

## Complete mitochondrial genome of *Niphades castanea* (Coleoptera: Curculionidae)

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### ABSTRACT

*Niphades castanea* Chao is an important insect pest on many plants which belong to genus *Castanea*. The complete mitochondrial genome of *N. castanea* was sequenced and analyzed. The phylogenetic relationships between *N. castanea* and other 41 species in the family Curculionidae were reconstructed using maximum likelihood (ML) methods based on the concatenated nucleotide sequences, the phylogenetic analysis showed that *N. castanea* is closely related to *Hylobitelus xiaoi*, which is in accordance with the traditional morphological classification.

### ARTICLE HISTORY

Received 21 April 2020  
Accepted 16 May 2020

### KEYWORDS

Curculionidae; *Niphades castanea*; mitochondrial genome; phylogeny

*Niphades castanea* belong to subfamily Molytinae, its host plants is *Castanea mollissima* and other plants which belong to genus *Castanea*, family Fagaceae (Zhao and Chen 1980; Liu et al. 1995; Zhao et al. 2004; Ji et al. 2008; Xiao et al. 2017).

The specimen in this study was collected from Liuan City (Anhui Province, China) (115°33'24"E, 31°20'24"N) in 2019 and deposited in the Biodiversity Herbarium of Huanggang Normal University (no. HGNU-191201). The species was sequenced using Illumina Miseq platforms and annotated using MITOS web server. PhyloSuite (Zhang et al. 2020) was used for the phylogenetic analyses with several plug-in programs: MAFFT (Katoh and Standley 2013) using '-auto' strategy and codon alignment mode. PartitionFinder2 (Lanfear et al. 2016) was used to select best-fit partitioning schemes and models using AICc criterion. Maximum likelihood phylogenies were inferred using IQ-TREE (Minh et al. 2013; Nguyen et al. 2015). The topology of the trees were visualized and edited in iTOL (Letunic and Bork 2019). The mitogenome sequence of *Carabus changeonleei* (MG253028) was used as the outgroup.

The complete mitogenome of *Niphades castanea* is 17,494 bp in size (GenBank accession number: MT232762). It includes 13 protein-coding genes (PCGs), 22 tRNA genes and 2 rRNA genes, a total of 37 genes, and 1 control region. There are 16 gene overlapping regions appeared, with a total overlapping length of 70 bp, the longest overlapping region (29 bp) located between trnF and nad5. There are

9 intergenic spacers with a total length of 561 bp, ranging from 2 to 452 bp. The longest intergenic was located between trnI and trnQ. The genomic nucleotide composition is A:T:C:G = 39.33%:37.38%:14.02%:9.27%. The total length of 13 PCGs in the mitochondrial genome is 11,133 bp. The initiation codons of PCGs comply with the ATN rule: there are 7 genes (nat2, cox1, cox2, atp8, nad3, nad5, nad6) with ATT as the start codon, 5 genes (atp6, cox3, nad4, nad4l, and cob) with ATG as the start codon, and 1 gene (nad1) with ATA as the start codon. Except for atp8, nad5, and nad1 with TAG as the stop codon, others use TAA, TA(A), or T (AA) as the stop codon. The length of tRNA genes ranked from 63 bp to 71 bp, 1458 bp in total length. The length of 12S rRNA and 16S rRNA are 775 bp and 1272 bp in length, respectively. The control region is 2364 bp, between rrnS and trnI, the AT content is 81.35%.

ML (Figure 1) analyses showed that the subfamily Cryptorhynchinae and Molytinae were clustered together as sister to each other with at 90% bootstrap value of support, Platypodinae and Dryophthorinae were clustered together as sister to each other with at low bootstrap value of support, which is consistent with previous phylogenetic analyses (Marvaldi 1997; Haran et al. 2013; Gillett et al. 2014). The phylogenetic analysis showed that *N. castanea* is closely related to *Hylobitelus xiaoi*, both belong to Molytinae, which is in accordance with the traditional morphological classification.

