MITOCHONDRIAL DNA PART B
2020, VOL. 5, NO. 1, 1073–1074
https://doi.org/10.1080/23802359.2020.1721366

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MITOGENOME ANNOUNCEMENT

Mitochondrial genome of *Trichagalma acutissimae* (Hymenoptera: Cynipoidea: Cynipidae) and phylogenetic analysis

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ABSTRACT

Trichagalma acutissimae (Monzen) (Hymenoptera: Cynipidae) is a major pest of *Quercus variabilis* Blume in the Taihang Mountains in China. In this study, we sequenced and analyzed the mitochondrial genome (mitogenome) of *T. acutissimae*. This mitogenome was 16,078 bp long and encoded 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), and 2 ribosomal RNA unit genes (rRNAs). The whole mitogenome exhibited heavy AT nucleotide bias (86.2%). Except for *nad4L* that started with TTG, all other PCGs started with the standard ATN codon. All 13 PCGs terminate with the stop codon TAA. Phylogenetic analysis showed that *T. acutissimae* got together with *Synergus* sp. with high support value, indicating the close relationship of these two genus. All five Cynipoidea species constituted a major clade and formed a sister group to Proctotrupoidea and Chalcidoidea.

ARTICLE HISTORY
Received 15 January 2020
Accepted 19 January 2020

KEYWORDS
Cynipidae; mitochondrial genome; *Trichagalma acutissimae*; phylogenetic analysis

Cynipoidea is the third-largest superfamily of parasitic Hymenoptera, which includes species exhibiting a wide range of life modes (Ronquist 1999). Most of the phytophagous Cynipidae can induce a great variety of galls, among them, are some of the most complex of all insect galls (Nieves-Aldrey et al. 2005). The Cynipini are restricted to plants of the family Fagaceae, predominantly oaks (*Quercus* spp.), on which they induce galls of diverse structures in leaves, buds, stems, flowers, fruits, and roots (Stone et al. 2002). *Trichagalma acutissimae* (Hymenoptera: Cynipidae) is one of the important pests harming afforestation plants *Quercus variabilis* and is very difficult to control by chemical pesticides.

Specimens of *T. acutissimae* were collected from Linzhou City, Henan Province, China (36°07′N, 113°43′E, October 2019) and were stored in Entomological Museum of Anyang Institute of Technology (Accession number AIT-E-TRI07). After morphological identification, total genomic DNA was extracted from tissues using DNeasy DNA Extraction kit (Qiagen, Hilden, Germany). The mitogenome sequence of *T. acutissimae* was generated using Illumina HiSeq 2500 Sequencing System (Illumina, San Diego, CA). In total, 6.2 G raw reads were obtained, quality-trimmed, and assembled using MITObim v 1.7 (Hahn et al. 2013). By comparison with the homologous sequences of other Cynipoidea species from GenBank, the mitogenome of *T. acutissimae* was annotated using the software Geneious R8 (Biomatters Ltd., Auckland, New Zealand).

The nearly complete mitogenome of *T. acutissimae* is 16,078 bp (Genbank accession, MN928529) in length and contains 13 protein-coding genes (PCGs), 22 tRNA genes, and 2 rRNA genes. The overall base composition of the mitogenome was estimated to be A 42.9%, T 43.3%, C 7.6%, and G 6.2%, with a high AT content of 86.2%. Compared with the ancestral insect mitochondrial genome, the mitogenome of *T. acutissimae* exhibits dramatic mitochondrial gene rearrangement, which is usually found in Cynipoidea species (Mao et al. 2015; Tang et al. 2019). Most PCGs of *T. acutissimae* had the conventional start codons ATN (five ATG, five ATT, and two ATA), with the exception of *nad4L* (TTG). All 13 PCGs terminate with the stop codon TAA. The lengths of *rrnL* and *rrnS* in *T. acutissimae* were 1396 and 853 bp, with the AT contents of 89.5 and 91.1%, respectively. The 22 tRNA genes vary from 64 bp (*trnT*) to 75 bp (*trnC* and *trnK*).

