

Mitochondrial DNA Part A

DNA Mapping, Sequencing, and Analysis

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of *Endoclita signifer* (Lepidoptera, Hepialidae)Xiushuai Yang¹, Xiuhao Yang², Dayong Xue¹, and Hongxiang Han¹¹Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China and ²Department of Guangxi Forestry Pest Management, Nanning 530022, Guangxi, China**Abstract**

The ghost moth *Endoclita signifer* is a new wood-boring pest of eucalyptus in south of China. It infests dozens of native plant species, and causes severe damage to the plantations of exotic eucalyptus. We sequenced the complete mitochondrial genome (mitogenome) of *E. signifer*, which has the typical 37 mitochondrial genes of insects. Contrary to most of the Lepidoptera, the *E. signifer* mitogenome has the putative ancestral insect gene order. Atypical start codon (TTG) and incomplete stop codon (one T-nucleotide) were found for *COX2*. The *E. signifer* control region is 389 bp without tandem repeats, and two (TA)_n stretches were observed.

Keywords

Endoclita signifer, Hepialidae, mitochondrial genome

History

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Endoclita signifer (Walker, 1856) is a species of Hepialidae, a primitive lepidopteran family with 66 genera and about 563 species (Wikipedia, 2011). *Endoclita signifer* is widely distributed in eastern Asia. In forestry plantations, *Endoclita* larvae are stem-borers on teak, firs, or eucalyptus often causing significant economic loss (Nair, 2007). *Endoclita signifer* is highly polyphagous and is known to infest more than 20 native plant species in China. *Endoclita signifer* is now one of the most significant pests of eucalyptus plantations in southern China, and it can cause losses of million dollars annually (Yang et al., 2013).

In this study, we determined the complete mitogenome of *E. signifer*, which is collected from Bobai Forestry Farm, Guangxi

Province, China. Three legs from one side of the body were removed and stored in 100% ethanol at -20°C , and the specimens were deposited at the Museum of the Institute of Zoology, Chinese Academy of Sciences. The complete mitogenome of *E. signifer* is 15 285 bp (GenBank accession no. KT780172), with the entire set of 37 genes (13 PCGs, 22 tRNA genes, and two rRNA genes) and the putative control region (also called the A + T-rich region).

The arrangement of the 37 genes and the control region was identical to the inferred ancestral gene order for insects, and was consistent with that of the three hepialid species recently published (Cao et al., 2012; Yi et al., 2014). The nucleotide compositions of *E. signifer* are significantly A and T biased with an A + T content of 81.9% for the majority strand and 95.4% for the control region. The mitogenome is slightly T-skewed and moderately C-skewed. Eleven PCGs were predicted to start with ATN codons, while CGA and TTG were predicted to be start codons of *COX1* and *COX2* genes respectively. A *trnM*-like structure with a high coverage score of 22.54 was observed in the control region using tRNAscan-SE (lowelab.ucsc.edu/tRNAscan-SE/). The sequence of *trnM*-like has a much higher AT content (97.4%) than the normal tRNA genes, and it is supposed to be a random bit sequence which could be folded into a similar clover leaf secondary structure. The putative control region of *E. signifer* is 389 bp long, with more T than A and a little more G than C. One poly-T stretch was observed downstream of srRNA, and two (TA)_n stretches were observed upstream of *trnI*.

Bayesian phylogenetic analysis was conducted using MrBayes 3.2.6 (MrBayes Inc., Tallahassee, FL) with 13 mitochondrial protein-coding genes (Figure 1). *Endoclita signifer* is clustered

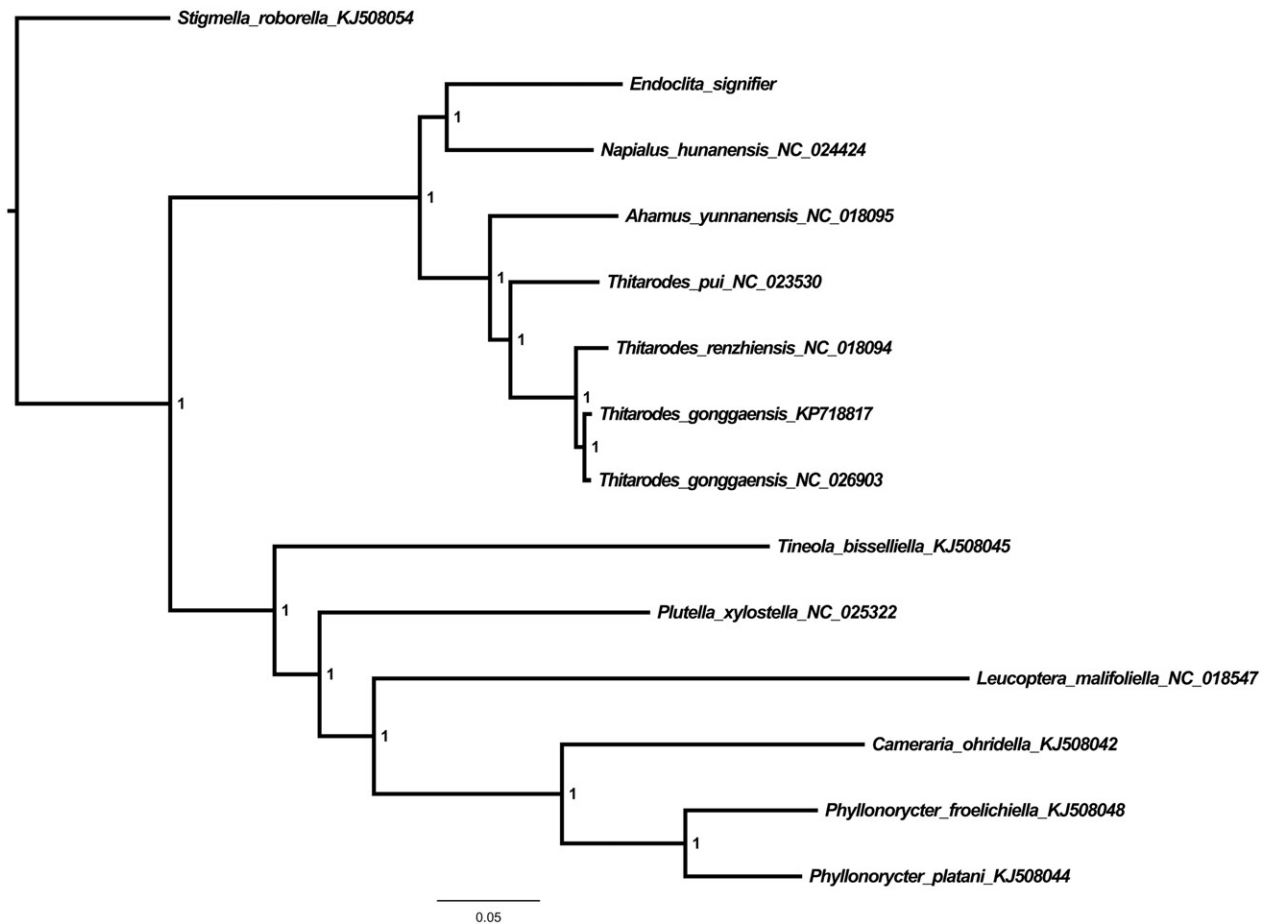


Figure 1. Bayesian phylogenetic tree inferred from 13 protein-coding sequences. *Stigmella roborella* was used to root the tree.

with the other hepialid species, and it is more closely related to *Napialus hunanensis*.

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Declaration of interest

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