

The complete mitochondrial genome of *Ricania shantungensis* (Hemiptera: Ricaniidae) in Korea

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ABSTRACT

In this study, we have sequenced and annotated the complete mitochondrial genome of *Ricania shantungensis* (Hemiptera: Ricaniidae) for the first time. The circular mitogenome of *R. shantungensis* was 15,789 bp, including 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single control region of 1,363 bp. Its AT ratio was 74.6%. According to the phylogenetic tree, *R. shantungensis* was clustered with the genus *Ricania*.

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It has been reported that there are 40 genus and 400 species in the family Ricaniidae, including *Ricania shantungensis* and the genus *Ricania* includes about 40 species distributed in Asia including China and India (Xu et al. 2006). The original distribution of *R. shantungensis* is assumed to be Zhejiang and Shandong provinces in China (Chou and Lu 1977). It damages host plants by sucking and spawning and causes sooty mold disease. This incurs economic losses for various fruit trees such as blueberries and apples. Recently, it has been continuously spreading throughout Korea and has been detected in 43 cities (Kim et al. 2015). In this study, we determined the mitogenome of *R. shantungensis*.

In August 2018, the sample was collected from Daejeon, Korea (36.114775 N, 127.330402E). Genomic DNA was extracted using DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany). The specimen's genome DNA (Accession number: 973) was deposited in the National Institute of Ecology, Seocheon, Korea. Raw sequences obtained from Illumina HiSeqX (Macrogen Inc., South Korea) were filtered by Trimmomatic 0.33 (Bolger et al. 2014) and *de novo* assembled by Velvet 1.2.10 (Zerbino and Birney 2008) and gap sequences were closed with SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17, and SAMtools 1.9 (Li et al. 2009; Li 2013). Geneious R11 11.1.5 (Biomatters Ltd, Auckland, New Zealand) was used to annotate the mitochondrial genome of *R. shantungensis* with referring mitogenomes of *R. speculum* (NC_031369 and MT834932) and *R. marginalis* (NC_019597).

The complete mitogenome of *R. shantungensis* (GenBank accession number: MT898421) was 15,789 bp with 74.6% AT content, which was longer than any other available *Ricania* mitochondrial genome (*R. speculum*: 15,729bp). It contained all 39 genes of a standard insect mitochondrial genome, including 13 protein-coding genes, two rRNAs, and 22 tRNAs. The order of the 39 genes was conserved as in all other hemipteran mitogenomes. The single large non-coding control region was also found in the mitogenome, and was 1,363 bp long, the largest of all known *Ricania* mitogenomes.

We inferred phylogenetic relationships based on multiple sequence alignments of 16 planthopper mitogenomes including two outgroup species, *Magicicada tredecula* (NC_041656) and *Philaenus spumarius* (NC_005944) (Song and Liang 2013) except variable control regions. Multiple sequence alignment was conducted using MAFFT 7.450 (Katoh and Standley 2013). Phylogenetic trees were constructed by maximum likelihood (ML) using MEGA X (Kumar et al. 2018) and Bayesian inference (BI) using MrBayes 3.2.6 (Ronquist et al. 2012). The tree topology of ML and BI were identical (Figure 1). According to the tree, *R. shantungensis* was clustered with two species, *R. marginalis* and *R. speculum*, belonging to the genus *Ricania*. In addition, Ricaniidae was included in a clade with Flatidae. This study will be helpful to understand the phylogenetic relationships of Ricaniidae.

