

# Structural Features and Phylogenetic Implications of Two New Mitogenomes of Erythroneurine Leafhoppers (Hemiptera: Cicadellidae: Typhlocybinae)

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## Research article

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# Abstract

**Background:** Complete mitochondrial genome sequences facilitate species identification and analyses of phylogenetic relationships. However, the available data are limited for the diverse and widespread insect family Cicadellidae. In this study, we sequenced complete mitochondrial genomes of two species of Erythroneurini.

**Results:** The mitogenomes of *Empoascanara wengangensis* and *E. gracilis* were 14,830 and 14,627 bp in length, respectively, and similar to other published leafhopper mitogenomes in terms of gene size, base composition, gene order, PCGs codon usage, and tRNA secondary structure. Most protein coding genes start with ATN and end with TAA or TAG. Two rRNA genes are highly conserved and encoded on the minority strand, and the AT content in 16S is higher than that of 12S. The control regions in the genus *Empoascanara* are highly variable and contain various numbers of repeat sequences.

**Conclusions:** The mitogenomes of these two species closely resemble those of most other sequenced leafhoppers in various structural and compositional aspects. Phylogenetic analysis of 13 PCGs yielded a well-supported topology with most branches receiving maximum support and most relationships agreeing with those of other recent phylogenetic studies. Nucleotide diversity analysis show that *nad4* and *nad5* can be evaluated as potential DNA markers that define the Cicadellidae insect species. Like other studies, the main evolutionary event of leafhoppers occurred in the Tertiary, and its divergence time is estimated to be 10.03~122.48 Ma. This study confirms results of previous studies indicating that mitochondrial genome sequences are informative of leafhopper phylogeny.

## Full Text

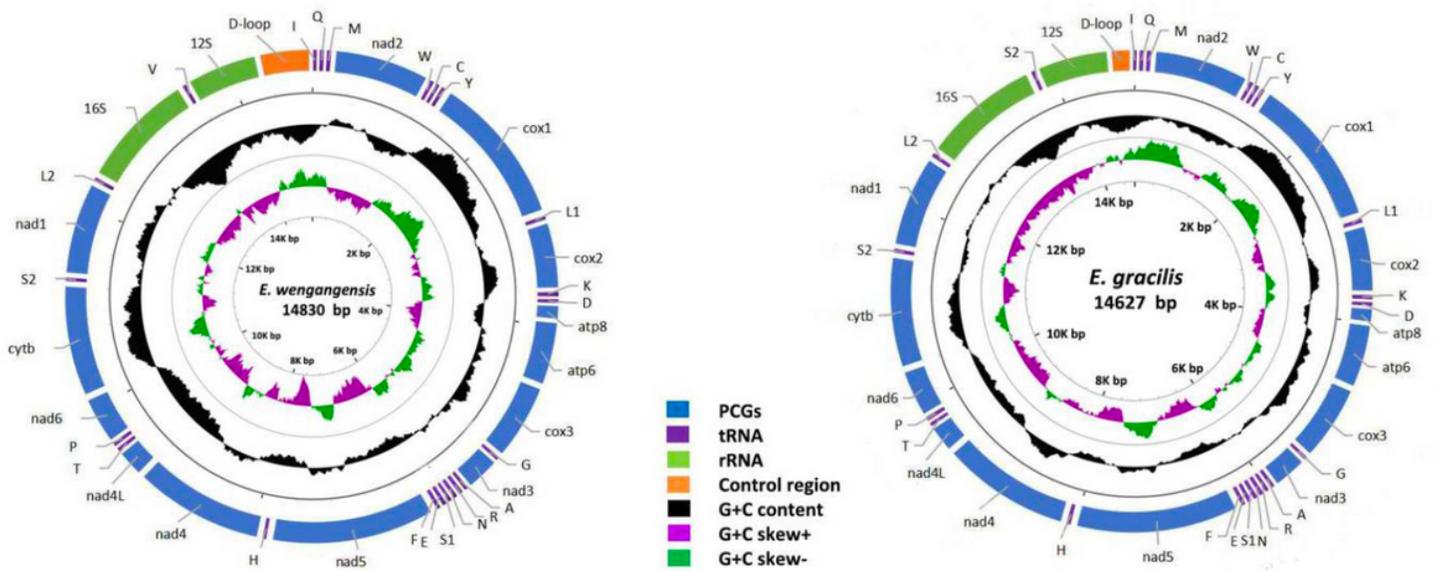
This preprint is available for [download as a PDF](#).

