

The complete mitochondrial genome of the tea weevil, *Mylokerinus aurolineatus* (Coleoptera: Curculionidae)

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ABSTRACT

The tea weevil, *Mylokerinus aurolineatus* (Voss), is a serious pest of tea plants. We have obtained and annotated the complete mitochondrial genome of *M. aurolineatus* (GenBank accession No. MH197100). The entire mt genome is 17,762 bp long with an A + T content of 75.45%. The mt genome of *M. aurolineatus* encodes all 37 genes that are typically found in animal mt genomes, consists of 13 protein-coding genes, 2 ribosomal RNA and 22 transfer RNA genes. The gene order is consistent with other weevil mt genomes in Entiminae, within a typical gene order of "RANSEF". Phylogenetic analysis was performed using 13 protein-coding genes among 18 weevils showed that *M. aurolineatus* is closely related to another Entiminae species, *Sympiezomias velatus*.

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The tea weevil, *Mylokerinus aurolineatus* (Voss), is one of the main leaf-feeding insects of *Camellia sinensis*. The adult weevils feeding on young, tender leaves, seriously deteriorating tea yield and quality (Sun et al. 2010). In this study, we obtained and described the complete mitochondrial genome of *M. aurolineatus* for the first time. Adult specimens were collected from a tea plantation at Yongchuan, Chongqing, China (N29°23', E105° 54'), that the tea plantation is belong to Chongqing Academy of Agricultural Science. Samples have been deposited in the insect specimen room of Tea Research Institute of Chongqing Academy of Agricultural Science with an accession number of CQNKY-CO-01-01-01.

The complete mt genome of the tea weevil is a typical closed-circular and double stranded DNA molecule with 17,762 bp in length (GenBank accession MH197100). The overall nucleotide composition of the major strand of the mt genome as follows: A = 39.55% (7025), C = 14.53% (2580), G = 10.02% (1780) and T = 35.90% (6377), with a total A + T content of 75.45%, that is heavily biased toward A and T nucleotides. AT- and GC-skew of the whole J-strand of *M. aurolineatus* is 0.048 and -0.183, respectively. The mt genome of *M. aurolineatus* encodes all 37 genes usually found in animal mt genomes, including 13 protein-coding genes, 2 ribosomal RNAs and 22 transfer RNAs. In this mt genome, there are two long non-coding region like control region. One non-coding region locates between *rns* and *trnI*, is 1161 bp long with a high A + T content of 82.26%, and the other one locates between *trnL* and *trnQ*, is 2012 bp long with a low A + T content of 69.23%. The gene arrangement of the tea weevil is identical to other weevil mt genome in Entiminae, contains gene order "RANSEF" instead of the

ancestral order "ARNSEF" (Tang et al. 2017). Twenty-three of all 37 gene are encoded on the majority strand (J-strand) and the others encoded by the minority strand (N-strand).

Twelve of the 13 PCGs start with ATN codons (ATG for *atp6*, *cox3*, *cob* and *nad4L*; ATT for *cox2*, *nad2*, *nad3*, *nad5* and *nad6*; ATA for *nad1* and *nad4*; ATC for *atp8*) and *cox1* used AAT as start codon, same situation exists in the mt genome of *Naupactus xanthographus* (Song et al. 2010). Three PCGs (*cox1*, *nad4* and *nad5*) have incomplete terminal codons consisting of single T nucleotide, and the other PCGs stop with TAA and TAG. The nucleotide length of tRNA genes is ranging from 63 bp (*trnC*, *trnH* and *trnN*) to 71 bp (*trnK*), and A + T content is ranging from 62.69% (*trnS₁*) to 87.50% (*trnC* and *trnD*). Twenty-one tRNA genes have the conventional cloverleaf shaped secondary structure and *trnS₁* gene lacks the dihydrouridine (DHU) arm. The gene *trnS₁* almost lacks the DHU arm in all metazoan mt genomes (Cameron 2014). The two rRNA genes have been identified on the N-strand in the *M. aurolineatus* mt genome. The length of *rnl* and *rns* genes was 1288 bp and 786 bp, and their A + T content was 80.51 and 79.13%, respectively.

