

The complete mitochondrial genome of *Limassolla lingchuanensis* (Hemiptera: Cicadellidae: Typhlocybinae)

Xiaowei Yuan^{a,b,c}, Kangning Xiong^{a,b}, Can Li^c and Yuehua Song^{a,b}

^aSchool of Karst Science, Guizhou Normal University, Guiyang, Guizhou, China; ^bState Engineering Technology Institute for Karst Desertification Control, Guiyang, Guizhou, China; ^cGuizhou Provincial Key Laboratory for Rare Animal and Economic Insect of the Mountainous Region, Guiyang University, Guiyang, Guizhou, China

ABSTRACT

The complete mitochondrial genome of the leafhopper *Limassolla lingchuanensis* was determined. It is 15,716 bp in length and consists of 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 rRNA genes, and a putative control region. ATN and TTG were initiation codons, and TAA, TAG, and T were termination codons. The phylogenetic relationships based on the neighbor-joining method were revealed using 13 PCGs with 10 leafhopper species of family Cicadellidae, which agree with the conventional taxonomy.

ARTICLE HISTORY

Received 13 November 2019
Accepted 23 November 2019

KEYWORDS

Limassolla lingchuanensis;
leafhopper; mitochon-
drial genome

The leafhopper species *Limassolla lingchuanensis* (Chou and Zhang 1985) belongs to the subfamily Typhlocybinae (Hemiptera: Cicadellidae), the genus *Limassolla* includes 44 known species distributed across the world (Md et al. 2019). Many leafhopper species in this genus are all herbivorous insects with a broad diet and can feed on a variety of plants (Zhang et al. 2011). In this study, all examined samples were collected from Luodian in Guizhou Province of China (N25°56', E106°86'). The whole body specimen was preserved in ethanol and stored in the insect specimen room of Guizhou Normal University with an accession number GZNU-ELS-2019001.

The overall base composition is 43.18% A, 35.64% T, 11.62% C, and 9.56% G, with A+T the complete mitogenome of *L. lingchuanensis* (GenBank accession number MN605256) is a typical closed-circular molecule of 15,716 bp in length, containing 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 rRNA genes (*rrnL* and *rrnS*), and a putative control region. The orientation and gene order of *L. lingchuanensis* are identical with other leafhoppers' mitogenomes (Xing and Wang 2019; Yang et al. 2019). Thirteen genes were coded on the minor strand (J-strand), whereas the others were oriented on the major strand (N-strand). Gene overlaps in the *L. lingchuanensis* mitogenome were found at 16 gene junctions and involved a total of 45 bp with length varying from 1 to 8 bp. The longest overlap was situated between *trnC* and *trnW*.

There are 11 intergenic spacer sequences in a total of 47 bp and the largest overlap is 26 bp long intergenic spacer, which is located between *nad5* and *trnH*.

The overall nucleotide composition was A (43.18%), T (35.64%), C (11.62%), and G (9.56%), The AT-skew and GC-skew of this genome were 0.0957 and -0.0972, respectively. The A+T content of the 13 PCGs ranged from 70.37% (*cox1*) to 83.01% (*atp8*). The length of 22 tRNAs ranged from 53 bp (*trnH*) to 71 bp (*trnK*), and A+T content varied from 73.02% (*trnS1*) to 89.06% (*trnG*). The *rrnL* and *rrnS* were spaced by *trnV*, with a length of 1168 and 743 bp, respectively. And all of them were encoded on the J-strand. The control region was 1416 bp length and 91.38% A+T content.

In the mitogenome of *L. lingchuanensis*, the total length of 13 PCGs is 10,787 bp, which accounts for 75.26% of the total genome. The *nad4* initiated with A as the start codon, *atp8* began with TTG, *nad3*, *nad5*, and *nad6* started with ATA, *cox2*, *nad1*, and *nad4l* started with ATT, and remaining six PCGs started with ATG. Nine PCGs including *atp6*, *atp8*, *cox3*, *nad1*, *nad3*, *nad4l*, *nad5*, *nad6*, and *cob* are terminated with TAA as stop codon, *cox1* and *nad2* end with TAG, *cox2* and *nad4* end with a single T residue. We analyzed the amino acid sequences of 13 PCGs with neighbor-joining method to reveal the phylogenetic relationship of *L. lingchuanensis* with other leafhoppers in family Cicadellidae. The result shows that *L. lingchuanensis* forms a clade with *Empoasca vitis*