## Figures



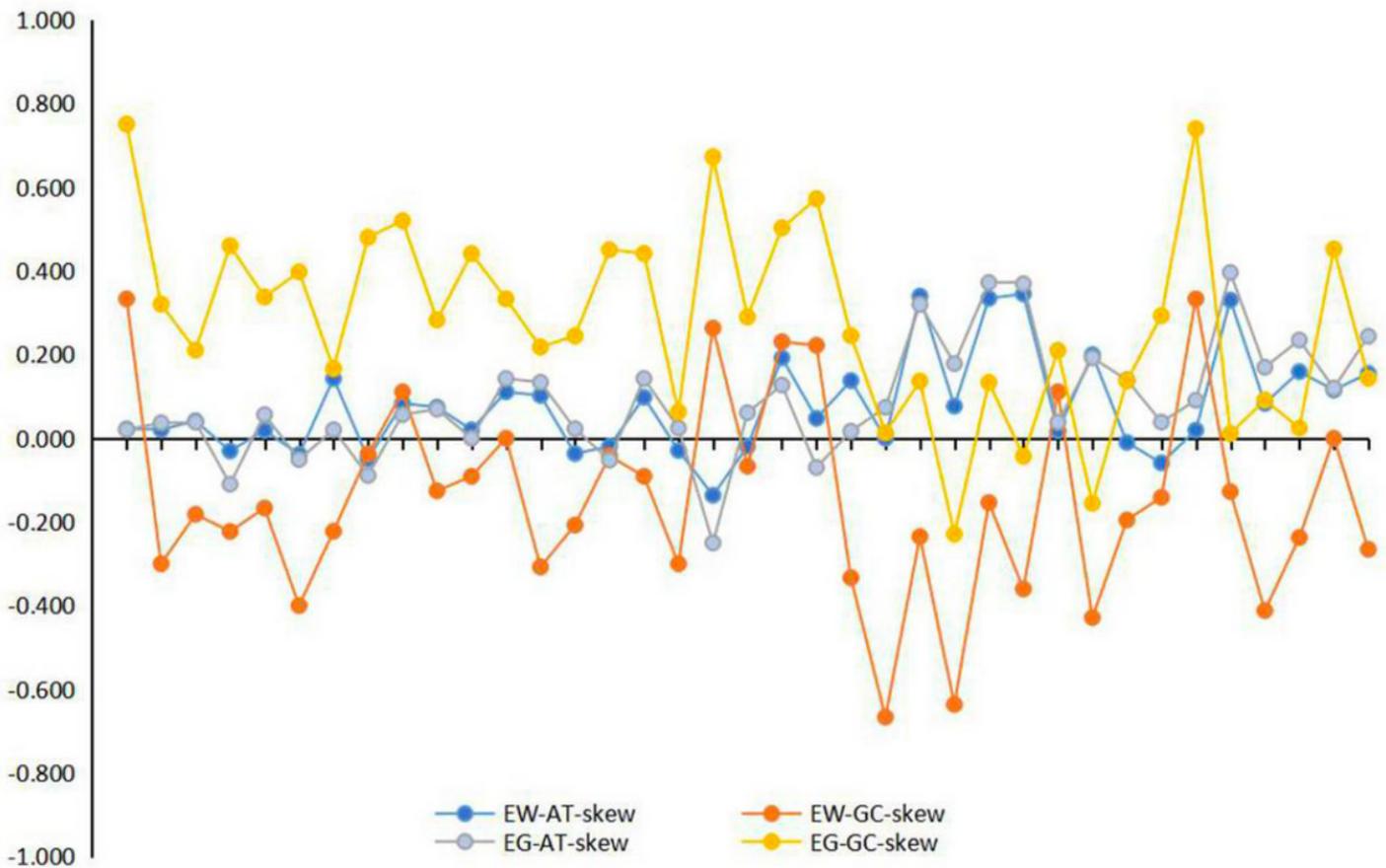
**Figure 1**

Four species of Empoasca. 1 *E. wengangensis* Chen & Song, 2020; 2 *E. gracilis* Dworakowska, 1992; 3 *E. sipra* Dworakowska, 1980; 4 *E. dwalata* Dworakowska, 1971.



