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

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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 lrRNA-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/).
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.

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