

The complete mitochondrial genome of the jewel beetle *Trachys variolaris* (Coleoptera: Buprestidae)

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ABSTRACT

The complete mitochondrial genome (mitogenome) of the jewel beetle, *Trachys variolaris*, was sequenced and described. The mitogenome of *T. variolaris* is a typical circular DNA molecule with 16,771 bp in length. It contains the typical 37 mitochondrial genes (13 protein-coding genes, two rRNA genes, and 22 tRNA genes) and a long non-coding region called the control region. Twelve protein-coding genes initiate with ATN codons except *ND1* uses TTG. Most of the protein-coding genes use TAA or TAG as the stop codon, but *COII*, *COIII*, *ND4*, and *ND5* terminate with a single T— or TA—. The length of the 22 tRNAs ranges from 61 to 70 bp and they all have the clover-leaf structure except for *tRNA^{Ser(AGN)}*. The control region is 2155 bp long with the A+T content of 69.4%. The result of our phylogenetic analysis showed that Buprestoidea is monophyletic, and it is the sister group to (Byrrhoidea + Elateroidea).

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Jewel beetles (Buprestidae) are famous for their beautiful metallic sheen but most of them are important forestry pests as their larvae are either xylophagous and wood-boring, or stem- and leaf-mining. Generally, the bodies of Buprestidae are elongated or even narrow and cylindrical, but species in the genus *Trachys* possess a short body with a round or drop-shaped form (Bernhard et al. 2005). Among them, *Trachys variolaris* was firstly described by Saunders in 1873 (Saunders 1873) and can be collected from *Quercus* trees. Here, we sequenced and described the complete mitogenome of the jewel beetle, *T. variolaris*. Voucher specimen (No. VCim-00112) was deposited at the Entomological Museum of Chinese Academy of Forestry and the sequence was submitted to GenBank under the accession number MN178497.

The complete mitochondrial genome of *T. variolaris* is a typical circular DNA with 16,771 bp in length, containing 37 genes (13 protein-coding genes, 22 tRNA genes, and two rRNA genes) and a long non-coding region. The arrangement of genes is identical with the gene order of *Drosophila yakuba*, which is regarded as the putative ancestral one (Clary and Wolstenholme 1985; Cameron 2014). Totally, there are 51 bp overlapped nucleotides between adjacent genes in 17 locations, ranging from 1 to 8 bp in size. Except for control region, seven inter-genic regions were found in this mitogenome, ranging from 1 bp to 25 bp.

The nucleotide composition of the whole mitogenome is significantly biased toward A and T. The A+T content is

72.1% with positive AT-skew (0.11) and negative GC-skew (−0.21). All protein-coding genes initiate with ATN codons except for *ND1* uses TTG. The stop codon TAA and TAG are assigned to nine protein-coding genes, whereas *COII*, *COIII*, *ND4*, and *ND5* terminate with TA— or a single T— residue. Using a single T— or TA— as stop codon is commonly found in many other insect mitogenomes (Hong et al. 2009; Zhao et al. 2019; Cao and Wang 2019).

This mitogenome contains all set of typical 22 tRNA genes and the length ranges from 61 bp to 70 bp. Among them, only *tRNA^{Ser(AGN)}* cannot be folded into the clover-leaf secondary structure as the result of the deficiency of the dihydrouridine (DHU) arm. The *tRNA^{Ser(AGN)}* with a simply looped DHU arm is also found in many insects (Li et al. 2012; Song et al. 2016). The *lrRNA* is 1320 bp long with a high A+T content (79.3%), and the *srRNA* is 791 bp long with an A+T content of 77.2%. The control region is located between *srRNA* and *tRNA^{Leu}* with 2155 bp in length.

Phylogenetic tree of Elateriformia based on the dataset of 13 PCGs was conducted by maximum-likelihood (ML) method (Figure 1). The results confirmed that the four superfamilies within Elateriformia are all monophyly. Buprestoidea is shown as the sister group to the clade (Byrrhoidea + Elateroidea). These results are congruent with previous hypotheses on the phylogenetic relationships among Elateriformia using molecular data (Bocakova et al. 2007; Kundrata et al. 2017).