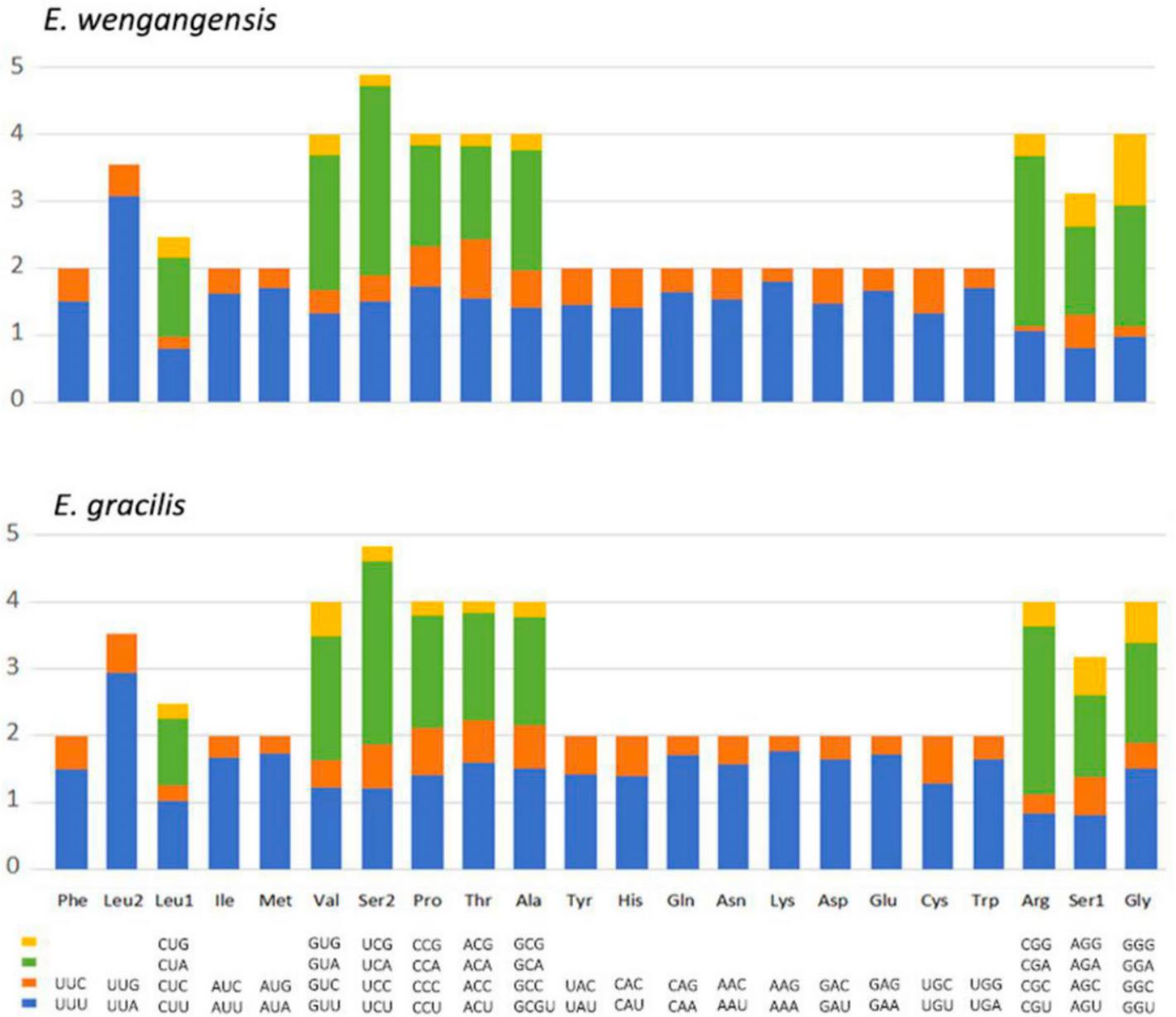
**Figure 2**

Circular map of the mitochondrial genome of *E. wengangensis* and *E. gracilis*.



