



## The complete mitochondrial genome of *Annamanum lunulatum* (Coleoptera: Lamiinae) and its phylogeny

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### ABSTRACT

The complete mitochondrial genome of the *Annamanum lunulatum* is 15,610 bp in length, which contains 13 protein-coding genes, 22 transfer RNAs, two ribosomal RNAs, and the A + T-rich region. The arrangement of genes is identical to all known longhorn beetles mitochondrial genomes. The overall AT content of the mitochondrial genome is 75.3%, whereas the AT content of A + T-rich region is 84.3%. In ML and BI phylogenetic analyses, *A. lunulatum* is a sister clade to *Blephephaeus succinator*, and the monophyly of Lamiinae is supported.

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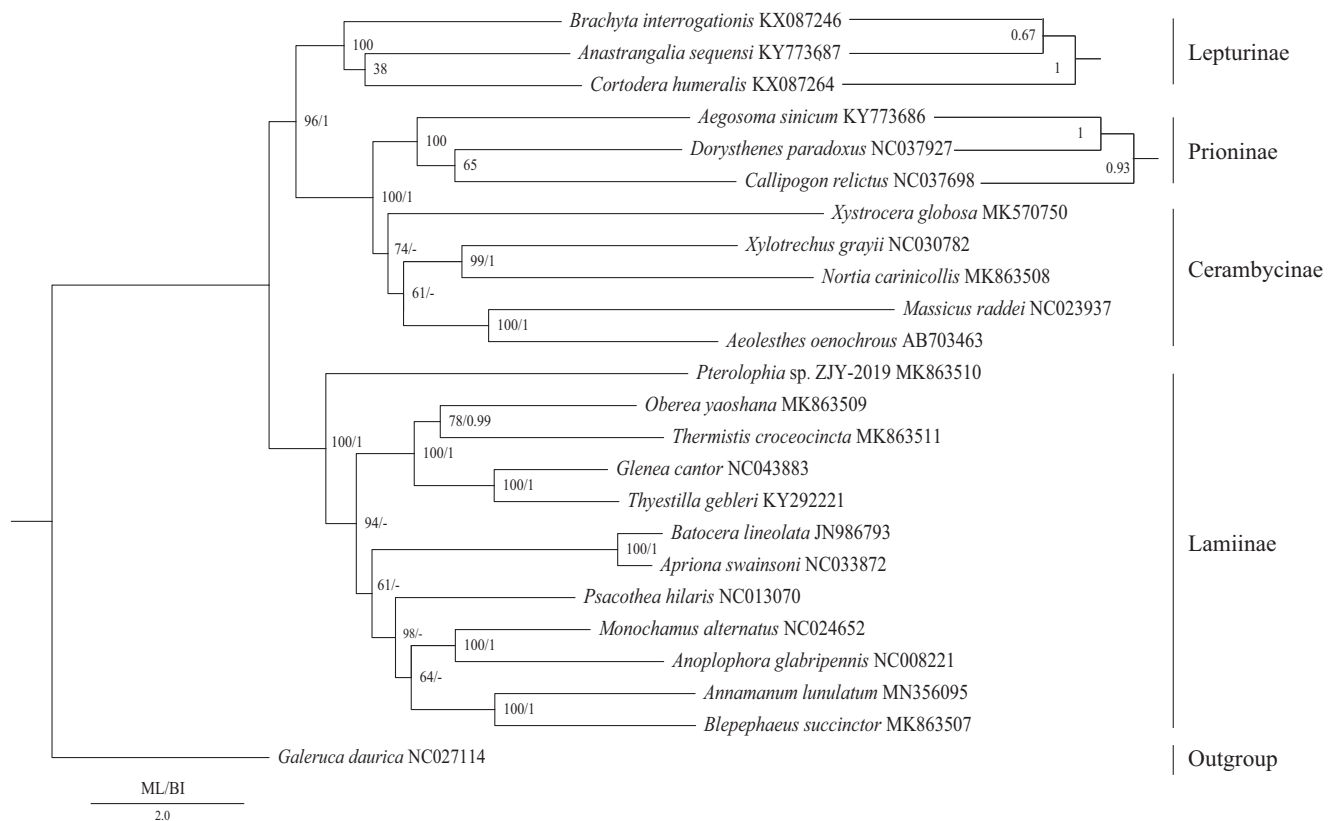
Coleoptera (Hexapoda: Insecta) are a group of insects with over 360,000 described species of beetles (Hunt et al. 2007). It is in the larval stage that some species of Coleoptera belonging to pests make strong damage to plants. *Annamanum lunulatum* (Cerambycidae: Lamiinae) is a longhorn beetle firstly reported by Pic (1934) and *Uraecha longzhouensis* is considered as one of its junior synonyms (Lin and Lingafelter 2018). The genus *Annamanum* includes 31 described species located in South China, Japan, Vietnam, Laos, Cambodia, India, Myanmar, and Malaysia, among which 15 species were reported from China (Holzschuh 2017; Lin and Ge 2017; Tavakilian and Chevillotte 2018; Yang and Yang 2019). However, there were few genetic information on the mitochondrial genome reported in this genus. Hence, we sequenced the mitochondrial genome of *A. lunulatum* to benefit the studies of the genetic diversity in *Annamanum* and to discuss its phylogenetic relationship within Lamiinae.

