



Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

Complete mitochondrial genome of the spotted lanternfly, *Lycorma delicatula* White, 1845 (Hemiptera: Fulgoridae)

Na Ra Jeong, Min Jee Kim, Wonhoon Lee, Gwan-Seok Lee & Iksoo Kim

To cite this article: Na Ra Jeong, Min Jee Kim, Wonhoon Lee, Gwan-Seok Lee & Iksoo Kim (2020) Complete mitochondrial genome of the spotted lanternfly, *Lycorma delicatula* White, 1845 (Hemiptera: Fulgoridae), *Mitochondrial DNA Part B*, 5:1, 370-372, DOI: [10.1080/23802359.2019.1703577](https://doi.org/10.1080/23802359.2019.1703577)

To link to this article: <https://doi.org/10.1080/23802359.2019.1703577>



© 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 16 Jan 2020.



Submit your article to this journal [↗](#)



Article views: 52



View related articles [↗](#)



View Crossmark data [↗](#)

Complete mitochondrial genome of the spotted lanternfly, *Lycorma delicatula* White, 1845 (Hemiptera: Fulgoridae)

Na Ra Jeong^a, Min Jee Kim^{a,b}, Wonhoon Lee^c, Gwan-Seok Lee^d and Iksoo Kim^a

^aDepartment of Applied Biology, College of Agriculture and Life Sciences, Chonnam National University, Gwangju, Republic of Korea; ^bHerbal Medicine Resources Research Center, Korea Institute of Oriental Medicine, Naju, Republic of Korea; ^cDepartment of Plant Medicine and Institute of Agriculture and Life Sciences, Gyeongsang National University, Jinju, Republic of Korea; ^dDepartment of Agro-food Safety and Crop Protection, Crop Protection Division, National Institute of Agricultural Sciences, RDA, Wanju, Republic of Korea

ABSTRACT

The spotted lanternfly, *Lycorma delicatula* White, 1845 (Hemiptera: Fulgoridae), is an invasive pest that attacks forest as well as agricultural trees. We sequenced the 15,798-bp long complete mitochondrial genome (mitogenome) of this species; it consists of a typical set of genes (13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes) and one major non-coding A+T-rich region. The orientation and gene order of the *L. delicatula* mitogenome are identical to that of the ancestral type found in majority of the insects. Bayesian inference (BI) and maximum-likelihood (ML) phylogeny placed the *L. delicatula* examined in our study, together with other geographical samples of the species in a group with the highest nodal support, forming the subfamily Aphaeninae to which *L. delicatula* belongs.

ARTICLE HISTORY

Received 18 November 2019
Accepted 7 December 2019

KEYWORDS

Lycorma delicatula;
mitochondrial genome;
Fulgoridae

Introduction

The spotted lanternfly, *Lycorma delicatula* White, 1845 (Hemiptera: Fulgoridae), is native to northern China (Liu 1939) and was detected as an exotic species in South Korea in 2004 (Kim and Kim 2005) and in Pennsylvania, USA in 2015 (Barringer et al. 2015). This pest damages a wide variety of forest trees, and particularly the agricultural grape tree, by feeding on the phloem sap and secreting honeydew, thereby inhibiting transpiration and leading to growth of sooty mold on the trees (Han et al. 2008; Lee et al. 2009; Park et al. 2009; Dara et al. 2015).

In previous studies, mitochondrial NADH dehydrogenase (ND) subunit 2 (ND2) and ND6 regions were analyzed from specimens collected from China, Korea, and Japan (Kim et al. 2013). However, specimens from Korea and Japan revealed identical sequences, warranting the need for variable markers for population genetics data.

Methods

For our study, one wild adult lanternfly was caught on the tree of heaven (*Ailanthus altissima*) in the Nam-gu, Gwangju Metropolitan City, Republic of Korea (35°05'07.2" N, 126°52'02.0" E) and its DNA was extracted from one of the hind legs. Leftover DNA and the specimen were deposited at the Chonnam National University, Gwangju, Korea, under the accession number CNU11113.