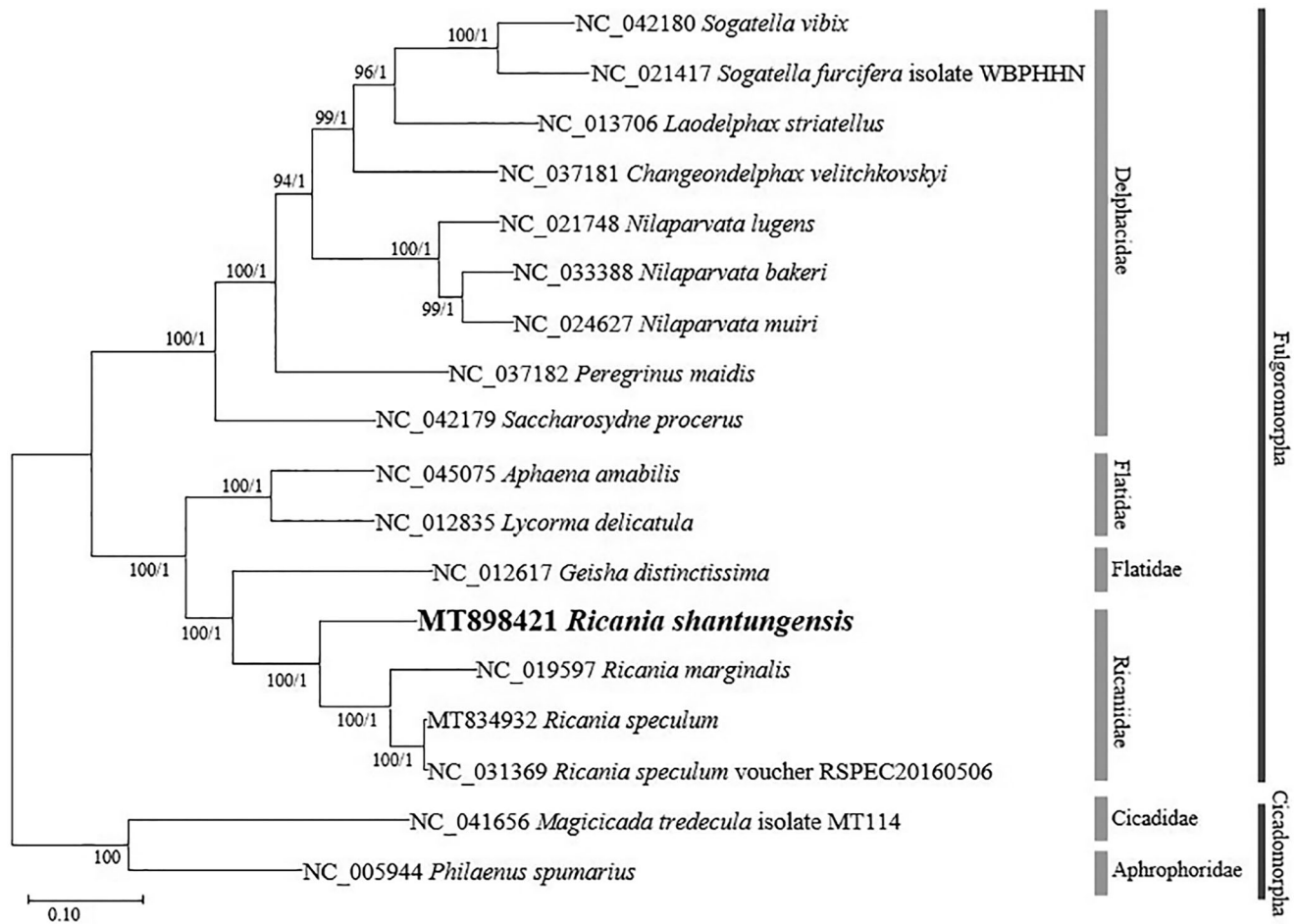


Figure 1. Maximum likelihood (1,000 bootstrap repeats) and Bayesian inference phylogenetic trees of 16 Fulgoromorpha mitochondrial genomes including two out-group species (*Magicicada tredecula* and *Philaenus spumarius*). Numbers on internodes indicate maximum likelihood bootstrap proportions (left) and Bayesian posterior probabilities (right).

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The data that support the findings of this study are openly available in GenBank at <https://www.ncbi.nlm.nih.gov/genbank/>, accession number [MT898421].

References

- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*. 30(15):2114–2120.
- Chou Y, Lu CS. 1977. On the Chinese Ricaniidae with descriptions of eight new species. *Acta Entomol Sin*. 20:314–322.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol*. 30(4):772–780.
- Kim DE, Lee H, Kim MJ, Lee DH. 2015. Predicting the potential habitat, host plants, and geographical distribution of *Pochazia shantungensis* (Hemiptera: Ricaniidae) in Korea. *Korean J Appl Entomol*. 54(3): 179–189.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol*. 35(6):1547–1549.
- Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R. 2009. The sequence alignment/map format and SAMtools. *Bioinformatics*. 25(16):2078–2079.
- Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint arXiv:1303.3997.
- Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol*. 61(3):539–542.
- Song N, Liang AP. 2013. A preliminary molecular phylogeny of planthoppers (Hemiptera: Fulgoroidea) based on nuclear and mitochondrial DNA sequences. *PLOS One*. 8(3):e58400
- Xu CQ, Liang AP, Jiang GM. 2006. The genus *Euricania melichar* (Hemiptera: Ricaniidae) from China. *Raffl Bull Zool*. 54(1):1–10.
- Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res*. 18(5):821–829.
- Zhao QY, Wang Y, Kong YM, Luo D, Li X, Hao P. 2011. Optimizing *de novo* transcriptome assembly from short-read RNA-Seq data: a comparative study. *BMC Bioinf*. 12(Suppl 14):S2.