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 *tml-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 Meesiidae was obtained with the highest support, leaving Psychidae occupying the basal lineage of the two families.

**KEYWORDS**

Mitochondrial genome; *Monopis longella*; phylogeny; Tineidae

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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, NDS-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 (Wernerson 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 *tml-trnM-trnQ* sequence in the A + T-rich region and ND2 junction. Previously, ditrysian Lepidoptera were reported to have the gene order *trnM-trnL-trnQ* at the same junction (Kim et al. 2010), which contrasts with the ancestral *tml-trnL-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 NDS 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).
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.

**Funding**

This study was supported by the Basic Science Research Program through the National Research Foundation of Korea, funded by the Ministry of Education, Science, and Technology [2015R1D1A3A03018119].

**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/nuccore/MH992770.1.
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