

The complete mitochondrial genome of *Monopis longella* Walker, 1863 (Lepidoptera: Tineidae)

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ABSTRACT

The complete mitochondrial genome (mitogenome) of *Monopis longella* Walker, 1863 (Lepidoptera: Tineidae) comprises 15,541 bp and contains a typical set of genes and one non-coding region. The gene arrangement of *M. longella* is unique for Lepidoptera in that it has a *trnI-trnM-trnQ* sequence in the A + T-rich region and *ND2* junction. Unlike most other lepidopteran insects, in which the *COI* gene has CGA as the start codon, *M. longella COI* has an ATT codon. Phylogenetic analyses based on the concatenated sequences of 13 protein-coding genes and two rRNA genes, using the Bayesian inference (BI) method, placed *M. longella* in the Tineidae, sister in position to the cofamilial species, *Tineola bisselliella*, with the highest nodal support. Tineidae, represented by three species including *M. longella*, formed a monophyletic group with high support (Bayesian posterior probability = 0.99). Within Tineoidea the sister relationship between Tineidae and Meessiidae was obtained with the highest support, leaving Psychidae occupying the basal lineage of the two families.

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Monopis longella Walker, 1863 (Lepidoptera: Tineidae) is distributed in Korea, Japan, China, Russia (Far East), Thailand, Malaysia, The Philippines, Vietnam, Pakistan, and India (Huang et al. 2011; Lee et al. 2016). This species was initially recorded from Korea as *Monopis pavlovskii* Zagulajev, 1955 (Ponomarenko and Park 1996), but was later synonymized to *M. longella* based on morphological and mitochondrial *COI* data (Huang et al. 2011). The larvae of this moth feed on animal hair and feathers, typically living in tubular larval tunnels in the nests of birds (Huang et al. 2011).

In 2013, an adult male *M. longella* was collected from Jeollanam-do Province, South Korea (34°29'31.6" N, 126°16'07.0" E) and subsequently deposited as a voucher specimen at the Chonnam National University, Gwangju, Korea, under accession no. CNU7297 (Iksoo Kim, ikkim81@chonnam.ac.kr). DNA was extracted from the hind legs of this specimen using a commercial kit (Promega, Madison, WI, USA). Using this DNA three long overlapping fragments (LFs; *COI-ND4*, *ND5-IrRNA*, and *IrRNA-COI*) were amplified and served as templates for the amplification of 26 short overlapping fragments using the primers reported in Kim et al. (2012).

Phylogenetic analysis was performed using available species in the superfamilies Gracillarioidea, Yponomeutoidea, and Tineoidea (21 species including *M. longella*). Thirteen protein-coding genes (PCGs) and two rRNA genes including those of two outgroup species, were aligned using RevTrans

ver. 2.0 (Wernersson and Pedersen 2003) and concatenated using SequenceMatrix ver. 1.8 (Vaidya et al. 2011). An optimal partitioning scheme (six partitions) and substitution model (GTR + Gamma + I) were determined using PartitionFinder 2 and the Greedy algorithm (Lanfear et al. 2012, 2014, 2016). Bayesian inference (BI) analysis that is implemented on the CIPRES Portal ver. 3.1 (Miller et al. 2010) were used for the phylogenetic analyses.

The complete 15,541 bp mitogenome of *M. longella* is composed of typical gene sets (two rRNAs, 22 tRNAs, and 13 PCGs) and a major non-coding A + T-rich region (GenBank acc. no. MH992770). The gene arrangement of the *M. longella* mitogenome is, however, unique in Lepidoptera, in that it has a *trnI-trnM-trnQ* (where underlining indicates a gene inversion) gene arrangement in the A + T-rich region and *ND2* junction. Previously, ditrysian Lepidoptera were reported to have the gene order *trnM-trnI-trnQ* at the same junction (Kim et al. 2010), which contrasts with the ancestral *trnI-trnQ-trnM* order found in the majority of insects (Boore 1999) including a few species of Lepidoptera (Cao et al. 2012; Wang et al. 2014). Twelve of the identified PCGs, including *COI*, contain a typical ATN start codon, whereas *ND5* has an infrequent TTG codon. The ATT start codon for *COI* differs from majority of other available species of Tineoidea, Gracillarioidea, and Yponomeutoidea (data not shown), as well as most species of Lepidoptera, which has CGA (Kim et al. 2012, 2018, 2020).