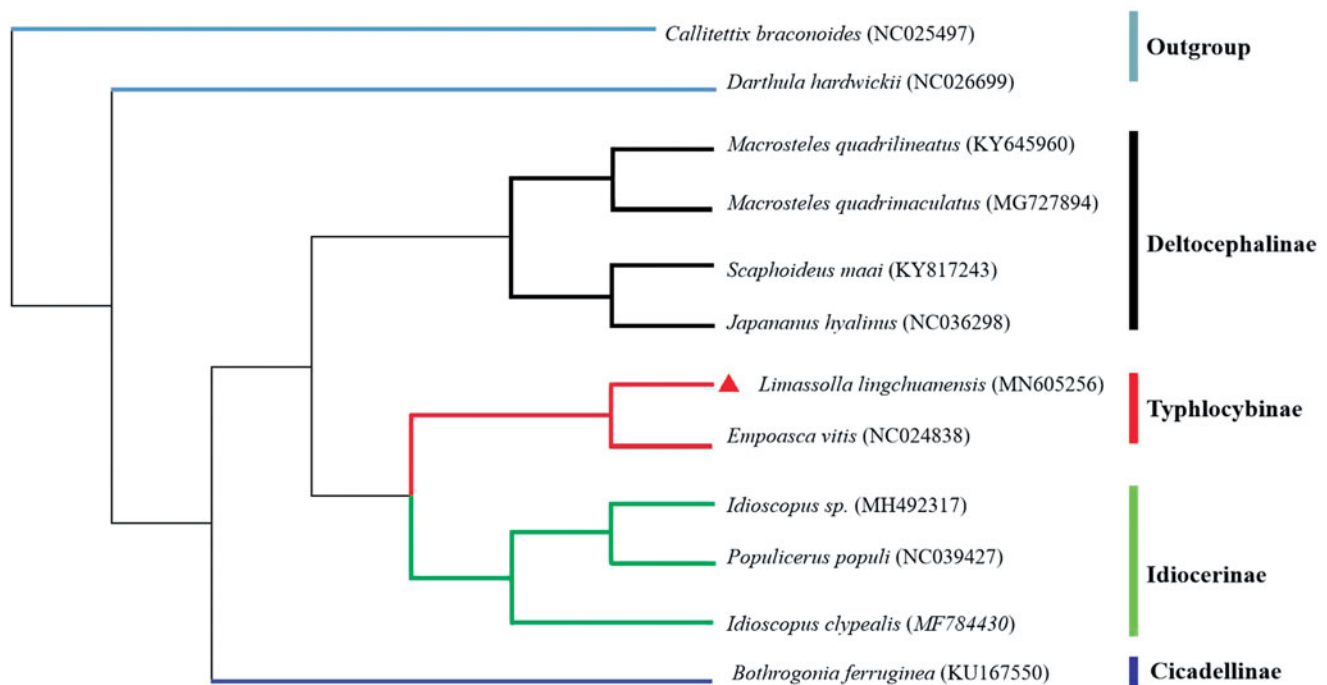


Figure 1. The neighbor-joining phylogenetic tree of *L. lingchuanensis* and 9 other leafhoppers in inner group. *Callitettix braconoides* and *Darthula hardwickii* were used as an outgroup. GenBank accession numbers of each species are listed in the tree.

(Figure 1), both of them belongs to the subfamily Typhlocybinae. It is consistent with the traditional classification.

Disclosure statement

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

Funding

This study was supported in part by the Project of Innovation Program for Postgraduate Education of Guizhou Province: Xiong Kangning's Studio of Postgraduate Supervisors for the Karst Environment of Guizhou Province [201604], the Project for National Top Discipline Construction of Guizhou Province: Geography in Guizhou Normal University [201785-01], the Guizhou Provincial Science and Technology Foundation [(2018)1411], the Training Program for High-level Innovative Talents of Guizhou Province [(2016)4020] and the Program for First-class Discipline

Construction in Guizhou Province [(2017)85], and the Guizhou Science and Technology Support Project [(2019)2855].

References

- Chou Y, Zhang YL. 1985. On the tribe *Zyginellini* from China (Hemiptera: Cicadellidae: Typhlocybinae). *Entomotaxonomia*. 4:287–296.
- Md SH, Jin HK, Sang JS, Yong JK. 2019. Taxonomic revision of the micro-leafhopper genus *Limassolla* Dlabola from Korea (Hemiptera: Cicadellidae: Typhlocybinae). *Zootaxa*. 3:1175–5326.
- Xing JC, Wang JJ. 2019. Complete mitochondrial genome of *Paralaevicephalus gracilipenis* (Hemiptera: Cicadellidae: Deltocephalinae) from China. *Mitochondrial DNA Part B*. 4(1):1372–1373.
- Yang WJ, Gao YR, Li C, Song YH. 2019. The complete mitochondrial genome of *Chlorotettix nigromaculatus* (Hemiptera: Cicadellidae: Deltocephalinae) with phylogenetic consideration. *Mitochondrial DNA Part B*. 4(1):624–625.
- Zhang YL, Gao X, Huang M. 2011. Two new species of *Yangisunda* Zhang (Hemiptera: Cicadellidae: Typhlocybinae: Zyginellini) from China, with a key to species. *Zootaxa*. 3097(1):45–52.