

The mitochondrial genome of *Nigidius miwai* Nagel (Coleoptera: Lucanidae), a carnivorous lucanid from South Korea

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ABSTRACT

The complete mitochondrial genome of carnivorous *Nigidius miwai* was analyzed prior to a study on evolution of carnivorous pathway within the family. This species' genome had a total length of 18,462 bp (GenBank accession number: OL597607), comprising 36 genes along with 13 protein-coding genes, 21 tRNA genes, two rRNA genes, and an A+T rich region. The nucleotide composition was 37.2% A, 33.8% T, 9.2% G, and 19.8% C (GC contents 29.0%). The phylogenetic tree indicated that *N. miwai* is a distinctive species within Nigidiini of Lucaninae.

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Lucanidae contains about 1300 species worldwide (e.g. Fujita 2010; Kim and Farrell 2015). Regarding their biological traits, most members are saproxylic at larval stage and sap eating at adult stage. However, some species turn to carnivorous at adult stage. So far as known, carnivory occurs only in Figulini and Nigidiini within the family (Kim and Kim 2014).

Nigidius miwai Nagel, 1941 in Nigidiini is a Korean endemic species of which distribution is extremely limited only to Is. Jeju, South Korea, and is known to become carnivorous at adult stage (Kim and Kim 2014). With the consent of the Korea Forest Service, several adults were collected from the island (N33°15'26.3" E126°21'10.4") in May 2021. They were deposited at the Korea National Arboretum (Il-Kwon Kim, ilkwons91@korea.kr) under the specimen code 21LUC16.

The complete mitochondrial genome of *N. miwai* was sequenced using Illumina MiSeq (Macrogen, Inc., Seoul, South Korea). In total, 2,210,362,196 read bases were analyzed to generate 18,462 base pairs of sequence and assembled in Geneious Prime ver. 2021.1.1 (Kearse et al. 2012). The gene annotation and circularity check were performed using MITOS2 webserver (Bernt et al. 2013, <http://mitos2.bioinf.uni-leipzig.de>). The mitochondrial genome comprises 36 genes along with 13 protein-coding genes, 21 tRNA genes, two rRNA genes, and an A+T rich region. The overall nucleotide composition is 37.2% A, 33.8% T, 9.2% G, and 19.8% C (GC contents 29.0%).

The maximum-likelihood analysis (GTR model) was conducted using MEGA X ver. 10.2.4 (Kumar et al. 2018) with 1000 bootstrap replications. Twenty-nine mitochondrial genome sequences of 19 lucanid species were included, with *Sinodendron yunnanense* Kral, 1994 as an outgroup. A robust

phylogenetic tree indicated that *N. miwai* is a distinctive species, as a sister taxon to *Nigidius* sp., in Nigidiini which forms a monophyletic clade with Figulini just as Kim and Farrell (2015) previously analyzed (Figure 1). The mitochondrial genome of *N. miwai* will be used to infer the evolutionary pathway of carnivory in Lucanidae.

Author contributions

Jeong-Hwan Choi: data curation, formal analysis, visualization, and writing – original draft; Chang-Jun Kim: conceptualization and resources; Moo-Sung Kim and Jun-Young Kang: investigation; Il-Kwon Kim: project administration, funding acquisition, and writing – review and editing. All authors have read and approved the final manuscript.

Disclosure statement



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

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Data availability statement

The complete mitochondrial genome sequence of *Nigidius miwai* is openly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov/>) under the accession no. OL597607 with Biosample SAMN22256801, SRA SRR16362025, and Bioproject PRJNA771208.

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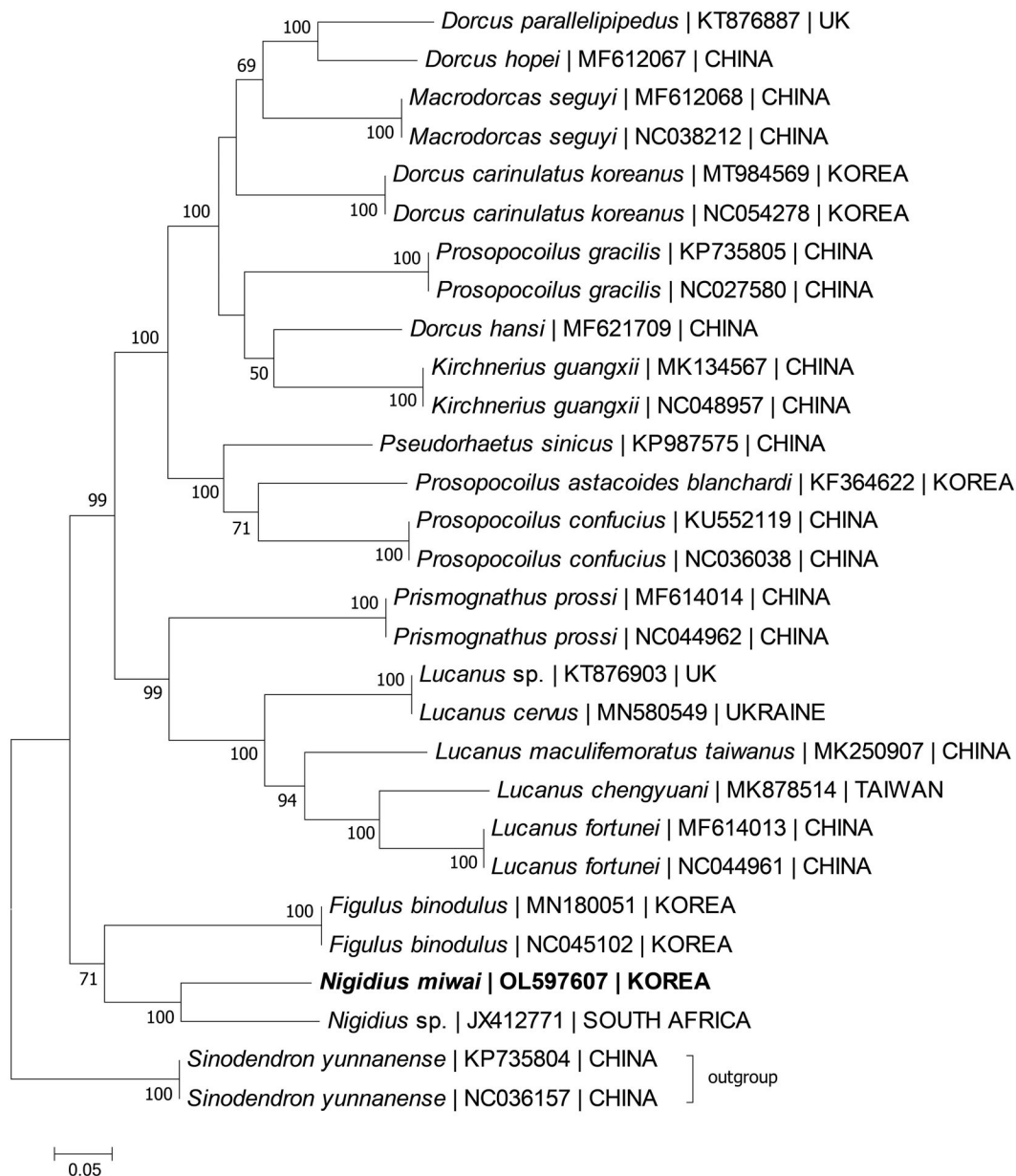


Figure 1. A maximum-likelihood tree inferred from concatenated amino acid sequences of 13 mitochondrial protein coding genes of *N. miwai* (OL597607) and the other lucanid species. The numbers beside the nodes indicate bootstrap values.

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