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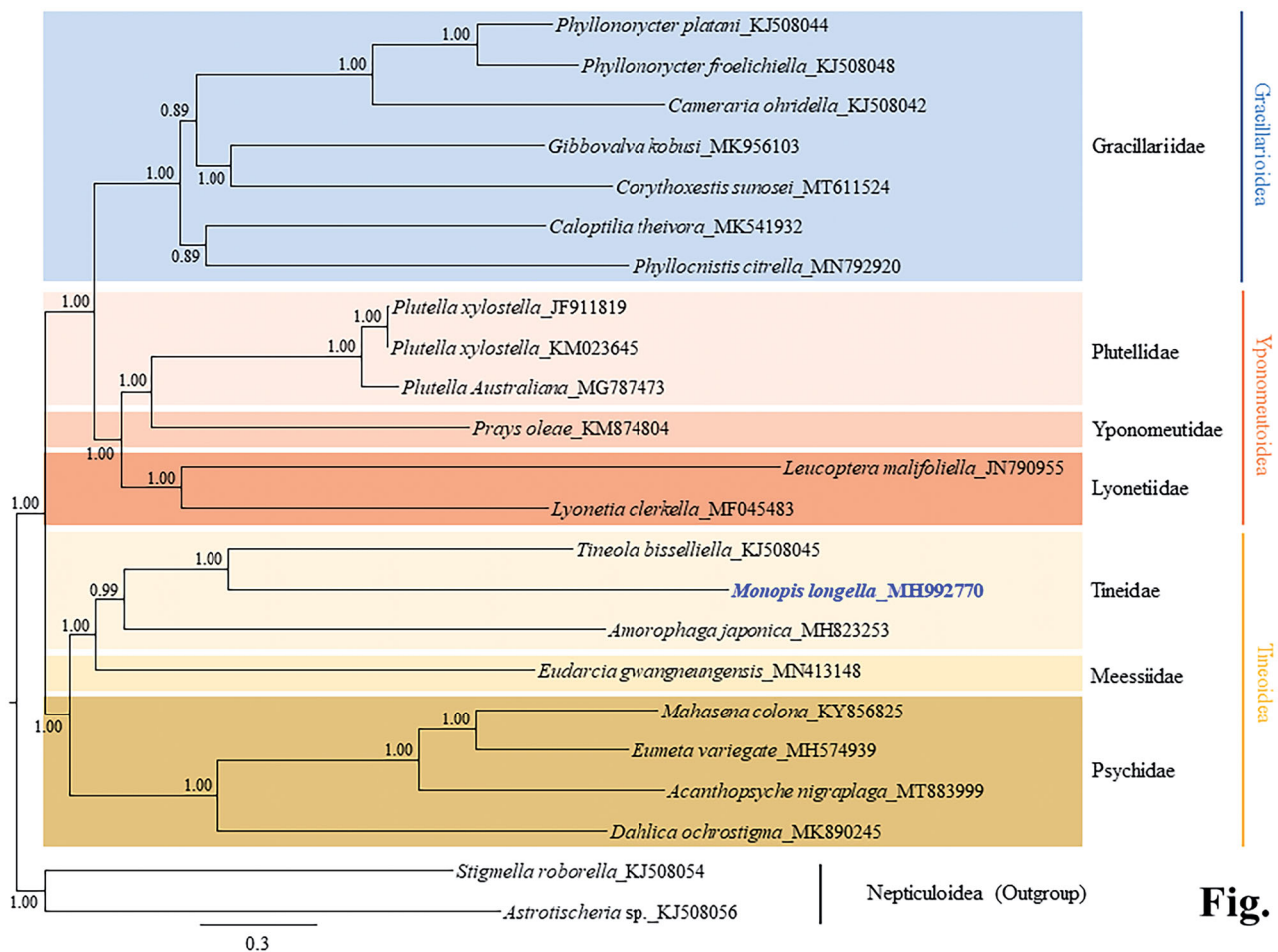


Fig. 1.

