The complete mitochondrial genome of *Monochamus dubius* Gahan (Coleoptera: Cerambycidae)

Jiankai Wu, Ren Chen, Yi Wan, Shaozhen Wang and Jiayi Ma

The characteristics of PCGs, tRNAs, rRNAs, and AT-rich region were obtained from the annotated result of mitoMaker (Bernt et al. 2013). The complete mitogenome sequence has been submitted to NCBI Genbank with accession number MW067124. In this study, 37 genes were annotated, including 13 PCGs, 22 tRNAs, 2 rRNAs. Thirteen PCGs are 10,911 bp in total, encoding 3,637 amino acids. Nine PCGs (ATP6, ATP8, COX1, COX2, COX3, CYTB, ND2, ND3, ND6) are clockwise coding, while four PCGs (ND1, ND4, ND4L, ND5) are counterclockwise coding. All PCGs stop with usual codons such as TAA and TAG, except ND5 which stopped with the incomplete condon T. The *rrnS* and *rrnL* genes are 810 bp and 1234 bp in length.

To investigate its taxonomic status of *M. dubius*, the sequence alignment was performed with the MAFFT, according to mitochondrial genome sequence of 17 species from Chrysomeloidea which had been selected from Genbank with accession number MW067124. In this study, 37 genes were annotated, including 13 PCGs, 22 tRNAs, 2 rRNAs. Thirteen PCGs are 10,911 bp in total, encoding 3,637 amino acids. Nine PCGs (ATP6, ATP8, COX1, COX2, COX3, CYTB, ND2, ND3, ND6) are clockwise coding, while four PCGs (ND1, ND4, ND4L, ND5) are counterclockwise coding. All PCGs stop with usual codons such as TAA and TAG, except ND5 which is stopped with the incomplete condon T. The *rrnS* and *rrnL* genes are 810 bp and 1234 bp in length.
alternatus alternatus (Figure 1). The complete mitochondrial genome of *M. dubius* will provide useful genetic information for the genetic evolution of *M. dubius*, as well as in other insects of Chrysomeloidea.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This work was supported by the [Forestry Science Research Project of Fujian Forestry Department] under Grant [number Minlinke [2017] 03]; [Forestry Programs of Science and Technology in Fujian Province] under Grant [number Minlinke [2020] 29]; [horizontal research projects] under Grant [number KH200083A]; and [Undergraduate Training Program for Innovation and Entrepreneurship of China] under Grant [number 202010389003].

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov/nuccore/MW067124.1/) under the accession no. MW067124. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA688627, SRP300485, and SAMN17183230 respectively.

**References**

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 313–319.

Ge DY, Chesters D, Gómez-Zurita J, Zhang LJ, Yang XK, Vogler AP. 2011. Anti-predator defence drives parallel morphological evolution in flea beetles. Proc Biol Sci. 278(1715):2133–2141.

Haddad S, Shin S, Lemmon AR, Lemmon EM, Svacha PETR, Farrell B, Ślipiński ADAM, Windsor D, Mckenna DD. 2018. Anchored hybrid enrichment provides new insights into the phylogeny and evolution of longhorned beetles (Cerambycidae). Syst Entomol. 43(1):68–89.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33(7):msw054.

Nie R, Vogler AP, Yang XK, Lin M. 2020. Higher-level phylogeny of longhorn beetles (Coleoptera: Chrysomeloidea) inferred from mitochondrial genomes. Syst Entomol. 45(1):188–204.

Nurk S, Meleshko D, Korobeynikov A, Pevzner PA. 2017. metaSPAdes: a new versatile metagenomic assembler. Genome Res. 27(5):824–834.

Reid CAM. 2000. Spilopyrinae Chapuis: a new subfamily in the Chrysomelidae and its systematic placement (Coleoptera). Invert Systematics. 14(6):837–862.

Salvato P, Simonato M, Battisti A, Negrissolo E. 2008. The complete mitochondrial genome of the bag-shelter moth *Ochrogaster lunifer* (Lepidoptera, Notodontidae). BMC Genomics. 9:331.