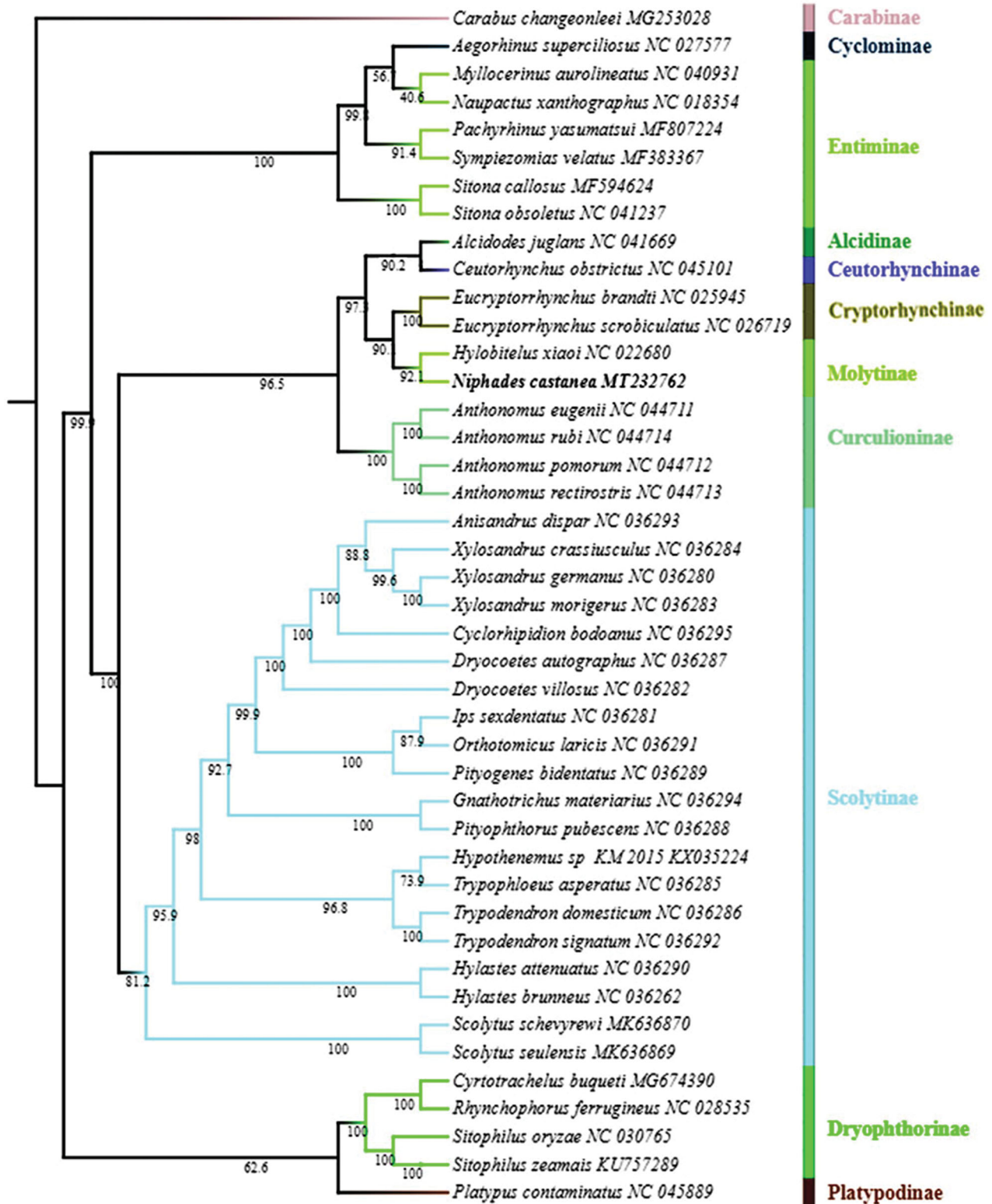


Figure 1. Phylogenetic tree based on 37 genes of mitogenomes of 42 Curculionidae species inferred by maximum likelihood method (ML tree).

## Disclosure statement

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

## Funding

The project was supported by the National Natural Science Foundation of China (NSFC) [Grant No. 31702048] and the Scientific Research Starting Foundation for Doctor, Huanggang Normal University (Grant No. 2020010).

## Data availability statement

The data that newly obtained at this study are available in the NCBI under accession number of MT232762 (<https://www.ncbi.nlm.nih.gov/nucleotide/MT232762>).

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