Complete mitochondrial genome of Neotoxoptera formosana (Takahashi, 1921) (Hemiptera: Aphididae), with the phylogenetic analysis

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Abstract

In this study, we sequenced and annotated the complete mitochondrial genome (mitogenome) of Neotoxoptera formosana (Takahashi) (Hemiptera: Aphididae). The complete mitogenome of N. formosana is 15,642 bp in length, and includes 13 protein-coding genes (PCGs), 2 ribosome RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, and one control region. The overall base composition was as follows: 45.2% of A, 5.8% of G, 10.5% of C, and 38.4% of T, with a total of A+T content of 83.6%. The phylogenetic tree showed that N. formosana and Myzus persicae were clustered into one branch. This result will enrich the mitogenome of family Aphididae.

The complete mitogenome of N. formosana was a circular double-stranded and 15,642 bp in length (GeneBank accession number MW534268), containing 37 encoding genes (13 PCGs, 22 tRNA genes, and 2 rRNA genes) and one control region. The whole base composition was as follows: 45.2% of A, 5.8% of G, 10.5% of C, and 38.4% of T, with a total of A+T content of 83.6%. All PCGs began with the typical ATN codons (ATT for COX1, ATP6, ATP8, ND3, ND5, ND6, and ND1; ATG for COX3, ND4, ND4L, and CYTB; ATA for ND2 and COX2). All protein coding genes used TAA as stop codon. The 16s rRNA gene was 1,263 bp in size and was located between trnL and trnV, while the 12s rRNA gene was 812 bp in size and was located behind trnV.

The nucleotide sequences of 13 PCGs (delete the third codon position) and 2 rRNA genes from 15 Aphidoidea species and one outgroup taxa from Pyrrhocoroidea species were aligned using MAFFT v7.394 with L-INS-I algorithm (Katoh and Standley 2013). The poorly aligned results were removed by trimAl v1.4.1 (Capella-Gutierrez et al. 2009). A phylogenetic tree was constructed for 16 species by maximum likelihood method using IQ-TREE v1.6.3 software under the GTR + I + G model (Nguyen et al. 2015). The result confirmed that N. formosana and Myzus persicae were clustered into one branch (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the author(s).
The data that support the findings of this study are openly available in [NCBI] at [https://www.ncbi.nlm.nih.gov/], reference number [MW534268]. The associated BioProject, BioSample, and SRA numbers are PRJNA703062, SAMN18011301, SRR13753265, respectively (https://www.ncbi.nlm.nih.gov/sra/?term=SRR13753265).

**Date availability statement**

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**Figure 1.** Maximum likelihood phylogeny of 15 Aphidoidea species based on concatenated nucleotide sequences of 13 PCGs (delete the third codon position) and 2 rRNA. Number at nodes represent SH-aLRT support (%)/ultrafast bootstrap support (%).