


## The complete mitochondrial genome of *Laodelphax striatellus* (Fallén, 1826) (Hemiptera: Delphacidae) collected in a mid-Western part of Korean peninsula

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### ABSTRACT

*Laodelphax striatellus* (Fallén, 1826) is one of key rice pests in Northeast Asia. We have determined the mitochondrial genome of *L. striatellus* collected in a mid-western part of Korean peninsula. The circular mitogenome of *L. striatellus* is 16,359 bp long including 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single large non-coding region of 1,972 bp. The base composition was AT-biased (77.3%). In comparison of the two Chinese *L. striatellus* mitogenomes with Korean mitogenome, total 140 and 40 single nucleotide polymorphisms and 166 and 118 insertions and deletions were identified, presenting intra-species variations based on geographical distribution.

### ARTICLE HISTORY

Received 1 May 2019  
Accepted 17 May 2019

### KEYWORDS

Mitochondrial genome;  
*Laodelphax striatellus*;  
Delphacidae; intra-species  
variations; Korean peninsula

*Laodelphax striatellus* (Fallén, 1826) (small brown planthopper; SBPH), of which body size is less than 4 mm, is a hemimetabolous insect widely distributed in Asia, Europe, and Northern Africa (Wilson and Claridge 1991). High density of SBPH could cause severe economic damage on rice, *Oryza sativa* L., by directly sucking and indirectly transmitting viral pathogens, including rice stripe virus and rice streaked dwarf virus, with piercing mouthparts (i.e. stylets; Hibino 1996; Seo et al. 2016). Two mitogenomes (Song and Liang 2009; Zhang et al. 2013) and one whole genome (Zhu et al. 2017) originated from China (Jiansu province and Beijing) were published, insufficient to uncover geographical differences among SBPH populations in Northeast Asia, where SBPHs can overwinter and migrate from China to Korea and Japan by westerlies in early summer (Otuka et al. 2012).

Here we first mitochondrial genome of Korean SBPH collected in Suwon, South Korea in 1970 (37°16'20"N, 126°57'57"E; voucher was deposited in InfoBoss Cyber Herbarium (IN; Seo BY, INH-00018; South Korea). DNA was extracted using CTAB-based DNA extraction method manually (iNtRON biotechnology, Inc., Korea). Raw sequences obtained from Illumina NextSeq500 (Macrogen Inc., South Korea) were filtered using Trimmomatic 0.33 (Bolger et al. 2014) and *de novo* assembled using Velvet 1.2.10 (Zerbino and Birney 2008) and MITOBim 1.9.1 (Hahn et al. 2013) and gaps including 548-bp AT-rich region were closed with SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17, and SAMtools 1.9 (Li et al. 2009; Li 2013) as well as PCR, respectively. Geneious R11 11.1.5 (Biomatters Ltd, Auckland, New Zealand) was used to annotate mitochondrial genome based

on that of Chinese *L. striatellus* (NC\_013706; Zhang et al. 2013).

*Laodelphax striatellus* mitochondrial genome (GenBank accession is MK838101) is 16,359 bp, which is the shortest among three SBPH mitogenomes. Its nucleotide composition is AT-biased (A + T is 77.3%) and contains 13 protein-coding genes, two rRNAs, and 22 tRNAs. The control region, presumably corresponding to single largest non-coding AT-rich region (1,972 bp, A + T is 83.8%), is shorter than those of Chinese SBPH mitogenomes (2,040 bp in NC\_013706 and 2,042 bp in JX880068).