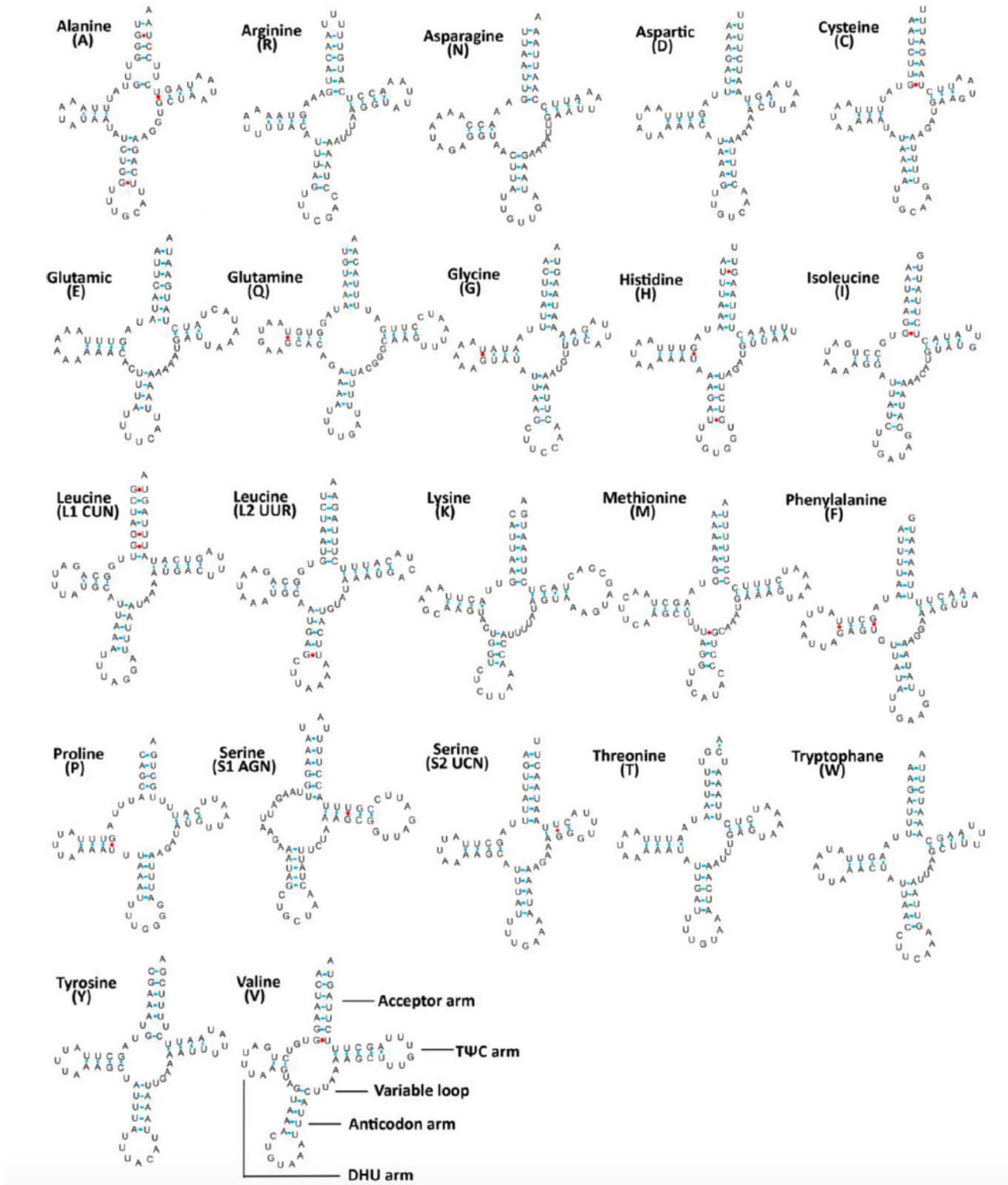
**Figure 3**

AT and GC skews calculated for the 37 mitochondrial genome of *E. wengangensis* and *E. gracilis*. Each point indicates an individual gene.