The phylogenetic tree was constructed using the maximum-likelihood method through raxmlGUI 1.5 (Silvestro and Michalak 2012) based on 13 mitochondrial protein-coding genes sequences. Results showed that the newly sequenced species *T. acutissimae* got together with *Synergus* sp. with high support value, indicating the close relationship between these two genera (Figure 1). All five Cynipoidea species constituted a major clade and formed a sister group to Proctotrupoidea and Chalcidoidea. In conclusion, the mitogenome of *T. acutissimae* is sequenced in this study and can provide essential DNA molecular data for further phylogenetic and evolutionary analysis of Cynipoidea.

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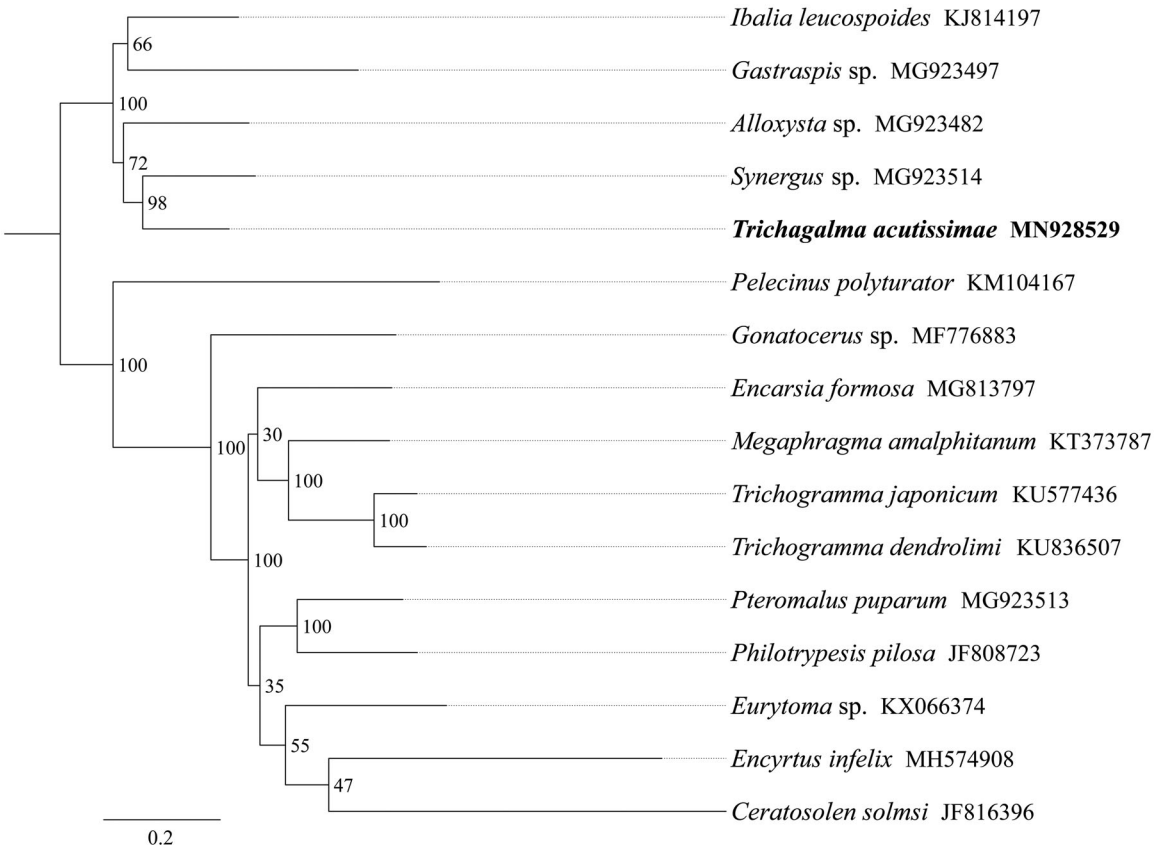

Figure 1. Phylogenetic relationships based on the 13 mitochondrial protein-coding genes sequences inferred from RaxML. Numbers on branches are Bootstrap support values (BS).

Disclosure statement

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the article.

Funding

This study was supported by the Scientific and Technological Project of Henan Province [182102110409] and a grant from Postdoctoral Innovation and Practice Base of Anyang Institute of Technology.

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