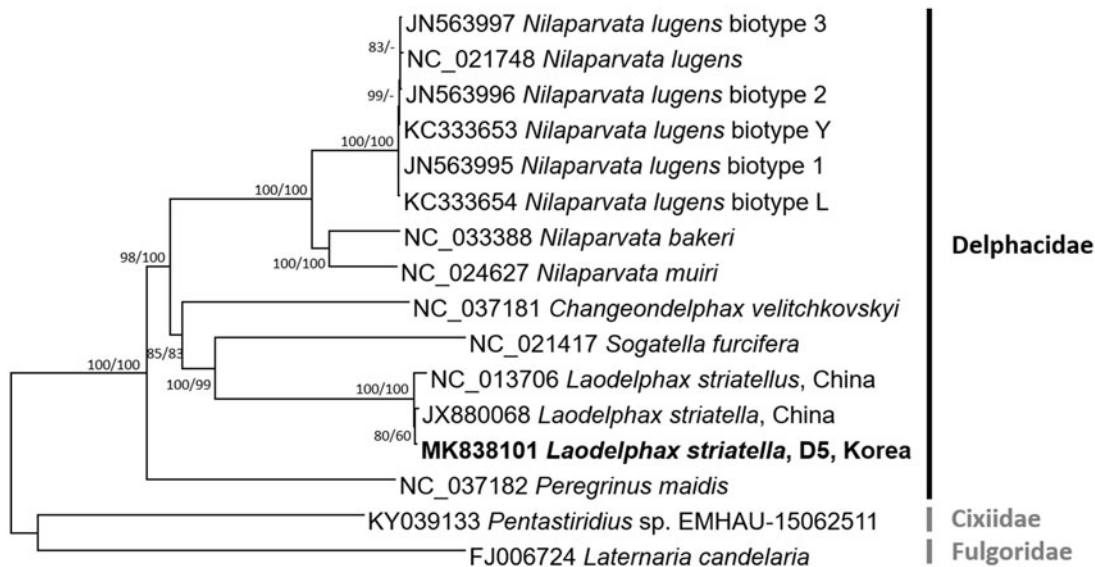
Gene order of three SBPH mitogenomes is identical. In comparison of two Chinese *L. striatellus* mitogenomes (NC\_013706 and JX880068) with Korean SBPH, 140 and 40 single nucleotide polymorphisms and 166 and 118 insertions and deletions were identified, respectively, presenting intra-species variations based on geographical distribution, similar to *Nilaparvata lugens* (Choi et al. 2019; Park, Kwon, et al. 2019) and *Chilo suppressalis* (Park, Xi, et al. 2019).

We inferred the phylogenetic relationship of 16 mitogenomes, seven species of Delphacidae including three *L. striatellus* and two outgroup species (*Pentastiridius* sp. and *Laternaria candelaria*). Multiple sequence alignment was conducted using MAFFT 7.388 (Katoh and Standley 2013). Neighbour-joining (10,000 bootstrap repeats) and maximum-likelihood (1,000 bootstrap repeats) phylogenetic trees were constructed using MEGA X (Kumar et al. 2018). Seven species in Delphacidae are monophyletic and three *L. striatellus* mitogenomes are more divergent than six *N. lugens* mitogenomes (Figure 1). This mitochondrial genome will be helpful in

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**Figure 1.** Neighbour-joining (10,000 bootstrap repeats) and maximum-likelihood (1,000 bootstrap repeats) phylogenetic trees of seven insect species in the family Delphacidae, three *Laodelphax striatellus* (MK838101 in this study, NC\_013706, and JX880068), six *Nilaparvata lugens* (NC\_021748, JN563997, JN563996, JN563995, KC333653, and KC333654), *Nilaparvata bakeri* (NC\_033388), *Nilaparvata muiri* (NC\_024627), *Sogatella furcifera* (NC\_021417), *Changeodelphax velitchkovskiy* (NC\_037181), and *Peregrinus maidis* (NC\_037182), and as outgroup species, *Pentastiridius* sp. (KY039133) and *Laternaria Candelaria* (FJ006724). Phylogenetic tree was drawn based on neighbour-joining tree. The numbers above branches indicate bootstrap support values of neighbour-joining and maximum-likelihood phylogenetic trees, respectively.

understanding geographical intraspecies variations of *L. striatellus*.

## Disclosure statement

No potential conflict of interest was reported by the authors.

## Funding

This study was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development [Project No. PJ010452]” and “Research Program for Agriculture Science & Technology Development [Project No. PJ011977]” Rural Development Administration, Republic of Korea.

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