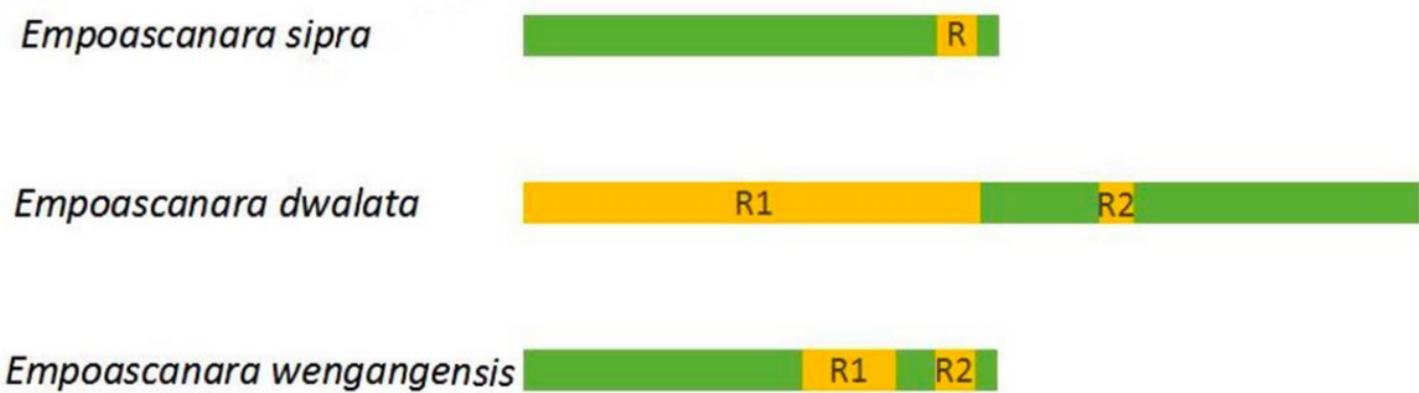
**Figure 4**

Relative Synonymous Codon Usage (RSCU) of mitochondrial genomes for *E. wengangensis* and *E. gracilis*.



