

The Complete Mitochondrial Genome of *Iassus latus* Shen & Cai, 2010 (Hemiptera: Cicadellidae)

Junfang He¹, Bin Zhang^{1,2*}

1. College of Life Sciences & Technology, Inner Mongolia Normal University, Hohhot, China, 010022

2. Key Laboratory of Biodiversity Conservation and Sustainable Utilization for College and University of Inner Mongolia Autonomous Region, Hohhot 010022, China

Abstract: The complete mitochondrial genome of *Iassus latus* Shen & Cai, 2010 (Hemiptera, Cicadellidae) was described, which was 15,181 bp in length, encoding the standard set of 22 transfer RNAs (tRNAs), two ribosomal RNAs (rRNAs), 13 protein-coding genes (PCGs) and one A-T rich region (also called control region). The content of A+T was 80.12% (A: 46.62%, T: 33.50%, C: 10.96%, G: 8.93%), which was much higher than that of G+C. The complete mitochondrial genome of *I. latus* and the other 25 species were used for phylogenetic analysis using the Bayesian method. The phylogenetic tree visualized that *I. latus* and species from the same subfamily were clustered in one branch, which was closely related to *Iassus dorsalis*. The identified mitochondrial genome of *I. latus* will provide fundamental data to explore the evolution of the mitochondrial genome in Iassinae.

Keywords: *Iassus latus*; Mitochondrial genome; Phylogenetic tree

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1. Introduction

The *Iassus latus* leafhopper Shen & Cai, 2010 belongs to the subfamily Iassinae (Hemiptera: Cicadellidae). There are more than 2200 species in 155 genera of 12 families in the world, and 89 species in 10 genera of 5 families (Yang & Dai 2022), which is a larger subfamily of the leafhopper. So far, little is known about the evolution of the mitochondrial genome in *I. latus*. Clarifying the mitochondrial genome of *I. latus* contributes to the species identification, and phylogenetic analyses of the members of Iassinae.

In this study, we reported the complete mitochondrial genome of *I. latus*, with the voucher number of PP085127. The specimen was collected from Tongliao (43.05614971°N, 123.20999124°E), Inner Mongolia, China on July 25, 2020, and was deposited in the insect specimen room of the Research Institute of Inner Mongolia Normal University (number IMNU20200721114). The entire body without abdomen was shipped to Tsingke Biotechnology Co., Ltd. (Beijing, China) for genomic extraction. Sequencing was performed on an Illumina NovaSeq instrument. De novo assembly of clean reads was performed using SPAdes v3.11.0 (Bankevich et al. 2012). A preliminary prediction of the mitochondrial genome of *I. latus* was made using the MITOS Web Server (Bernt et al. 2013). The secondary structure of tRNA gene was further verified by tRNAscan-SE, and the anti-codon and its site were read and the codon was then determined. The exact position of rRNA was difficult to determine, so it was inferred by the position between the two genes.

2. Mitochondrial genome data analysis

The mitochondrial genome of *I. latus* is 15181 bp in length, with the overall base composition of 33.5% (T), 10.95% (C), 46.62% (A) and 8.93% (G). The A+T content of the whole genome sequence was 80.12%, which was much higher than that of G+C, showing

an obvious A+T preference. Annotation of the mitochondrial genome revealed 13 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes, and one control region (CR or D-loop). The gene organization and order exhibited a typical invertebrate mitochondrial genome feature (Chen et al. 2020). The length of 22 tRNA genes encoded by the mitochondrial genome of the *I. latus* ranged at 60–69 bp. The lengths of 16S rRNA and 12S rRNA were 1010 bp and 705 bp respectively. Except for ATP8 that was initiated with TTG, most of the PCGs were initiated with the typical ATN codon. Meanwhile, most PCGs were terminated with the typical TAA and TAG codons, except for COX2 with the incomplete termination codon T.

