparation and execution of this manuscript. The authors are responsible for the content and writing of this paper.

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