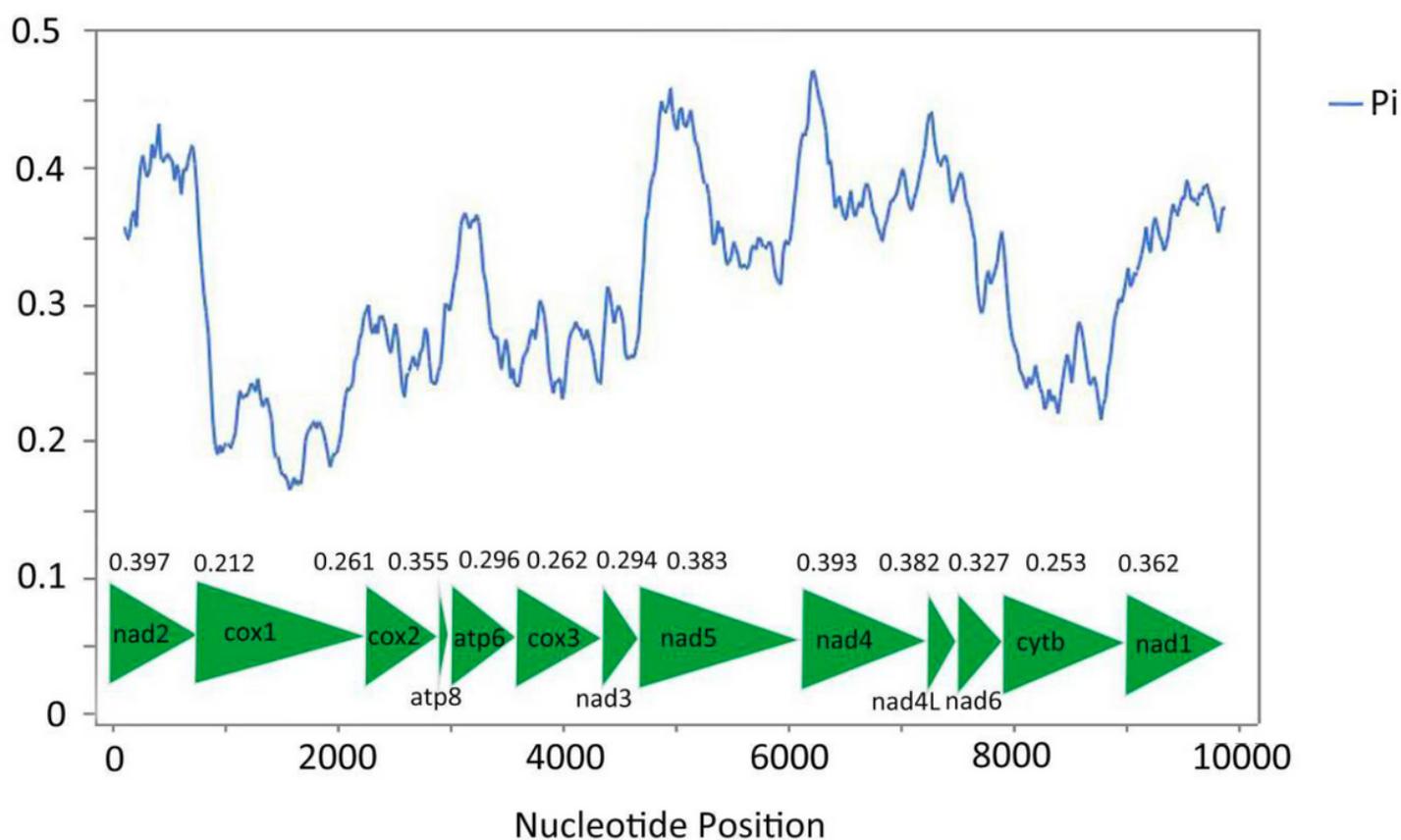
**Figure 5**

Inferred secondary structures of 22 tRNAs from *E. wengangensis*. Watson-Crick base pairings are illustrated by lines (-), whereas GU base pairings are illustrated by red dots. Structural elements in tRNA arms and loops are illustrated as for *trnV*.