Samples of *A. lunulatum* were collected from Jinxiu (22°57'28" N, 107°11'38" E), Guangxi province, China on 10 August 2016 and classified by JY Zhang. The sample (JX20160810) was identified and stored at 40 °C in the Animal Specimen Museum, College of Life Sciences and Chemistry, Zhejiang Normal University, China. The total genomic DNA was extracted from leg muscle tissue using an Ezup Column Animal Genomic DNA Purification Kit (Sangon Biotech Company, Shanghai, China) and stored in the Zhang's laboratory. Eight universal primers and six specific

primers (Simon et al. 2006; Zhang et al. 2008; Zhang, Cai, et al. 2018; Zhang, Yu, et al. 2018) were utilized for polymerase chain reaction (PCR) amplification. The mitochondrial genome was deposited in GenBank with an accession number MN356095.

The complete mitochondrial genome of *A. lunulatum* is 15,610 bp in length, including 13 protein-coding genes, 22 transfer RNAs, two ribosomal RNAs, and the A + T-rich region. The overall AT content of the mitochondrial genome is 75.3%, whereas the AT content of A + T-rich region is 84.3%. Almost all the protein-coding genes use ATN as an initiation codon excluding *ND1* with TTG. Eleven genes (*ND1*, *ND2*, *ND3*, *ND4L*, *COI*, *COII*, *COIII*, *ATP6*, *ATP8*, *ND6*, *Cyt b*) end the typical stop codon TAA or TAG, whereas *ND4* and *ND5* end with T—.

In order to reconstruct the phylogenetic relationships of Lamiinae, we used 13 protein-coding genes of 24 species, which contained *Galeruca daurica* as the outgroup (Kim et al. 2009; Lu et al. 2011; Chiu et al. 2016; Fang et al. 2016; Guo et al. 2016; Li et al. 2016; Wang et al. 2016; Lim et al. 2017; Liu et al. 2017; Yang et al. 2017; Liu et al. 2018; Que et al. 2019; Wang, Dai, et al. 2019; Wang, Lan, et al. 2019). MrBayes version 3.2 and the RAxML version 8 programs (Ronquist et al. 2012; Stamatakis 2014) were used to construct BI and ML trees, respectively (Figure 1). *Annamanum lunulatum* was a sister clade to *Blephephaeus*, and the monophyly of Lamiinae was supported in both BI and ML analyses.



**Figure 1.** Phylogenetic trees of the relationships among 24 species of Coleoptera, including *Anamanum lunulatum*, were based on the nucleotide dataset of the 13 mitochondrial protein-coding genes. The numbers showed between branches indicate the posterior probabilities from Bayesian inference (BI) and bootstrap percentages from maximum-likelihood (ML, 1000 replications) analyses. The GenBank accession numbers of all species were also shown.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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