Figure 1. A Bayesian inference-based phylogenetic tree for three superfamilies in Ditrysia (Tineoidea, Gracillarioidea, and Yponomeutoidea) obtained using concatenated sequences of 13 protein-coding genes and two rRNAs. The numbers at each node indicate Bayesian posterior probabilities. The scale bar indicates the number of substitutions per site. Two species of Nepticuloidea (*Astrotischeria* sp. and *Stigmella roborella*) were included as an outgroup. GenBank accession numbers of the species analyzed are as follows: *Amorophaga japonica*, MH823253 (Kim et al. 2020); *Tineola bisselliella*, KJ508045 (Timmermans et al. 2014); *Eumeta variegata*, MH574939 (Jeong et al. 2018); *Mahasena colona*, KY856825 (Li et al. 2017); *Dahlia ochrostigma*, MK890245 (Roh et al. 2019); *Acanthopsyche nigraplaga*, MT883999 (Lee et al. 2021); *Eudarcia gwangneungensis*, MN413148 (Roh et al. 2020); *Phyllonorycter froelichiella*, KJ508048 (Timmermans et al. 2014); *Phyllonorycter platani*, KJ508044 (Timmermans et al. 2014); *Cameraria ohridella*, KJ508042 (Timmermans et al. 2014); *Caloptilia theivora*, MK541932 (Chen, Jiang, et al. 2019); *Gibbovalva kobusi*, MK956103 (Chen, Liao, et al. 2019); *Phyllocnistis citrella*, MN792920 (Liu et al. 2020); *Corythoestis sunosei*, MT611524 (Zhang et al. 2020); *Plutella xylostella*, JF911819 and KM023645 (Wei et al. 2013; Dai et al. 2016); *Plutella australiana*, MG787473 (Wardz and Baxter 2018); *Leucoptera malifoliella*, JN790955 (Wu et al. 2012); *Lyonetia clerkella*, MF045483 (Unpublished); *Prays oleae*, KM874804 (van Asch et al. 2016); *Astrotischeria* sp., KJ508056 (Timmermans et al. 2014); *Stigmella roborella*, KJ508054 (Timmermans et al. 2014).

Phylogenetic analyses placed *M. longella* in the Tineidae in a sister position to the cofamilial species *Tineola bisselliella* with full support (Figure 1). Tineidae, represented by three species including *M. longella* formed a monophyletic group, with high nodal support (Bayesian posterior probability = 0.99) (Figure 1). Within the Tineoidea the sister relationship between the Tineidae and Meessiidae was also obtained with full support, leaving the Psychidae as the basal lineage of the two families. All families and superfamilies represented by multiple taxa formed respective monophyletic groups, with high nodal supports (Bayesian posterior probability = 0.99–1.0). Superfamilies in the Ditrysia showed the sister relationships between the Gracillarioidea and Yponomeutoidea, leaving Tineoidea as the basal lineage of the two superfamilies with the high supports (Figure 1). Currently, only limited species belonging to the Gracillarioidea, Yponomeutoidea, and Tineoidea are available for their mitogenome sequences in Ditrysia. In order to gain a more comprehensive picture of the phylogenetic

relationships among lepidopteran superfamilies in Ditrysia, further analyses based on extended taxonomic sampling will be necessary.

Disclosure statement

No potential conflicts of interest are reported by the authors.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov/nucleotide/MH992770.1>.

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