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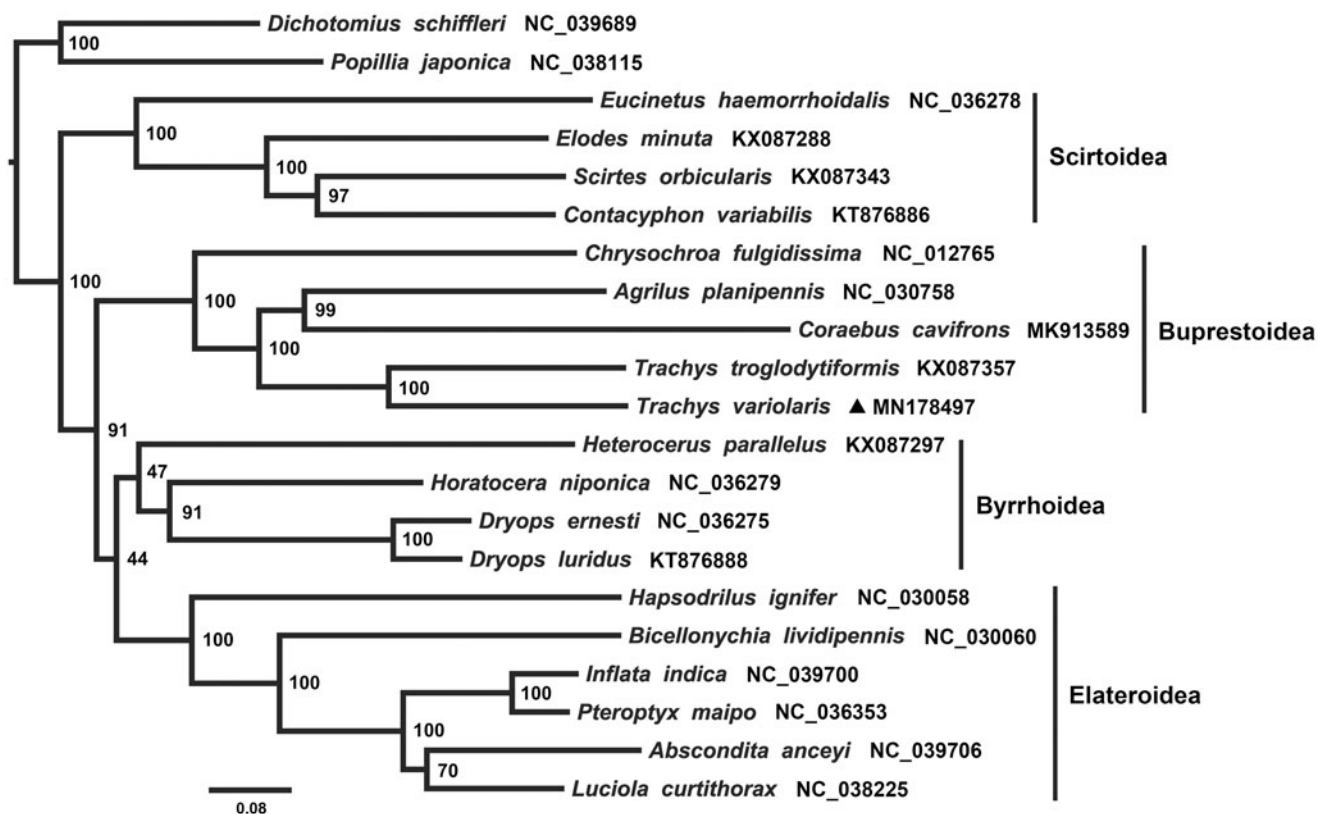


Figure 1. Phylogenetic relationship of 19 species among Elateriformia. The phylogenetic tree was conducted by ML analysis of the 13 protein-coding genes (10,992 bp) with IQ-TREE 1.6.5 (Trifinopoulos et al. 2016). The nodal values indicate the bootstrap percentages obtained with 10,000 replicates. Alphanumeric terms indicate the GenBank accession numbers.

Disclosure statement

No potential conflict of interest was reported by the authors.

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