Using the extracted DNA, four long overlapping fragments (LFs: *COI-trnN*, *COIII-CytB*, *ND6-srRNA*, and *IrrRNA-COI*) were amplified using four sets of primers designed using data regarding the previously published species of Fulgoroidea, with special consideration for geographically close specimens of *L. delicatula*, published in earlier studies (Hua et al. 2009; Song et al. 2012). Using the LFs as templates, 36 overlapping short fragments (SF) were amplified using the aforementioned primers.

Phylogenetic analysis was performed using 11 available mitogenomes from Fulgoroidea, including the one obtained in this study (Figure 1). Nucleotide sequences of all protein-coding genes (PCGs) and rRNAs were aligned and well-aligned blocks were selected using GBlocks 0.91b software (Castresana 2000) with the maximum number of contiguous non-conserved positions set to 11 and no gap positions allowed. Subsequently, 13 PCGs and 2 rRNAs were concatenated in alignment (11,301 bp excluding gaps). Bayesian inference (BI) and maximum-likelihood (ML) methods were applied using MrBayes version 3.2.6 (Ronquist et al. 2012) and RAxML-HPC2 version 8.0.24 (Stamatakis 2014), respectively, which were incorporated into the CIPRES Portal version 3.1 (Miller et al. 2010). An optimal partitioning scheme (nine partitions) and substitution model (GTR + Gamma + I) were determined using PartitionFinder 2 with the Greedy algorithm (Lanfear et al. 2012, 2014, 2016). Phylogenetic trees were visualized using FigTree version 1.42 (<http://tree.bio.ed.ac.uk/software/figtree/>).