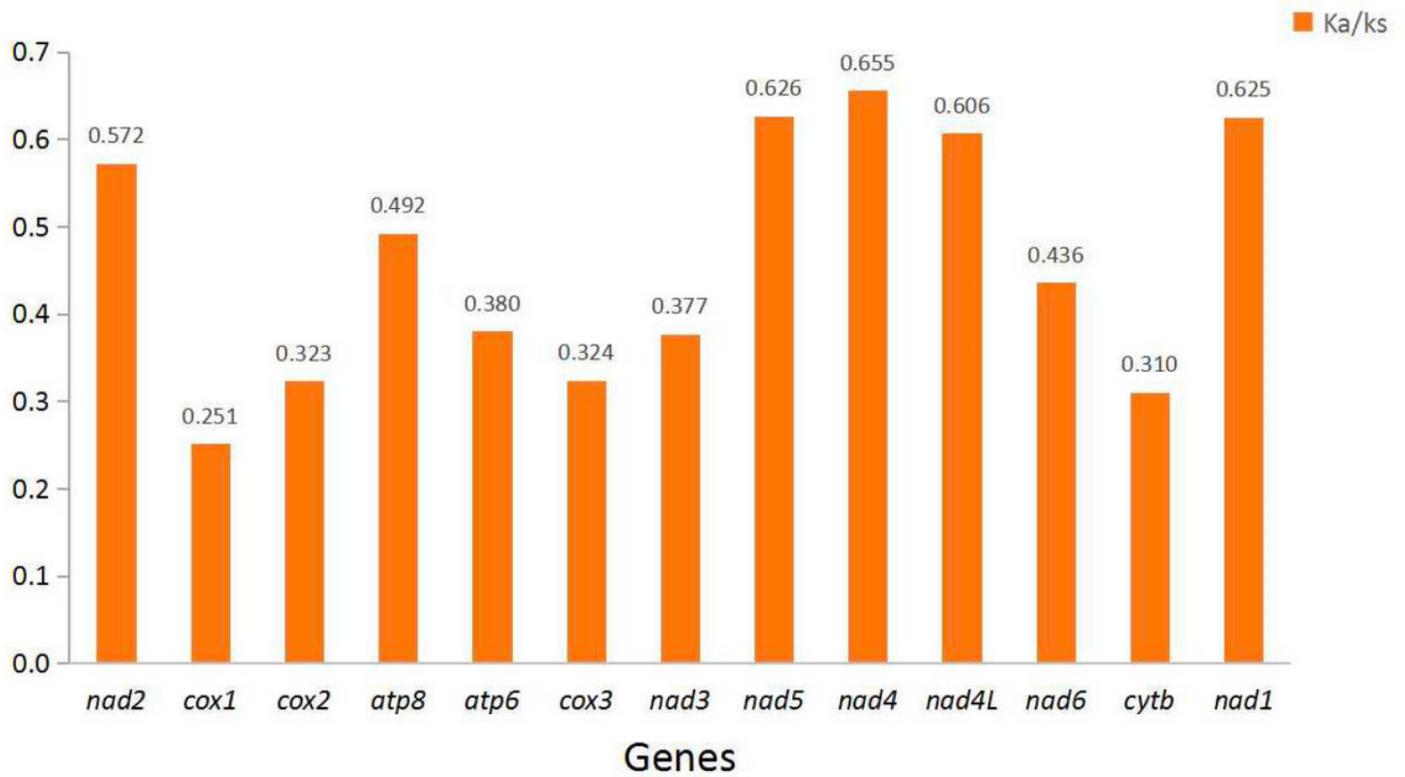
**Figure 6**

Organization of the control region structure in the mitochondrial genomes of three *Empoasca* species. R: repeat unit.



**Figure 7**

Nucleotide diversities and sliding window analysis of 13 PCGs of the 45 Cicadellidae species. Blue curve shows the value of nucleotide diversity (Pi). Pi value of each PCG was shown above the arrows.



**Figure 8**

The ratio of non-synonymous (Ka) to synonymous (Ks) substitution rates of each 13 PCGs among 45 Cicadellidae species.