Fig. 1 Gene map of the *I. latus* mitogenome

Fig. 2 The relative synonymous codon usage (RSCU) of the PCGs of *I. latus* mitogenomes

Phylogenetic analyses of *I. latus* and other 25 leafhopper species were conducted based on the concatenated PCGs using Bayesian inference (BI) method in MrBayes v3.2.1 (Ronquist et al. 2012) under the GTR + Gamma substitution model. The phylogenetic tree (Figure 3) visualized that *I. latus* was clustered in one branch with 12 species of Iassinae, and it was closely related to *Iassua dorsalis*. Collectively, the complete mitochondrial genome of *I. latus* in Inner Mongolia China identified in this study enriches the genomic data of Iassinae and provides a strong support for analyzing the phylogenetic relationship of Iassinae.

No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of this article.

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov/> under the Accession no. PP085127. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA741086, SRR14924734, and SAMN19844606, respectively.

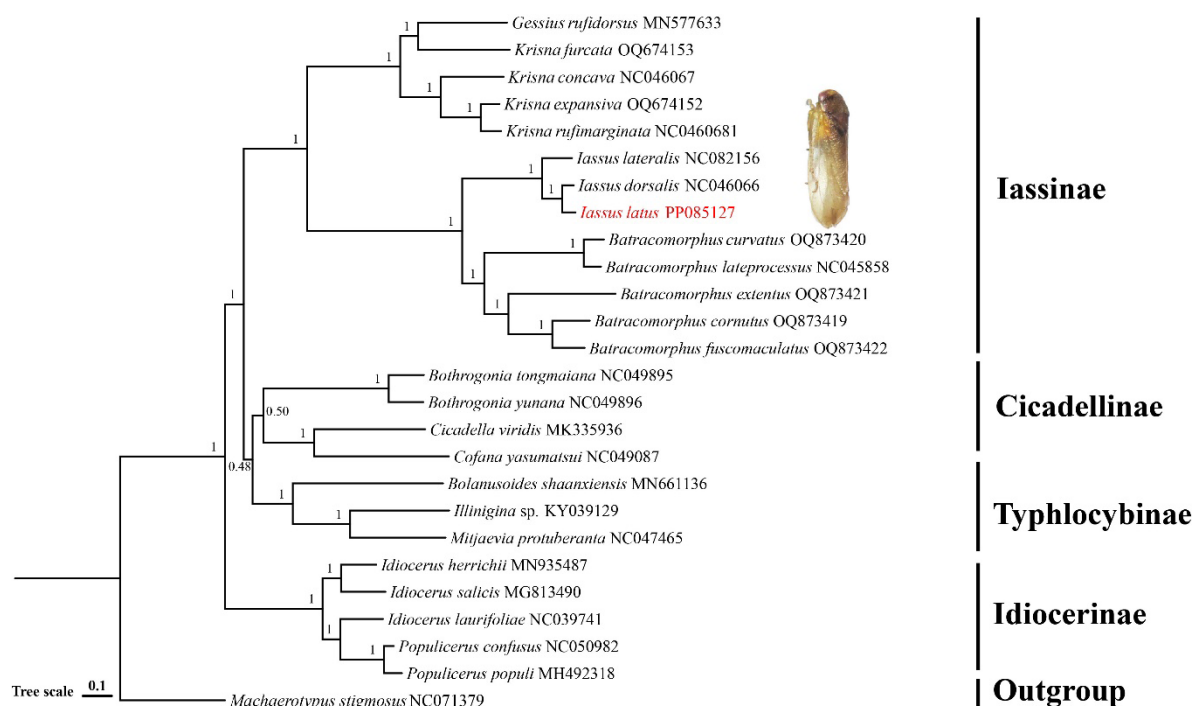


Figure 3. The phylogenetic tree of 4 subfamilies containing 25 species was constructed by Bayesian method. The phylogenetic placement of *I. latus* is highlighted. The number of nodes represents the support rate. GenBank accession numbers are given with species names.

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*Correspondence

About the author:

Name: Junfang He , gender: female, nationality: Han, Native place: Yanggao County, Datong City, Shanxi Province, Education: Bachelor's degree, institution: Inner Mongolia Normal University, title: None, research direction: Animal Biology

Name: Bin Zhang , gender: male, nationality: Han, native place: Kangping County, Shenyang City, Liaoning Province, Education: PhD, institution: Inner Mongolia Normal University, title: Professor, research direction: Zoology