We analyzed amino acid sequence of 13 PCGs with maximum likelihood (ML) method to understand the phylogenetic relationship of *M. aurolineatus* with other weevils. The mt genome sequence of *Ascalohybris subjacens* (GenBank accession no. NC_011277) was used as an outgroup. The tea weevil and another Entiminae weevil, *Sympiezomias velatus*, are clustered into a branch of the phylogenetic tree with 100% bootstrap value (Figure 1).

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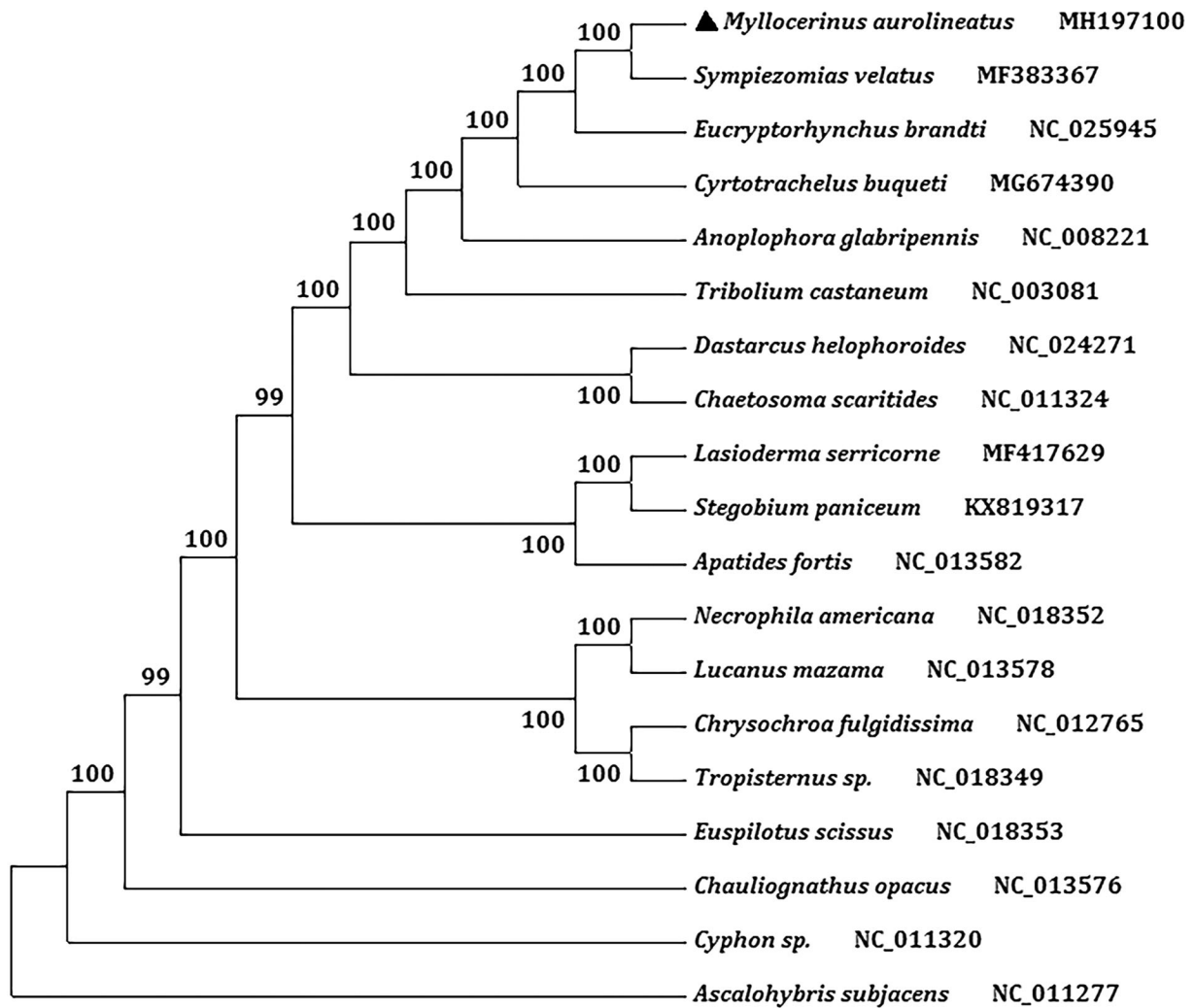


Figure 1. The maximum likelihood (ML) phylogenetic tree of *Myllocerinus aurolineatus* and other weevils.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>, reference number MH197100.

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