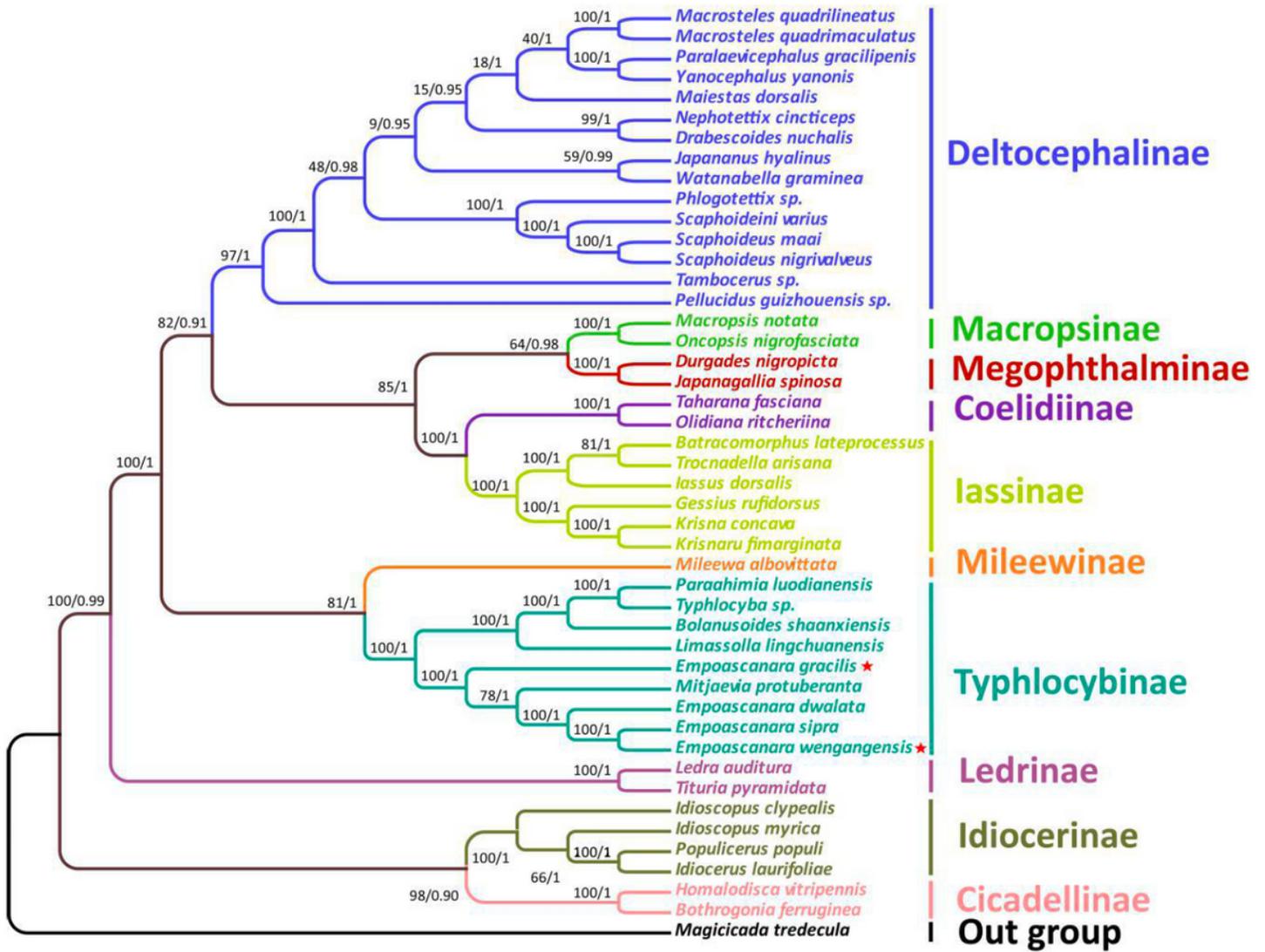


Figure 9

ML and BI Phylogenetic tree inferred from 13 PCGs of Cicadellidae. The first number at each node is bootstrap proportion (BP) of maximum likelihood (ML) analyses, and the second number is Bayesian (BI) posterior probability (PP).



- [SupplementaryMaterials.pdf](#)