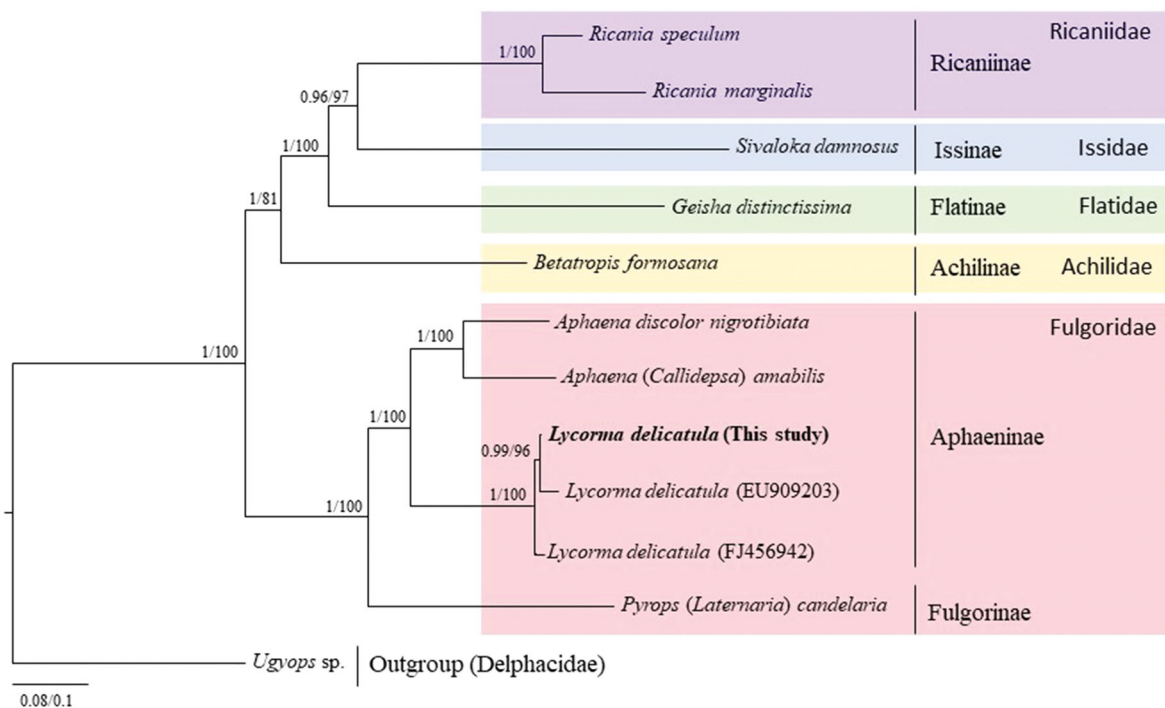


Figure 1. Phylogenetic tree for the superfamily Fulgoroidea. The tree was constructed using the concatenated 13 PCGs and 2 rRNAs via the maximum-likelihood (ML) and Bayesian Inference (BI) methods. The numbers at each node specify bootstrap percentages of 1000 pseudoreplicates by ML analysis and Bayesian posterior probabilities in percent by BI analysis. The scale bar indicates the number of substitutions per site. Delphacidae (*Ugyops sp.*, MH352481, Yu and Liang 2018) was used as outgroup. GenBank accession numbers are as follows: *Ricania speculum*, KX371891 (Zhang et al. 2016); *Ricania marginalis*, JN242415 Song et al. 2012); *Sivaloka damnosus*, FJ360694 (Song et al. 2010); *Geisha distinctissima*, FJ230961 (Song and Liang 2009); *Betatropis formosana*, MH324927 (Xu et al. 2019); *Aphaena discolor nigrotibiata*, MN025523 (Wang et al. 2019); *Aphaena (Callidepsa) amabilis*, MN025522 (Wang et al. 2019); *Lycorma delicatula*, EU909203 (Song et al. 2012); *Lycorma delicatula*, FJ456942 (Hua et al. 2009); and *Pyrops (Laternaria) candelaria*, FJ006724 (Song et al. 2012).

Results

The *L. delicatula* mitogenome was found to be 15,789 bp in length, with typical gene sets – 2 rRNAs, 22 tRNAs, and 13 PCGs – and a major non-coding A + T-rich region of 1495 bp length (GenBank accession number MN607209), whereas previous studies showed that the mitogenome was 15,946 bp long (Song et al. 2012) and 15,410 bp (Hua et al. 2009). The largest size variation was detected in the A + T-rich region (1043 bp in Hua et al. (2009), 1495 bp in this study, and 1642 bp in Song et al. (2012)). The gene arrangement of *L. delicatula* was identical to that of the ancestral type found in majority of the insects (Boore 1999).

Phylogenetic analyses using both, BI and ML methods, using 13 PCGs and two rRNAs, placed *L. delicatula* from Korea, along with previously analyzed geographical samples, into one group, with the highest nodal support in both analyses. The subfamily Aphaeninae, to which *L. delicatula* belongs, forms a cohesive monophyletic group with the highest nodal supports indicated by BI and ML analyses.

Disclosure statement

No potential conflicts of interest are reported by the authors.

Funding

This research was supported by the ‘Cooperative Research Program for Agriculture Science and Technology Development [Project No. PJ01338901]’, Rural Development Administration, Republic of Korea.

References

- Barringer LE, Donovall LR, Spichiger S-E, Lynch D, Henry D. 2015. The first new world record of *Lycorma delicatula* (Insecta: Hemiptera: Fulgoridae). *Entomol News*. 125(1):20–23.
- Boore JL. 1999. Animal mitochondrial genomes. *Nucleic Acids Res*. 27(8): 1767–1780.
- Castresana J. 2000. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Mol Biol Evol*. 17(4): 540–552.
- Dara SK, Barringer L, Arthurs SP. 2015. *Lycorma delicatula* (Hemiptera: Fulgoridae): a new invasive pest in the United States. *J Integr Pest Manag*. 6(1):20.
- Han JM, Kim H, Lim EJ, Lee S, Kwon YJ, Cho S. 2008. *Lycorma delicatula* (Hemiptera: Auchenorrhyncha: Fulgoridae: Aphaeninae), finally, but suddenly arrived in Korea. *Entomol Res*. 38(4):281–286.
- Hua J, Li M, Dong P, Cui Y, Xie Q, Bu W. 2009. Phylogenetic analysis of the true water bugs (Insecta: Hemiptera: Heteroptera: Nepomorpha): evidence from mitochondrial genomes. *BMC Evol Biol*. 9(1):134.
- Kim SS, Kim TW. 2005. *Lycorma delicatula* (White) (Hemiptera: Fulgoridae) in Korea. *Lucanus*. 5:9–10.
- Kim H, Kim M, Kwon DH, Park S, Lee Y, Huang J, Kai S, Lee HS, Hong KJ, Jang Y, et al. 2013. Molecular comparison of *Lycorma delicatula* (Hemiptera: Fulgoridae) isolates in Korea, China, and Japan. *J. Asia Pac. Entomol*. 16(4):503–506.
- Lanfear R, Calcott B, Ho SY, Guindon S. 2012. PartitionFinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Mol Biol Evol*. 29(6):1695–1701.
- Lanfear R, Calcott B, Kainer D, Mayer C, Stamatakis A. 2014. Selecting optimal partitioning schemes for phylogenomic datasets. *BMC Evol Biol*. 14(1):82.
- Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B. 2016. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Mol Biol Evol*. 34:772–773.

- Lee JE, Moon SR, Ahn HG, Cho SR, Yang JO, Yoon CM, Kim GH. 2009. Feeding behavior of *Lycorma delicatula* (Hemiptera: Fulgoridae) and response on feeding stimulants of some plants. *Korean J Appl Entomol.* 48(4):467–477.
- Liu G. 1939. Some extracts from the history of entomology in China. *Psyche.* 46(1):23–28.
- Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES science gateway for inference of large phylogenetic trees. *Proceedings of the 9th Gateway Computing Environments Workshop (GCE), New Orleans (LA): GCE;* p. 1–8.
- Park JD, Kim MY, Lee SG, Shin SC, Kim HH, Park IK. 2009. Biological characteristics of *Lycorma delicatula* and the control effects of some insecticides. *Korean J Appl Entomol.* 48(1):53–57.
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck J P. 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 A. 2009. The complete mitochondrial genome sequence of *Geisha distinctissima* (Hemiptera: Flatidae) and comparison with other hemipteran insects. *Acta Biochim Biophys Sin.* 41(3):206–216.
- Song N, Liang AP, Bu CP. 2012. A molecular phylogeny of Hemiptera inferred from mitochondrial genome sequences. *PLOS One.* 7(11): e48778.
- Song N, Liang AP, Ma C. 2010. The complete mitochondrial genome sequence of the planthopper, *Sivaloka damnosus*. *J Insect Sci.* 10:76.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30(9): 1312–1313.
- Wang W, Huang Y, Bartlett CR, Zhou F, Meng R, Qin D. 2019. Characterization of the complete mitochondrial genomes of two species of the genus *Aphaena* Guérin-Méneville (Hemiptera: Fulgoridae) and its phylogenetic implications. *Int J Biol Macromol.* 141:29–40.
- Xu SY, Long JK, Chen XC. 2019. Comparative analysis of the complete mitochondrial genomes of five Achilidae species (Hemiptera: Fulgoroidea) and other Fulgoroidea reveals conserved mitochondrial genome organization. *PeerJ.* 7:e6659.
- Yu F, Liang AP. 2018. The complete mitochondrial genome of *Ugyops* sp. (Hemiptera: Delphacidae). *J Insect Sci.* 18:1–13.
- Zhang QX, Guan DL, Niu Y, Sang LQ, Zhang XX, Xu SQ. 2016. Characterization of the complete mitochondrial genome of the Asian planthopper *Ricania speculum* (Hemiptera: Fulgoroidea: Ricanidae). *Conservation Genet Resour.* 8(4):463–466.